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117827

From: Swope, Sheridan  
Sent: Thursday, March 25, 2004 1:02 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/771,161

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MAR 25 2004  
STIC

For 09/771,161, pls search:

SID 2: Full-length and oligo search ( $\geq 20$ NTs) against the NT and AA data bases.

SID 93: Full-length and oligo search ( $\geq 20$ AAs) against the NT and AA data bases.

THANKS SO VERY MUCH TO THE GREAT STAFF OF STIC!!!!

Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652  
Recombinant Enzymes  
571-272-0943 (voice)  
E03A70 Remsen Bld (Office)  
E03C70 Remsen Bld (Mailbox)

Scan this page

Paul Schuchwitz

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 4/1  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:31:34 ; Search time 76 Seconds  
(without alignments)  
11492.462 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 531

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1065169 seqs, 261661801 residues

Word size: 20

Total number of hits satisfying chosen parameters: 24

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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1	232	43.7	232	9	US-09-771-161A-93	Sequence 93, Appl
2	227	42.7	540	9	US-09-771-161A-184	Sequence 184, App
3	227	42.7	540	9	US-09-862-037-28	Sequence 28, Appl
4	227	42.7	540	10	US-09-981-397A-14	Sequence 14, Appl
5	227	42.7	544	9	US-09-925-301-1015	Sequence 1015, Ap
6	128	24.1	540	9	US-09-748-537-1	Sequence 1, Appli
7	128	24.1	540	9	US-09-728-721-2	Sequence 2, Appli
8	128	24.1	540	13	US-10-133-780-1	Sequence 1, Appli
9	128	24.1	540	13	US-10-105-931-2	Sequence 2, Appli
10	128	24.1	540	13	US-10-118-984-2	Sequence 2, Appli
11	128	24.1	540	14	US-10-295-981-2	Sequence 2, Appli
12	109	20.5	109	9	US-09-728-721-6	Sequence 6, Appli
13	109	20.5	109	13	US-10-105-931-6	Sequence 6, Appli
14	109	20.5	109	13	US-10-118-984-6	Sequence 6, Appli
15	109	20.5	109	14	US-10-295-981-6	Sequence 5, Appli
16	98	18.5	131	13	US-09-728-721-5	Sequence 5, Appli
17	98	18.5	131	13	US-10-105-931-5	Sequence 5, Appli
18	98	18.5	131	13	US-10-118-984-5	Sequence 5, Appli
19	98	18.5	131	14	US-10-295-981-5	Sequence 5, Appli
20	92	17.3	92	13	US-10-014-269-21	Sequence 21, Appl
21	92	17.3	92	13	US-10-002-974-21	Sequence 21, Appl
22	92	17.3	92	14	US-10-314-506-21	Sequence 21, Appl
23	90	16.9	90	9	US-09-841-879B-10	Sequence 10, Appl
24	89	16.8	89	9	US-09-931-071-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-771-161A-93  
; Sequence 93, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005-1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724, 676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 93  
; TYPE: PRT  
; LENGTH: 232  
; ORGANISM: Homo sapiens  
US-09-771-161A-93

Alignment Scores:  
Pred. No.: 4.95e-230 Length: 232  
Score: 232.00 Matches: 232  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 43.69% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-771-161A-93 (1-232)

QY	320	ATGTATTTCATTACAGTTACAGAGTCTTTCAAGTGCACCTATGTGCAAGAGAA	379
DB	1	MetTyrSerLeuGlnLeuGlnSerValSerSerAlaHisLeuCysAspLysLys	20
QY	380	ATGGAATTATCTCTGAACATACCTGTAATCATGTGTCACACAGAGAAATCATGTGATCC	439
DB	21	MetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySer	40
QY	440	TCTCAGCTCCATGAATAAGTGTCTCTCCTGAAACTTCAAGGTCCCTGCAGCTCTCTCAA	499
DB	41	SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGln	60

Qy	500	GACAAATGATTTTATCTAGAAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGT	559
Db	61	AspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCys	80
Qy	560	CCTGGAATACACAGTTGGGATAGCACCAATTTCTGGATCTCAAGGGCTGCATTTCTGTGAT	619
Db	81	ProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAsp	100
Qy	620	CACAAGACCACTCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGAGAACTCA	679
Db	101	HisLysThrThrProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSer	120
Qy	680	GAACGCTCCAGCCTGGTATACCCAGACAGTGGATCCAGAGCAAAAGGGAAGACATTGTG	739
Db	121	GluArgLeuGlnProGlyLeuAlaGlnTrpIleGlnSerLysArgGluAspIleVal	140
Qy	740	AACCAAATCACAGAGCCCTGCTTAACACAGTCGGTGTAGATGCCCTTCGTCCAGGGACTTG	799
Db	141	AsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeu	160
Qy	800	ATCATGAAAGAGGACTATGAACCTGTTAGTACCAAGCTACAAGGACCTCAAAAGTCAGA	859
Db	161	IleMetLysGluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArg	180
Qy	860	CAATTACTAGACACTACTGACATCAAGGAGAGAATTCGCAAGTATATAGTACAAAAA	919
Db	181	GlnLeuLeuAspThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLys	200
Qy	920	TTGAAGATACAAAAAATGGGCTTTCAGCGCTTACC CGGAAATACTTGTGGTTCTTACA	979
Db	201	LeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleValValSerArg	220
Qy	980	TCACCATCTTTAAATTACTTCAAAATPAAAAAGCATG	1015
Db	221	SerProSerLeuAsnLeuGlnAsnLysSerMet	232

## RESULT 2

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US-09-771-161A-184
; Sequence 184, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 184
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-184

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Alignment Scores:		
Pred. No.:	6, 75a-225	Length:
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Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	42.75%	Indels:
DB:	9	Gaps:

US-09-771-161A-2 (1-1669) x US-09-771-161A-184 (1-540)

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 QY 395 AACATACCTGTAATAATCATGGTCCACAAGAGGAATCATGTGATCTCTCAGCTCCATGAA 454  
 Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353  
 QY 455 AATAGTGGTTCTCTCGAAACTTCAAGGTCCCTGCAGCTCTCTCAAGCAATGATTTTTTA 514  
 Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
 QY 515 TCTAGAAAAGCTCAAGACTGTTATTATTAAGCTGTCATCACTGTCCTTGGAAATCACACT 574  
 Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393  
 QY 575 TGGATAGCACCATTTCTGGATCTCAAGGCTGCATTTCTGTGATCACAAAGACCCTCCA 634  
 Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 413  
 QY 635 TGCTCTTCACGAATAATAATCCACTCTCAACTGCAGGAAGCTCAGAACGTCCTGCAGCT 694  
 Db 414 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
 QY 695 GGTATAGCCACGACGTGGATCCAGAGCAAAAGGAAGACATTTGTCAACCAATGCACAA 754  
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 QY 755 GCCTGCCTTACCAGTGCCTAGATGCCCTCTGTCCAGGGACTTGATCATGAAGAGGAC 814  
 Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
 QY 815 TATGAACCTGTTAGTACCAGCCTACAAGGACCTCAAAAGTCAGACAAATTACTAGACACT 874  
 Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
 QY 875 ACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTGAAAGATTAACAA 934  
 Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
 QY 935 CAATGGTCTCTCAGCTTACCCCGAATACTTGTGGTTTCTAGATCACCACTCTTTAAAT 994  
 Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 533  
 QY 995 TTACTTCAAAATAAAGCATG 1015  
 Db 534 LeuLeuGlnAsnLysSerMet 540  
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 US-09-862-027-28  
 ; Sequence 28, Application US/09862027  
 ; Patent No. US20020142428A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hodge, Martin R.  
 ; TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof  
 ; FILE REFERENCE: 35800/234862  
 ; CURRENT APPLICATION NUMBER: US/09/862,027  
 ; CURRENT FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: US 09/345,473  
 ; PRIOR FILING DATE: 1999-06-30  
 ; NUMBER OF SEQ ID NOS: 82  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-862-027-28  
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 Pred. No.: 6,75e-225 Length: 540  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 9 Gaps: 0

### RESULT 3

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US-09-862-027-28
; Sequence 28, Application US/09862027
; Patent No. US2002014228A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US/09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-027-28

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Best Local Similarity: 100.00%
Query Match: 42.75%
DB: 9
Length: 540
Matches: 227
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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QY 455 AATAGTGGTTCCTCAAACTTCAAGTCCCTGAGCTCCCTCAAGACAAATGATTTTAA 514
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTCTCGAATACACAGT 574
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Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433
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QY 875 ACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAATTTGAAAGATACAAA 934
Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513
QY 935 CAAATGGGTCTTCAGCTTACCGGAAATCTTGGTGTCTTAGATCACCATTCTTTAAAT 994
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Db 534 LeuLeuGlnAsnLysSerMet 540

RESULT 4
US-09-981-397A-14
; Sequence 14, Application US/09981397A
; Publication No.: US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axxima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; FILE OF INVENTION: Inhibition
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981,397A
; CURRENT FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 540
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-981-397A-14
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Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.75% Indels: 0
DB: 10 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-981-397A-14 (1-540)
QY 335 TTACAGAGTGTTCCTCAAGTCCCATTTACCTATGTGACAGAGAGAAATGGAATATCTCTG 394
Db 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333
QY 395 AACATACCTGTAAATCATGCTGCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454
Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353
QY 455 AATAGTGGTTCCTCAAACTTCAAGTCCCTGAGCTCCCTCAAGACAAATGATTTTAA 514
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTCTCGAATACACAGT 574
Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393
QY 575 TGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACTCCA 634
Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 413
QY 635 TGCTCTTACAGCAATTAATCAATCCACTCTCAAGTCCCTGAGGAACTCAGAACCTCTG 694
Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433
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Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513
QY 935 CAAATGGGTCTTCAGCTTACCGGAAATCTTGGTGTCTTAGATCACCATTCTTTAAAT 994
Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533
QY 995 TTACTTCAAAATAAAGCATG 1015
Db 534 LeuLeuGlnAsnLysSerMet 540

RESULT 5
US-09-925-301-1015
; Sequence 1015, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
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APPLICANT: Bertin, John  
APPLICANT: Chao, Moses V.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-316001  
CURRENT APPLICATION NUMBER: US/09/748,537  
CURRENT FILING DATE: 2000-12-26  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-748-537-1

Alignment Scores:  
Pred. No.: 6.75e-225 Length: 544  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 9 Gaps: 0

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Db	318	LeuGlnSerValSerSerAlaIleHisLeuCyAspLysLysMetGluLeuSerLeu	337
QY	395	AACATACCTCTAAATCATGTGCACAAAGAGAAATCATGTGCATCCTCTCAGCTCCATGAA	454
Db	338	AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	357
QY	455	AATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGCAATGATTTTAA	514
Db	358	AsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	377
QY	515	TCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCTCTCTCGAAATTCACAGT	574
Db	378	SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer	397
QY	575	TGGATAGCACCATTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCATCCA	634
Db	398	TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro	417
QY	635	TGCTCTTCAGCAATAAATCCACTCTCACTGCAGGAACCTCAGAACCTCTGCAGCT	694
Db	418	CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro	437
QY	695	GGTATAGCCAGCAGTGGATCCAGACGAAAGGAGACATTGTGAACCAATGACAGAA	754
Db	438	GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu	457
QY	755	GCCTGCCTTAACCAAGTCAGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGGAC	814
Db	458	AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp	477
QY	815	TATGAATCTTGTAGTACCAAGCTTACAGGACCTCAAGACCTCAAGACATTTACTAGACAT	874
Db	478	TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr	497
QY	875	ACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA	934
Db	498	ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys	517
QY	935	CAATGGCTCTTACGCTTACCCGGAAATCTTGTGTTCTAGATCACCATCTTTAAAT	994
Db	518	GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn	537
QY	995	TTACTTCAAAATAAAGCATG 1015	
Db	538	LeuLeuGlnAsnLysSerMet 544	

RESULT 6  
US-09-748-537-1  
Sequence 1, Application US/09748537  
Patent No. US2002061833A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-124001  
CURRENT APPLICATION NUMBER: US/09/728,721  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/340,620  
PRIOR FILING DATE: 1999-06-28  
PRIOR APPLICATION NUMBER: US 09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942

APPLICANT: Bertin, John  
APPLICANT: Chao, Moses V.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-316001  
CURRENT APPLICATION NUMBER: US/09/748,537  
CURRENT FILING DATE: 2000-12-26  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-748-537-1

Alignment Scores:  
Pred. No.: 1.11e-122 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-748-537-1 (1-540)

QY	632	CCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACCTCAGAACCTCTGCAG	691
Db	413	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432
QY	692	CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAAATGTTGTAACCAAATGACA	751
Db	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	452
QY	752	GAAGCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG	811
Db	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472
QY	812	GACTATGAACTTGTAGTACCAAGCTCAGAGCACTCAAGGACCTCAAAAGCTCAGACAA	871
Db	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492
QY	872	ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC	931
Db	493	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512
QY	932	AAACAAATGGCTCTTACGCTTACCCGGAAATCTTGTGTTCTAGATCACCATCTTTA	991
Db	513	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	532
QY	992	AATTTACTTCAAAATAAAGCATG 1015	
Db	533	AsnLeuLeuGlnAsnLysSerMet 540	

RESULT 7  
US-09-728-721-2  
Sequence 2, Application US/09728721  
Patent No. US2002061845A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-124001  
CURRENT APPLICATION NUMBER: US/09/728,721  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/340,620  
PRIOR FILING DATE: 1999-06-28  
PRIOR APPLICATION NUMBER: US 09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-2

Alignment Scores:
Pred. No.: 1,11e-122 Length: 540
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.11% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-728-721-2 (1-540)
QY 632 CCATGCTTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGAACGCTCTGCAG 691
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGTATAGCCAGCAGTCGATCCAGACCAAAAGGAAAGACATTGTGAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAAACCAAGTCGCTAGATGCCCTTCTCAGGAGCTTGATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 472
QY 812 GACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCAAGGAGAAATTTGCCAAGTTATAGTACAAATAATTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCAGCCTTACCCGAAATACTTGTGTTCTAGATCACCATTCTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 8
US-10-133-780-1
; Sequence 1, Application US/10133780
; Publication No. US20020123115A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,780
; FILING DATE: 26-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,942

; FILING DATE: 06-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-133-780-1

Alignment Scores:
Pred. No.: 1,11e-122 Length: 540
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.11% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-133-780-1 (1-540)
QY 632 CCATGCTTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGAACGCTCTGCAG 691
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGTATAGCCAGCAGTCGATCCAGACCAAAAGGAAAGACATTGTGAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAAACCAAGTCGCTAGATGCCCTTCTCAGGAGCTTGATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 472
QY 812 GACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCAAGGAGAAATTTGCCAAGTTATAGTACAAATAATTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCAGCCTTACCCGAAATACTTGTGTTCTAGATCACCATTCTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9
US-10-105-931-2
; Sequence 2, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2  
 LENGTH: 540  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-105-931-2

Alignment Scores:

Pred. No.: 1.11e-122 Length: 540  
 Score: 128.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 24.11% Indels: 0  
 DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-105-931-2 (1-540)

QY 632 CCATGCTCTTCCAGCAATAATAATCACTCTCACTCCAGGAACTCAGAACTGCTGCGAG 691  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCCTGCCTTACCAAGTCCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATCAAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAATGTTAGTACAGCCTCAGAGCTCAGAGCACTCAAAAGTTCAGACAAATTAAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAATGGTCTTCCAGCCTTACCCGGAATACCTGCTGTTCTAGATCACCATTCTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
 QY 992 AATTACTTCAAAATAAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 10

US-10-118-984-2  
 ; Sequence 2, Application US/10118984  
 ; Publication No. US20020197693A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; FILE REFERENCE: 07334/18001  
 ; CURRENT FILING DATE: 2002-04-09  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US/09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-118-984-2

Alignment Scores:

Pred. No.: 1.11e-122 Length: 540

Score: 128.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 24.11% Indels: 0  
 DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-118-984-2 (1-540)

QY 632 CCATGCTCTTCCAGCAATAATAATCACTCTCACTCCAGGAACTCAGAACTGCTGCGAG 691  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCCTGCCTTACCAAGTCCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATCAAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAATGTTAGTACCAAGCCTCAGAGCACTCAAAAGTTCAGACAAATTAAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAATGGTCTTCCAGCCTTACCCGGAATACCTGCTGTTCTAGATCACCATTCTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
 QY 992 AATTACTTCAAAATAAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 11

US-10-295-981-2  
 ; Sequence 2, Application US/10295981  
 ; Publication No. US20030120055A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US/09/340,620  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-295-981-2

Alignment Scores:

Pred. No.: 1.11e-122 Length: 540  
 Score: 128.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 24.11% Indels: 0  
 DB: 14 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-295-981-2 (1-540)

QY 632 CCATGCTCTTCAGCAATATAATCCACTCTCACTGCGAGAACTCAGAAAGTCTGCGAG 691  
Db 413 ProCysSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTCTGAACCAAAATGACA 751  
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATGAAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAATCTTGTAGTACCAAGCCTACAGAGCACTCAAAAGTCAAGCAATCTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCCAAAGGAGAAGTTCGCAAGTTATAGTACAAAAATTTGAAAGATAAC 931  
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGGTCTCAGCCTTACCCGGAATATCTGTGTTTCTAGATCACCATCTTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTACTTCAAAATAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540  
RESULT 12  
US-09-728-721-6  
; Sequence 6, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728, 721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-728-721-6  
Alignment Scores:  
Pred. No.: 5.18e-103 Length: 109  
Score: 109.00 Matches: 109  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 20.53% Indels: 0  
DB: 9 Gaps: 0  
US-09-771-161A-2 (1-1669) x US-09-728-721-6 (1-109)  
QY 689 CAGCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAGT 748  
Db 1 GlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMet 20  
QY 749 ACAGAAGCCTGCCTTAAACCAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAA 808  
Db 21 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLys 40  
QY 809 GAGGACTATGAATCTTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAAGCAATCTACTA 868  
Db 41 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 60  
QY 869 GACACTACTGACATCCAAAGGAGAAGTTCGCAAGTTATAGTACAAAAATTTGAAAGAT 928  
Db 61 AspThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAsp 80  
QY 929 ACAACAATGGGTCTTCCAGCCTTACCCGGAATATCTGTGTTTCTAGATCACCATCT 988  
Db 81 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSer 100  
QY 989 TTAATTTACTTCAAAATAAAGCATG 1015  
Db 101 LeuAsnLeuLeuGlnAsnLysSerMet 109

QY 809 GAGGACTATGAATCTTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAAGCAATCTACTA 868  
Db 41 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 60  
QY 869 GACACTACTGACATCCAAAGGAGAAGTTCGCAAGTTATAGTACAAAAATTTGAAAGAT 928  
Db 61 AspThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAsp 80  
QY 929 ACAACAATGGGTCTTCCAGCCTTACCCGGAATATCTGTGTTTCTAGATCACCATCT 988  
Db 81 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSer 100  
QY 989 TTAATTTACTTCAAAATAAAGCATG 1015  
Db 101 LeuAsnLeuLeuGlnAsnLysSerMet 109  
RESULT 13  
US-10-105-931-6  
; Sequence 6, Application US/10105931  
; Publication No. US20020150987A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/10/105,931  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-931-6  
Alignment Scores:  
Pred. No.: 5.18e-103 Length: 109  
Score: 109.00 Matches: 109  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 20.53% Indels: 0  
DB: 13 Gaps: 0  
US-09-771-161A-2 (1-1669) x US-10-105-931-6 (1-109)  
QY 689 CAGCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAGT 748  
Db 1 GlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMet 20  
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; Sequence 6, Application US/10118984  
; Publication No. US20020197693A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/10/118,984  
; PRIORITY FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-118-984-6

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; Sequence 6, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/10/295,981  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/340,620  
; PRIOR FILING DATE: 1999-06-28

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; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US/09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: 1998-06-17  
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Db 61 AspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsp 80  
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1079	64.6	2709	9 US-09-925-301-173	Sequence 173, App
3	812	48.7	2501	10 US-09-981-397A-13	Sequence 13, Appl
4	682	40.9	1931	9 US-09-748-537-2	Sequence 2, Appli
5	682	40.9	1931	9 US-09-728-721-1	Sequence 1, Appli
6	682	40.9	1931	13 US-10-133-780-2	Sequence 2, Appli
7	682	40.9	1931	13 US-10-105-931-1	Sequence 1, Appli
8	682	40.9	1931	13 US-10-118-984-1	Sequence 1, Appli
9	682	40.9	1931	14 US-10-295-981-1	Sequence 1, Appli
10	632	37.9	1620	9 US-09-728-721-3	Sequence 3, Appli
11	632	37.9	1620	13 US-10-105-931-3	Sequence 3, Appli
12	632	37.9	1620	13 US-10-118-984-3	Sequence 3, Appli
13	632	37.9	1620	14 US-10-295-981-3	Sequence 3, Appli
14	363	21.7	491	10 US-09-918-995-20565	Sequence 20565, A
15	220	13.2	299	9 US-09-919-580-544	Sequence 544, App

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26	22	1.3	1119	9	US-09-912-020-215	Sequence 215, App
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28	21	1.3	1942	10	US-09-822-846-166	Sequence 166, App
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44	20	1.2	1007	15	US-10-027-632-249981	Sequence 249981,
45	20	1.2	1536	14	US-10-072-438-31	Sequence 31, Appl

ALIGNMENTS

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US-09-771-161A-2  
; Sequence 2, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1669  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY:  
; LOCATION: (1)..(1669)  
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'  
US-09-771-161A-2

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RESULT 3
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; Sequence 13, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axxima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; TITLE OF INVENTION: Inhibition
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981.397A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-397A-13

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; Patent No. US20020061833A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE  
; FILE REFERENCE: 07334-316001  
; CURRENT APPLICATION NUMBER: US/09/748,537  
; CURRENT FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-748-537-2

Query Match 40.9%; Score 682; DB 9; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCAGGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTC 392  
Db 1151 AGTTACAGAGTGTTCAGGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTC 1210  
QY 393 TGAACATACCTGTAATATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 452  
Db 1211 TGAACATACCTGTAATATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 1270  
QY 453 AAAATAGTGGTTCCTCGAAACCTTCAAGGTCCTCGCCAGCTCCTCAAGACAATGTTTTT 512

Db 1271 AAAATAGTGGTTCCTCGAAACCTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTT 1330  
QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAAGTGCATCACTGCTCGGAAATCACA 572  
Db 1331 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAAGTGCATCACTGCTCGGAAATCACA 1390  
QY 573 GTTGGATAGCACCATTTCTGGATCTCAAGGGCTCATTTCTGTGATCACAAGACCACTC 632  
Db 1391 GTTGGATAGCACCATTTCTGGATCTCAAGGGCTCATTTCTGTGATCACAAGACCACTC 1450  
QY 633 CATGCTCTTTCAGCAATAATAATCCACTCTCAACTCAGAGAAACTCAGAACTGCTCGAGC 692  
Db 1451 CATGCTCTTTCAGCAATAATAATCCACTCTCAACTCAGAGAAACTCAGAACTGCTCGAGC 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAG 752  
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAG 1570  
QY 753 AAGCCTGCTTTAACCAAGTGGTGGATGCTGCTGCTCCAGGGACTTGTATCATGAAAGAGG 812  
Db 1571 AAGCCTGCTTTAACCAAGTGGTGGATGCTGCTGCTCCAGGGACTTGTATCATGAAAGAGG 1630  
QY 813 ACTATCAACTTGTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 872  
Db 1631 ACTATCAACTTGTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 1690  
QY 873 CTACTGACATCCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
Db 1691 CTACTGACATCCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750  
QY 933 AACAAATGGGTCTTTCAGACCTTACCCGGAATACCTTGGTGGTTCTAGATCACCATCTTTAA 992  
Db 1751 AACAAATGGGTCTTTCAGACCTTACCCGGAATACCTTGGTGGTTCTAGATCACCATCTTTAA 1810  
QY 993 ATTTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTTCAAGGAAGAAATGTTGTTTCATAA 1052  
Db 1811 ATTTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTTCAAGGAAGAAATGTTGTTTCATAA 1870  
QY 1053 AAGGATATTTATA 1065  
Db 1871 AAGGATATTTATA 1883

RESULT 5  
US-09-728-721-1  
; Sequence 1, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-09-728-721-1



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QY 933 AACAAATGGTCTTCCAGCTTACCCGGAATACATCTGTGTTTCTAGATCACCATCTTTAA 992
Db 1751 AACAAATGGTCTTCCAGCTTACCCGGAATACATCTGTGTTTCTAGATCACCATCTTTAA 1810
QY 993 ATTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTTCAGGAAGAAATGTTTTCATAA 1052
Db 1811 ATTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTTCAGGAAGAAATGTTTTCATAA 1870
QY 1053 AAGGATATTATA 1065
Db 1871 AAGGATATTATA 1883

RESULT 7
US-10-105-931-1
; Sequence 1, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-105-931-1

Query Match 40.9%; Score 682; DB 13; Length 1931;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATCTC 392
Db 1151 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATCTC 1210
QY 393 TGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
Db 1211 TGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 1270
QY 453 AAAATAGTGGTCTCTGAACTTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATCTC 512
Db 1271 AAAATAGTGGTCTCTGAACTTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATCTC 1330
QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCTCCTGGAATATCTC 572
Db 1331 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCTCCTGGAATATCTC 1390
QY 573 GTTGGATAGCACCATTTCTGATCTCAAGGGGTGCATCTGTGATCACAAGACCACTC 632
Db 1391 GTTGGATAGCACCATTTCTGATCTCAAGGGGTGCATCTGTGATCACAAGACCACTC 1450
QY 633 CATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACTCTGAGC 692
Db 1451 CATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACTCTGAGC 1510
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAAGGGAAGACATTTGTGAACCAATGACAG 752
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAAGGGAAGACATTTGTGAACCAATGACAG 1570
QY 753 AAGCTGCTTAAACAGTGGCTAGATGCTTCTGTCAGGGAATGATCATGAAGAGG 812

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Db 1571 AAGCCTGCTTAAACAGTCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGG 1630
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Db 1631 ACTATGAATCTGTAGTACCAAGCCTACAAGACCTCAAAAGTCAACAATTAATCTAGACA 1690
QY 873 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACA 932
Db 1691 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACA 1750
QY 933 AACAAATGGTCTTCCAGCTTACCCGGAATACATCTGTGTTTCTAGATCACCATCTTTAA 992
Db 1751 AACAAATGGTCTTCCAGCTTACCCGGAATACATCTGTGTTTCTAGATCACCATCTTTAA 1810
QY 993 ATTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTTCAGGAAGAAATGTTTTCATAA 1052
Db 1811 ATTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTTCAGGAAGAAATGTTTTCATAA 1870
QY 1053 AAGGATATTATA 1065
Db 1871 AAGGATATTATA 1883

RESULT 8
US-10-118-984-1
; Sequence 1, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-118-984-1

Query Match 40.9%; Score 682; DB 13; Length 1931;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATCTC 392
Db 1151 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATCTC 1210
QY 393 TGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
Db 1211 TGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 1270
QY 453 AAAATAGTGGTCTCTGAACTTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATCTC 512
Db 1271 AAAATAGTGGTCTCTGAACTTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATCTC 1330
QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCTCCTGGAATATCTC 572
Db 1331 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCTCCTGGAATATCTC 1390
QY 573 AAGCTGCTTAAACAGTGGCTAGATGCTTCTGTCAGGGAATGATCATGAAGAGG 812

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QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTC 632  
Db 1391 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTC 1450  
QY 633 CATGCTCTTCAACAATAATAATCAACTCACTCACTGCGAGGAACCTCAGAACGTCTGCAGC 692  
Db 1451 CATGCTCTTCAACAATAATAATCAACTCACTCACTGCGAGGAACCTCAGAACGTCTGCAGC 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAG 752  
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAG 1570  
QY 753 AAGCCTGCTTAAACAGTGGATGAGTGCCTTCTGTCCAGGACTTGTATCATGAAGAGG 812  
Db 1571 AAGCCTGCTTAAACAGTGGATGAGTGCCTTCTGTCCAGGACTTGTATCATGAAGAGG 1630  
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QY 873 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 932  
Db 1691 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 1750  
QY 933 AACAAATGGCTCTTACGCCCTTACCGGAAATACCTTGTGTTCTAGATCACCATTCTTAA 992  
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QY 993 ATTTACTTCAAAATAAAAGCATGTAAGTACCTGTTTTCAGAGAAATGTTTCATAA 1052  
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QY 1053 AAGGATATTATA 1065  
Db 1871 AAGGATATTATA 1883  
RESULT 9  
US-10-295-981-1  
; Sequence 1, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/10/295,981  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US/09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US/09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-10-295-981-1  
Query Match 40.9%; Score 682; DB 14; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAAAGAAAATGGAATATATCTC 392

Db 1151 AGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAAAGAAAATGGAATATATCTC 1210  
QY 393 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCCATG 452  
Db 1211 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCCATG 1270  
QY 453 AAAATAGTGGTTCCTCTGAAAACCTCAAGGTCCCTGCCAGCTCCTCAAGACATGATTTTT 512  
Db 1271 AAAATAGTGGTTCCTCTGAAAACCTCAAGGTCCCTGCCAGCTCCTCAAGACATGATTTTT 1330  
QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAGTCTCTGGAATATCA 572  
Db 1331 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAGTCTCTGGAATATCA 1390  
QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTC 632  
Db 1391 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTC 1450  
QY 633 CATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCGAGGAACCTCAGAACGTCTGCAGC 692  
Db 1451 CATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCGAGGAACCTCAGAACGTCTGCAGC 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAG 752  
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAG 1570  
QY 753 AAGCCTGCTTAAACAGTGGTGTAGTACCTTCTGTCCAGGACTTGTATCATGAAGAGG 812  
Db 1571 AAGCCTGCTTAAACAGTGGTGTAGTACCTTCTGTCCAGGACTTGTATCATGAAGAGG 1630  
QY 813 ACTATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTGTAGTACCAATTTACTAGACA 872  
Db 1631 ACTATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTGTAGTACCAATTTACTAGACA 1690  
QY 873 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 932  
Db 1691 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 1750  
QY 933 AACAAATGGCTCTTACGCCCTTACCGGAAATACCTTGTGTTCTAGATCACCATTCTTAA 992  
Db 1751 AACAAATGGCTCTTACGCCCTTACCGGAAATACCTTGTGTTCTAGATCACCATTCTTAA 1810  
QY 993 ATTTACTTCAAAATAAAAGCATGTAAGTACCTGTTTTCAGAGAAATGTTTCATAA 1052  
Db 1811 ATTTACTTCAAAATAAAAGCATGTAAGTACCTGTTTTCAGAGAAATGTTTCATAA 1870  
QY 1053 AAGGATATTATA 1065  
Db 1871 AAGGATATTATA 1883  
RESULT 10  
US-09-728-721-3  
; Sequence 3, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US/09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3



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; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-728-721-3

Query Match      37.9%; Score 632; DB 9; Length 1620;
Best Local Similarity 99.9%; Pred. No. 1.1e-298;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAGAGAAATGGAATATCTC 392
DB 938 AGTTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAGAGAAATGGAATATCTC 997
QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
DB 998 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 1057
QY 453 AAAATAGTGGTTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 512
DB 1058 AAAATAGTGGTTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1117
QY 513 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTGATCAAGACCACTC 572
DB 1118 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTGATCAAGACCACTC 1177
QY 573 GTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCAATCTGTGATCAAGACCACTC 632
DB 1178 GTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCAATCTGTGATCAAGACCACTC 1237
QY 633 CATGCTCTTCAGCAATAATAATCACTCACTCAAGTCCCTGCCAGTCAAGACCACTC 692
DB 1238 CATGCTCTTCAGCAATAATAATCACTCAAGTCCCTGCCAGTCAAGACCACTC 1297
QY 693 CTGGTATAGCCAGCAGTGCATCCAGAGCAAGAGGAGACATTTGTAACCAATGACAG 752
DB 1298 CTGGTATAGCCAGCAGTGCATCCAGAGCAAGAGGAGACATTTGTAACCAATGACAG 1357
QY 753 AAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGGACTTGCATCATGAAGAGG 812
DB 1358 AAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGGACTTGCATCATGAAGAGG 1417
QY 813 ACTATGAACCTTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGACA 872
DB 1418 ACTATGAACCTTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGACA 1477
QY 873 CTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 932
DB 1478 CTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 1537
QY 933 AACAAATGGGTCTTCAGCCTTACCCTGAAATATCTGTGGTTTCTAGATCAACCATCTTAA 992
DB 1538 AACAAATGGGTCTTCAGCCTTACCCTGAAATATCTGTGGTTTCTAGATCAACCATCTTAA 1597
QY 993 ATTTACTTCAAAATAAAGCATG 1015
DB 1598 ATTTACTTCAAAATAAAGCATG 1620

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RESULT 11
US-10-105-931-3
; Sequence 3, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 05/019,942
; PRIOR FILING DATE: 1998-02-06

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; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Past-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-931-3

Query Match      37.9%; Score 632; DB 13; Length 1620;
Best Local Similarity 99.9%; Pred. No. 1.1e-298;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAGAGAAATGGAATATCTC 392
DB 938 AGTTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAGAGAAATGGAATATCTC 997
QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
DB 998 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 1057
QY 453 AAAATAGTGGTTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 512
DB 1058 AAAATAGTGGTTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1117
QY 513 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTGATCAAGACCACTC 572
DB 1118 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTGATCAAGACCACTC 1177
QY 573 GTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCAATCTGTGATCAAGACCACTC 632
DB 1178 GTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCAATCTGTGATCAAGACCACTC 1237
QY 633 CATGCTCTTCAGCAATAATAATCACTCACTCAAGTCCCTGCCAGTCAAGACCACTC 692
DB 1238 CATGCTCTTCAGCAATAATAATCACTCAAGTCCCTGCCAGTCAAGACCACTC 1297
QY 693 CTGGTATAGCCAGCAGTGCATCCAGAGCAAGAGGAGACATTTGTAACCAATGACAG 752
DB 1298 CTGGTATAGCCAGCAGTGCATCCAGAGCAAGAGGAGACATTTGTAACCAATGACAG 1357
QY 753 AAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGGACTTGCATCATGAAGAGG 812
DB 1358 AAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGGACTTGCATCATGAAGAGG 1417
QY 813 ACTATGAACCTTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGACA 872
DB 1418 ACTATGAACCTTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGACA 1477
QY 873 CTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 932
DB 1478 CTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 1537
QY 933 AACAAATGGGTCTTCAGCCTTACCCTGAAATATCTGTGGTTTCTAGATCAACCATCTTAA 992
DB 1538 AACAAATGGGTCTTCAGCCTTACCCTGAAATATCTGTGGTTTCTAGATCAACCATCTTAA 1597
QY 993 ATTTACTTCAAAATAAAGCATG 1015
DB 1598 ATTTACTTCAAAATAAAGCATG 1620

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RESULT 12
US-10-118-984-3
; Sequence 3, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281

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; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-984-3

Query Match      37.9%; Score 632; DB 13; Length 1620;
Best Local Similarity 99.9%; Pred. No. 1.le-298;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAAAGAAATGGAATATATCTC 392
Db 938 AGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAAAGAAATGGAATATATCTC 997

QY 393 TGAACATACCTTAAATCATGTGCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
Db 998 TGAACATACCTTAAATCATGTGCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1057

QY 453 AAAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 512
Db 1058 AAAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1117

QY 513 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTCGGAAATCAACA 572
Db 1118 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTCGGAAATCAACA 1177

QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATCTGTGATCAACAAGACCACTC 632
Db 1178 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATCTGTGATCAACAAGACCACTC 1237

QY 633 CATGCTCTTCAGCAATAATAATCAACTCTCAACTGCAGGAACTCAGAACTCTGCGAGC 692
Db 1238 CATGCTCTTCAGCAATAATAATCAACTCTCAACTGCAGGAACTCAGAACTCTGCGAGC 1297

QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAG 752
Db 1418 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAG 1477

QY 873 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932
Db 1478 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1537

QY 933 AACAAATGGGCTTCCAGGCTTACCCGGAAATCTGTGGTTCTAGATCACCATCTTTAA 992
Db 1538 AACAAATGGGCTTCCAGGCTTACCCGGAAATCTGTGGTTCTAGATCACCATCTTTAA 1597

QY 993 ATTTACTTCAAAATAAAGCATG 1015
Db 1598 ATTTACTTCAAAATAAAGCATG 1620
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RESULT 13  
US-10-295-981-3  
; Sequence 3, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:

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; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3
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Query Match      37.9%; Score 632; DB 14; Length 1620;
Best Local Similarity 99.9%; Pred. No. 1.le-298;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAAAGAAATGGAATATATCTC 392
Db 938 AGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAAAGAAATGGAATATATCTC 997

QY 393 TGAACATACCTTAAATCATGTGCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
Db 998 TGAACATACCTTAAATCATGTGCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1057

QY 453 AAAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 512
Db 1058 AAAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1117

QY 513 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTCGGAAATCAACA 572
Db 1118 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTCGGAAATCAACA 1177

QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATCTGTGATCAACAAGACCACTC 632
Db 1178 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATCTGTGATCAACAAGACCACTC 1237

QY 633 CATGCTCTTCAGCAATAATAATCAACTCTCAACTGCAGGAACTCAGAACTCTGCGAGC 692
Db 1238 CATGCTCTTCAGCAATAATAATCAACTCTCAACTGCAGGAACTCAGAACTCTGCGAGC 1297

QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAG 752
Db 1298 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAG 1357

QY 753 AAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGGAATTTGATCATGAAAGAGG 812
Db 1358 AAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGGAATTTGATCATGAAAGAGG 1417

QY 813 ACTATGAACTTGTAGTACCAAGCCCTCAAGGACCTCAAAAGTCAAGCAATTTACTAGACA 872
Db 1418 ACTATGAACTTGTAGTACCAAGCCCTCAAGGACCTCAAAAGTCAAGCAATTTACTAGACA 1477

QY 873 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932
Db 1478 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1537

QY 933 AACAAATGGGCTTCCAGGCTTACCCGGAAATCTGTGGTTCTAGATCACCATCTTTAA 992
Db 1538 AACAAATGGGCTTCCAGGCTTACCCGGAAATCTGTGGTTCTAGATCACCATCTTTAA 1597

QY 993 ATTTACTTCAAAATAAAGCATG 1015
Db 1598 ATTTACTTCAAAATAAAGCATG 1620
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Db      1598 ATTACTTCAAAATAAAAGCATG 1620

RESULT 14
US-09-918-995-20565
; Sequence 20565, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20565
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-20565

Query Match      21.7%; Score 363; DB 10; Length 491;
Best Local Similarity 100.0%; Pred. No. 5.5e-167;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      333 AGTTACAGAGTGTTTCAAGTGCCATTCACTATGTGACAAAGAGAAAATGGAATTATCTC 392
Db      129 AGTTACAGAGTGTTTCAAGTGCCATTCACTATGTGACAAAGAGAAAATGGAATTATCTC 188

QY      393 TGAACATACCTGTAAATCATCTGTCGACAGAGGAATCATGTGATCTCTCAGCTCCATG 452
Db      189 TGAACATACCTGTAAATCATCTGTCGACAGAGGAATCATGTGATCTCTCAGCTCCATG 248

QY      453 AATAATAGTGGTCTCTCTGAAATTCAGGTCCCTGCCAGCTCCCTCAAGACAATGATTTT 512
Db      249 AATAATAGTGGTCTCTCTGAAATTCAGGTCCCTGCCAGCTCCCTCAAGACAATGATTTT 308

QY      513 TATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAATCACA 572
Db      309 TATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAATCACA 368

QY      573 GTTGGGATAGCACCATTCTCGGATCTCAAAAGGCTGCATTCTGTGATCAAGACCACTC 632
Db      369 GTTGGGATAGCACCATTCTCGGATCTCAAAAGGCTGCATTCTGTGATCAAGACCACTC 428

QY      633 CATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAAACTCAGAACGTCGTGAGC 692
Db      429 CATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAAACTCAGAACGTCGTGAGC 488

QY      693 CTG 695
Db      489 CTG 491

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US-09-919-580-544/c
; Sequence 544, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Serist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544

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Best Local Similarity 100.0%; Pred. No. 5.9e-97;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1441 TTAATTGCCCTACAAAGGGTTATTAAATTTAAAACTCCATTATTAGGATTACATTTTAAAG 1500
Db      242 TTAATTGCCCTACAAAGGGTTATTAAATTTAAAACTCCATTATTAGGATTACATTTTAAAG 183

QY      1501 TTTTATTATGAATTCCTTTTAAAAATGATATTTCAAAGGTAAACAATACATATTAAG 1560
Db      182 TTTTATTATGAATTCCTTTTAAAAATGATATTTCAAAGGTAAACAATACATATTAAG 123

QY      1561 AAAAAATAAATATATTAATACCGCTTCTCTGCCCATTTTAAACCTCAGGCTTCCCTTA 1620
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QY      1621 CTGTCAACCAACCAAGCTAAATAAAGTCAACAGCTGA 1660
Db      62 CTGTCAACCAACCAAGCTAAATAAAGTCAACAGCTGA 23

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Job time : 705 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 06:19:46 ; Search time 156 Seconds  
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Perfect score: 1669  
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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 20

Total number of hits satisfying chosen parameters: 37

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	812	48.7	2501	4	US-09-920-663-3
2	812	48.7	2502	4	US-09-069-023-2
3	682	40.9	1931	3	US-09-019-942-2
4	682	40.9	1931	4	US-09-099-041A-1
5	682	40.9	1931	4	US-09-245-281-1
6	682	40.9	1931	4	US-09-470-271-2
7	682	40.9	1931	4	US-09-207-359B-1
8	682	40.9	1931	4	US-09-340-620A-1
9	682	40.9	1931	4	US-09-865-364-1
10	682	40.9	1931	4	US-09-748-537-2
11	632	37.9	1620	4	US-09-099-041A-3
12	632	37.9	1620	4	US-09-245-281-3
13	632	37.9	1620	4	US-09-207-359B-3
14	632	37.9	1620	4	US-09-340-620A-3
15	632	37.9	1620	4	US-09-865-364-3
16	586	35.1	1060	4	US-09-023-655-684
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C 18	37	2.2	54	4	US-09-748-537-12
C 19	23	1.4	32	4	US-09-748-537-9
C 20	21	1.3	2674	4	US-09-673-395A-63
C 21	20	1.2	20	4	US-09-920-663-34
C 22	20	1.2	20	4	US-09-920-663-35
C 23	20	1.2	20	4	US-09-920-663-37
C 24	20	1.2	20	4	US-09-920-663-38
C 25	20	1.2	20	4	US-09-920-663-39
C 26	20	1.2	20	4	US-09-920-663-40
C 27	20	1.2	20	4	US-09-920-663-41

C 28	20	1.2	20	4	US-09-920-663-42	Sequence 42, Appl
C 29	20	1.2	20	4	US-09-920-663-43	Sequence 43, Appl
C 30	20	1.2	20	4	US-09-920-663-44	Sequence 44, Appl
C 31	20	1.2	20	4	US-09-920-663-45	Sequence 45, Appl
C 32	20	1.2	20	4	US-09-920-663-46	Sequence 46, Appl
C 33	20	1.2	20	4	US-09-920-663-47	Sequence 47, Appl
C 34	20	1.2	20	4	US-09-920-663-48	Sequence 48, Appl
C 35	20	1.2	20	4	US-09-920-663-49	Sequence 49, Appl
C 36	20	1.2	1830121	4	US-09-557-884-1	Sequence 1, Appl
C 37	20	1.2	1830121	4	US-09-643-990A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-920-663-3  
; Sequence 3, Application US/09920663  
; Patent No. 6426221  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION  
; FILE REFERENCE: RTS-0233  
; CURRENT APPLICATION NUMBER: US/09/920,663  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 3  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (225) ... (1847)  
US-09-920-663-3

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Gaps	0						
QY	333	AGTTACAGAGTGTTC	CAAGTGCCATT	CACCTATGTGACAAGAGAAATGGAATATATCTC	392		
DB	1162	AGTTACAGAGTGTTC	CAAGTGCCATT	CACCTATGTGACAAGAGAAATGGAATATATCTC	1221		
QY	393	TGAACATACCTGTAAT	CATGTCCACAAGAGAAATCATGTGGATCCTCTCAGCTCCATG	452			
DB	1222	TGAACATACCTGTAAT	CATGTCCACAAGAGAAATCATGTGGATCCTCTCAGCTCCATG	1281			
QY	453	AAATAGTGGTTCCTCTG	AAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATTTT	512			
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QY	513	TATCTAGAAAAGCTCA	AGACTGTATTTTATCAAGCTGCATCAGTCTCTCTGGAATCACA	572			
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QY	573	GTGGGATAGCACCATT	TTCTGATCTCAAGGGCTGCATTCTTGATCACAAGACCCTC	632			
DB	1402	GTGGGATAGCACCATT	TTCTGATCTCAAGGGCTGCATTCTTGATCACAAGACCCTC	1461			
QY	633	CATGCTTTTACGAAATA	TAATATCACTTCACTTCAAGGAACTCAGAACGCTCTGAGC	692			
DB	1462	CATGCTTTTACGAAATA	TAATATCACTTCACTTCAAGGAACTCAGAACGCTCTGAGC	1521			
QY	693	CTGGTATAGCCAGAGT	GGATCCAGACAAAGGAGACATTTGACCAAAATGACAG	752			
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DB	1582	AAGCCTGCTTAACAGT	CGCTAGATGCCCTTTCTGTCCAGGGACTTGATCATCAAGAGG	1641			
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Qy 1053 AAGGATATTTATATCTCTGTTGCTTTCAGCTTTTATATATAAATCCGTGAGTATTAAG 1112
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Qy 1113 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTT 1172
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Qy 1173 TTAATTAATCAAGTAAAAAGTT 1195
Db 2002 TTAATTAATCAAGTAAAAAGTT 2024

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RESULT 2
US-09-069-023-2
; Sequence 2, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-069-023-2

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Query Match 48.7%; Score 812; DB 4; Length 2502;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 333 AGTTACAGAGTGTTCAGAGTCCATTACCTATGTGACAGAGAAATGGAATATATCTC 392
Db 1163 AGTTACAGAGTGTTCAGAGTCCATTACCTATGTGACAGAGAAATGGAATATATCTC 1222
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Db 1223 TGAACATACCTGTAATCATGCTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 1282
Qy 453 AAAATAGTGGTTCCTCGAAATCTTCAAGGTCCTGCGAGCTCCCTCAAGACAAATGATTTT 512
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Qy 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAAGTGCATCTGCTGGAATCACA 572
Db 1343 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAAGTGCATCTGCTGGAATCACA 1402
Qy 573 GTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACTC 632
Db 1403 GTTGGGATAGCACCATTTCTGGTCTCAAGGGCTGCAATCTGTGATCACAAGACCACTC 1462

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Qy 633 CATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTCAGC 692
Db 1463 CATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTCAGC 1522
Qy 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAG 752
Db 1523 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAG 1582
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Db 1583 AAGCCTGCTTAACTACAGTGCCTTCTGCTCAGGGAGTCTGATCATCAAGAGAGG 1642
Qy 813 ACTATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTAAGTACACA 872
Db 1643 ACTATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTAAGTACACA 1702
Qy 873 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932
Db 1703 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1762
Qy 933 AACAAATGGGTCTTTCAGCCTTACCCTGGAATTAATCTGTTGGTTCTTAGATCACCATTCTTTAA 992
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Qy 993 ATTACTTCAAAATFAAAGCATGTAAGTGAAGTCTGTTTTCAGAGAGAAATGTTTTCATAA 1052
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Qy 1053 AAGGATATTTATATCTCTGTTGCTTTCAGCTTTTATATATAAATCCGTGAGTATTAAG 1112
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Qy 1113 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTT 1172
Db 1943 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTT 2002
Qy 1173 TTAATTAATCAAGTAAAAAGTT 1195
Db 2003 TTAATTAATCAAGTAAAAAGTT 2025

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RESULT 3
US-09-019-942-2
; Sequence 2, Application US/09019942
; Patent No. 6033855
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,942
; FILING DATE: 06-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:

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Db      1691 CTACTGACATCCAAAGGAGAAGATTTCGCAAGTTATAGTACAAAAATGAAAGATAACA 1750
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QY      933 AACAAATGGTCTTTCAGCCTTACCCGGAATATCTTGGTTCTAGATCACCATCTTAA 992
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Db      1751 AACAAATGGTCTTTCAGCCTTACCCGGAATATCTTGGTTCTAGATCACCATCTTAA 1810
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QY      993 ATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTCAAGAGAAATGTTTTCATAA 1052
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Db      1871 AAGGATATTATA 1883
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RESULT 6
US-09-470-271-2
; Sequence 2, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-470-271-2

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Query Match      40.9%; Score 682; DB 4; Length 1931;
Best Local Similarity 99.9%; Pred. No: 1.2e-309;
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      333 AGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTTATCTC 392
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Db      1151 AGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTTATCTC 1210
|||||
QY      393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
|||||
Db      1211 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270
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QY      453 AAATAGTGGTTCTCTCTGAAACTTTCAGGTCCTCCAGAGTTCCTCAGCTCCATG 512
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Query Match      40.9%; Score 682; DB 4; Length 1931;
Best Local Similarity 99.9%; Pred. No: 1.2e-309;
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      333 AGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTTATCTC 392
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Db      1151 AGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTTATCTC 1210
|||||
QY      393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
|||||
Db      1211 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270
|||||
QY      453 AAATAGTGGTTCTCTCTGAAACTTTCAGGTCCTCCAGAGTTCCTCAGCTCCATG 512
|||||
Db      1271 AAATAGTGGTTCTCTGAAACTTTCAGGTCCTCCAGAGTTCCTCAGACAAATGATTTT 1330
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QY      513 TATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTGGAAATCACA 572
|||||
Db      1331 TATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTGGAAATCACA 1390
|||||
QY      573 GTTGGGATAGCACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 632
|||||
Db      1391 GTTGGGATAGCACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 1450
|||||
QY      633 CATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCGTCAGC 692
|||||
Db      1451 CATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCGTCAGC 1510
|||||
QY      693 CTGGTATAGCCAGAGTGTGATCCAGAGCAAAAGGGAGACATGTGAAACCAATGACAG 752
|||||
Db      1511 CTGGTATAGCCAGAGTGTGATCCAGAGCAAAAGGGAGACATGTGAAACCAATGACAG 1570
|||||
QY      753 AAGCTGCTCTTAACCAAGTCTAGATGCCCTTCTGTCCAGGGACTTCATCATCAAGAGG 812
|||||
Db      1571 AAGCTGCTCTTAACCAAGTCTAGATGCCCTTCTGTCCAGGGACTTCATCATCAAGAGG 1630
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QY      813 ACTATGAATCTGTTAGTACCAAGCTCAAGAGCACTCAAAAGTCAAGCAATTTACTAGACA 872
|||||
Db      1631 ACTATGAATCTGTTAGTACCAAGCTCAAGAGCACTCAAAAGTCAAGCAATTTACTAGACA 1690
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QY      873 CTACTGACATCCAAAGGAGAAGATTTCGCAAGTTATAGTACAAAAATGGAAGATAACA 932
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Db 1271 AAATAGTGGTCTCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1330  
 QY 513 TATCTAGAAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCA 572  
 Db 1331 TATCTAGAAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCA 1390  
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 Db 1391 GTTGGATAGCAACATTTCTGATCTCAAGAGGCTGCATTTCTGTGATCAACAAGACCATC 1450  
 QY 633 CATGCTCTTCAAGCAATAAATCAATCTCACTCACTCACTCACTCACTCACTCACTCACT 692  
 Db 1451 CATGCTCTTCAAGCAATAAATCAATCTCACTCACTCACTCACTCACTCACTCACTCACT 1510  
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 QY 753 AAGCTGCTTAAACAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAATGACAG 812  
 Db 1571 AAGCTGCTTAAACAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAATGACAG 1630  
 QY 813 ACTATGAATCTTGTAGTACCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCT 872  
 Db 1631 ACTATGAATCTTGTAGTACCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCT 1690  
 QY 873 CTACTGACATCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 932  
 Db 1691 CTACTGACATCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 1750  
 QY 933 AACAAATGGTCTTCAAGCTTACCCGGAATACTTGTGTTTCTAGATCAACATCTTTAA 992  
 Db 1751 AACAAATGGTCTTCAAGCTTACCCGGAATACTTGTGTTTCTAGATCAACATCTTTAA 1810  
 QY 993 ATTACTTCAAAATAAAGCATGTAAGTACGTTTTCAGAGCAAAATGTTTCAATAA 1052  
 Db 1811 ATTACTTCAAAATAAAGCATGTAAGTACGTTTTCAGAGCAAAATGTTTCAATAA 1870  
 QY 1053 AAGGATATTATA 1065  
 Db 1871 AAGGATATTATA 1883

RESULT 7  
 US-09-207-359B-1  
 ; Sequence 1, Application US/09207359B  
 ; Patent No. 6469140  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/207,359B  
 ; CURRENT FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US/09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US/09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (214) ... (1833)  
 US-09-207-359B-1

Query Match 40.9%; Score 682; DB 4; Length 1931;  
 Best Local Similarity 99.9%; Pred. No. 1.2e-309;  
 Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTCTTCAAGTGCATTTCACTATGTGCAAGAAGAAAAATGGAATTTATCTC 392  
 Db 1151 AGTTACAGAGTGTCTTCAAGTGCATTTCACTATGTGCAAGAAGAAAAATGGAATTTATCTC 1210  
 QY 393 TGAACATACCTGTAAATCATGTGTCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
 Db 1211 TGAACATACCTGTAAATCATGTGTCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270  
 QY 453 AAAATAGTGGTCTCTCAAGACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 512  
 Db 1271 AAAATAGTGGTCTCTCAAGACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 1330  
 QY 513 TATCTAGAAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCA 572  
 Db 1331 TATCTAGAAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCA 1390  
 QY 573 GTTGGATAGCAACATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAACAAGACCATC 632  
 Db 1391 GTTGGATAGCAACATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAACAAGACCATC 1450  
 QY 633 CATGCTCTTCAAGCAATAAATCAATCTCACTCACTCACTCACTCACTCACTCACTCACT 692  
 Db 1451 CATGCTCTTCAAGCAATAAATCAATCTCACTCACTCACTCACTCACTCACTCACTCACT 1510  
 QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAATGACAG 752  
 Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAATGACAG 1570  
 QY 753 AAGCTGCTTAAACAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAATGACAG 812  
 Db 1571 AAGCTGCTTAAACAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAATGACAG 1630  
 QY 813 ACTATGAATCTTGTAGTACCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCT 872  
 Db 1631 ACTATGAATCTTGTAGTACCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCT 1690  
 QY 873 CTACTGACATCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 932  
 Db 1691 CTACTGACATCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 1750  
 QY 933 AACAAATGGTCTTCAAGCTTACCCGGAATACTTGTGTTTCTAGATCAACATCTTTAA 992  
 Db 1751 AACAAATGGTCTTCAAGCTTACCCGGAATACTTGTGTTTCTAGATCAACATCTTTAA 1810  
 QY 993 ATTACTTCAAAATAAAGCATGTAAGTACGTTTTCAGAGCAAAATGTTTCAATAA 1052  
 Db 1811 ATTACTTCAAAATAAAGCATGTAAGTACGTTTTCAGAGCAAAATGTTTCAATAA 1870  
 QY 1053 AAGGATATTATA 1065  
 Db 1871 AAGGATATTATA 1883

RESULT 8  
 US-09-340-620A-1  
 ; Sequence 1, Application US/09340620A  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/340,620A  
 ; CURRENT FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US/09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US/09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US/09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US/09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71



; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-09-340-620A-1

Query Match 40.9%; Score 682; DB 4; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 1.2e-309;  
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	333	AGTTACAGAGTGTTC	CAAGTGC	CAATTC	CACCTAT	GTGCA	CAAGAGAA	ATGGA	ATATCTC	392
DB	1151	AGTTACAGAGTGTTC	CAAGTGC	CAATTC	CACCTAT	GTGCA	CAAGAGAA	ATGGA	ATATCTC	1210
QY	393	TGAACATACCTG	TAAATCAT	TGGTCC	CAAGAGGA	ATCAT	TGTGGAT	CCTCT	CAGCTCCATG	452
DB	1211	TGAACATACCTG	TAAATCAT	TGGTCC	CAAGAGGA	ATCAT	TGTGGAT	CCTCT	CAGCTCCATG	1270
QY	453	AAATAGTGTTC	CTCTG	AAACTT	CAAGGT	CCCTG	CCAGCT	CTCT	CAAGCAATGATTTT	512
DB	1271	AAATAGTGTTC	CTCTG	AAACTT	CAAGGT	CCCTG	CCAGCT	CTCT	CAAGCAATGATTTT	1330
QY	513	TATCTAGAAAAGCT	CAAGACTG	TATTTAT	TGAAGCT	GCAT	CACTGT	CCCTG	GAAATCACA	572
DB	1331	TATCTAGAAAAGCT	CAAGACTG	TATTTAT	TGAAGCT	GCAT	CACTGT	CCCTG	GAAATCACA	1390
QY	573	GTGGGATAGCAC	CAATTTCT	GGATCT	CAAGGG	CTGCAT	CTCT	GTGAT	CAAGACCACTC	632
DB	1391	GTGGGATAGCAC	CAATTTCT	GGATCT	CAAGGG	CTGCAT	CTCT	GTGAT	CAAGACCACTC	1450
QY	633	CATGCTCTT	CAGCAATA	TAATTA	ATCCACT	CTCA	AGGCT	CAAGAACT	CAGACGCTCGAGC	692
DB	1451	CATGCTCTT	CAGCAATA	TAATTA	ATCCACT	CTCA	AGGCT	CAAGAACT	CAGACGCTCGAGC	1510
QY	693	CTGTATAGCC	CAGCAGTGGAT	CCAGAC	CAAAAGG	GAAGACAT	TGTGA	ACCAATGACAG	752	
DB	1511	CTGTATAGCC	CAGCAGTGGAT	CCAGAC	CAAAAGG	GAAGACAT	TGTGA	ACCAATGACAG	1570	
QY	753	AAGCCTGCTT	ACAGTGC	TAGATGCC	CTTCT	GTCC	AGGACT	TTGAT	CATGAAGAGG	812
DB	1571	AAGCCTGCTT	ACAGTGC	TAGATGCC	CTTCT	GTCC	AGGACT	TTGAT	CATGAAGAGG	1630
QY	813	ACTATGAAC	TGTGTAGT	TACCA	AGCTT	CAAGG	ACCTCA	AAAGT	CAGACAATTTAGACA	872
DB	1631	ACTATGAAC	TGTGTAGT	TACCA	AGCTT	CAAGG	ACCTCA	AAAGT	CAGACAATTTAGACA	1690
QY	873	CTACTGACAT	CCAGGAGA	AGAAAT	TTC	CCAA	AGTTAT	TAGTAC	AAAAATTTGAAAGATAACA	932
DB	1691	CTACTGACAT	CCAGGAGA	AGAAAT	TTC	CCAA	AGTTAT	TAGTAC	AAAAATTTGAAAGATAACA	1750
QY	933	ACAATATGGGT	CTTAC	CGGAA	TACT	CTTG	TGGTTT	CTAGAT	CAACATCTTTAA	992
DB	1751	ACAATATGGGT	CTTAC	CGGAA	TACT	CTTG	TGGTTT	CTAGAT	CAACATCTTTAA	1810
QY	993	ATTACTTCA	AAATAA	AAAGCAT	GTG	TTTTC	CAAG	AGAAAT	TGTTTTCATAA	1052
DB	1811	ATTACTTCA	AAATAA	AAAGCAT	GTG	TTTTC	CAAG	AGAAAT	TGTTTTCATAA	1870
QY	1053	AAGGATATTTATA	1065							
DB	1871	AAGGATATTTATA	1883							

RESULT 9  
US-09-865-364-1  
; Sequence 1, Application US/09865364  
; Patent No. 6613521  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/865,364  
; PRIOR FILING DATE: 2003-05-25  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-09-865-364-1

Query Match 40.9%; Score 682; DB 4; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 1.2e-309;  
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	333	AGTTACAGAGTGTTC	CAAGTGC	CAATTC	CACCTAT	GTGCA	CAAGAGAA	ATGGA	ATATCTC	392
DB	1151	AGTTACAGAGTGTTC	CAAGTGC	CAATTC	CACCTAT	GTGCA	CAAGAGAA	ATGGA	ATATCTC	1210
QY	393	TGAACATACCTG	TAAATCAT	TGGTCC	CAAGAGGA	ATCAT	TGTGGAT	CCTCT	CAGCTCCATG	452
DB	1211	TGAACATACCTG	TAAATCAT	TGGTCC	CAAGAGGA	ATCAT	TGTGGAT	CCTCT	CAGCTCCATG	1270
QY	453	AAATAGTGTTC	CTCTG	AAACTT	CAAGGT	CCCTG	CCAGCT	CTCT	CAAGCAATGATTTT	512
DB	1271	AAATAGTGTTC	CTCTG	AAACTT	CAAGGT	CCCTG	CCAGCT	CTCT	CAAGCAATGATTTT	1330
QY	513	TATCTAGAAAAGCT	CAAGACTG	TATTTAT	TGAAGCT	GCAT	CACTGT	CCCTG	GAAATCACA	572
DB	1331	TATCTAGAAAAGCT	CAAGACTG	TATTTAT	TGAAGCT	GCAT	CACTGT	CCCTG	GAAATCACA	1390
QY	573	GTGGGATAGCAC	CAATTTCT	GGATCT	CAAGGG	CTGCAT	CTCT	GTGAT	CAAGACCACTC	632
DB	1391	GTGGGATAGCAC	CAATTTCT	GGATCT	CAAGGG	CTGCAT	CTCT	GTGAT	CAAGACCACTC	1450
QY	633	CATGCTCTT	CAGCAATA	TAATTA	ATCCACT	CTCA	AGGCT	CAAGAACT	CAGACGCTCGAGC	692
DB	1451	CATGCTCTT	CAGCAATA	TAATTA	ATCCACT	CTCA	AGGCT	CAAGAACT	CAGACGCTCGAGC	1510
QY	693	CTGTATAGCC	CAGCAGTGGAT	CCAGAC	CAAAAGG	GAAGACAT	TGTGA	ACCAATGACAG	752	
DB	1511	CTGTATAGCC	CAGCAGTGGAT	CCAGAC	CAAAAGG	GAAGACAT	TGTGA	ACCAATGACAG	1570	
QY	753	AAGCCTGCTT	ACAGTGC	TAGATGCC	CTTCT	GTCC	AGGACT	TTGAT	CATGAAGAGG	812
DB	1571	AAGCCTGCTT	ACAGTGC	TAGATGCC	CTTCT	GTCC	AGGACT	TTGAT	CATGAAGAGG	1630
QY	813	ACTATGAAC	TGTGTAGT	TACCA	AGCTT	CAAGG	ACCTCA	AAAGT	CAGACAATTTAGACA	872
DB	1631	ACTATGAAC	TGTGTAGT	TACCA	AGCTT	CAAGG	ACCTCA	AAAGT	CAGACAATTTAGACA	1690
QY	873	CTACTGACAT	CCAGGAGA	AGAAAT	TTC	CCAA	AGTTAT	TAGTAC	AAAAATTTGAAAGATAACA	932
DB	1691	CTACTGACAT	CCAGGAGA	AGAAAT	TTC	CCAA	AGTTAT	TAGTAC	AAAAATTTGAAAGATAACA	1750
QY	933	ACAATATGGGT	CTTAC	CGGAA	TACT	CTTG	TGGTTT	CTAGAT	CAACATCTTTAA	992
DB	1751	ACAATATGGGT	CTTAC	CGGAA	TACT	CTTG	TGGTTT	CTAGAT	CAACATCTTTAA	1810
QY	993	ATTACTTCA	AAATAA	AAAGCAT	GTG	TTTTC	CAAG	AGAAAT	TGTTTTCATAA	1052
DB	1811	ATTACTTCA	AAATAA	AAAGCAT	GTG	TTTTC	CAAG	AGAAAT	TGTTTTCATAA	1870
QY	1053	AAGGATATTTATA	1065							
DB	1871	AAGGATATTTATA	1883							



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QY 1053 AAGGATATTATA 1065
Db 1871 AAGGATATTATA 1883

RESULT 10
US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THEREOF
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-537-2

Query Match 40.9%; Score 682; DB 4; Length 1931;
Best Local Similarity 99.9%; Pred. No. 1.2e-309; Mismatches 0; Indels 0; Gaps 0;
Matches 732; Conservative 0;

QY 333 AGTTACAGAGTGTTCACAGTGCATTACCTATGTGACAAAGAAATGGAATATATCTC 392
Db 1151 AGTTACAGAGTGTTCACAGTGCATTACCTATGTGACAAAGAAATGGAATATATCTC 1210

QY 393 TGAACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
Db 1211 TGAACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270

QY 453 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 512
Db 1271 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 1330

QY 513 TATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTGGAATCACA 572
Db 1331 TATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTGGAATCACA 1390

QY 573 GTTGGGATAGCACCATTCTGGATCTCAAAGGGCTGCACTTCTGTGATCAAGACCACTC 632
Db 1391 GTTGGGATAGCACCATTCTGGATCTCAAAGGGCTGCACTTCTGTGATCAAGACCACTC 1450

QY 633 CATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACCTCTGCAGC 692
Db 1451 CATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACCTCTGCAGC 1510

QY 693 CTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGACAG 752
Db 1511 CTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGACAG 1570

QY 753 AAGCCTGCCTTAAACCAAGTCGTAGTGCCTTCTGTCCAGGGACTTGTATCATGAAAGAGG 812
Db 1571 AAGCCTGCCTTAAACCAAGTCGTAGTGCCTTCTGTCCAGGGACTTGTATCATGAAAGAGG 1630

QY 813 ACTATGAACCTTGTAGTACCAAGCCCTCAAGACCTCAAAAGTCAGACAAATTTACTAGACA 872
Db 1631 ACTATGAACCTTGTAGTACCAAGCCCTCAAGACCTCAAAAGTCAGACAAATTTACTAGACA 1690

QY 873 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932
Db 1691 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1750

QY 933 AACAAATGGTCTTCAGCCTTACCCGAAATACCTTGTGGTTTCTAGATCACCATCTTTAA 992
Db 1751 AACAAATGGTCTTTCAGCCTTACCCGAAATACCTTGTGGTTTCTAGATCACCATCTTTAA 1810

QY 993 ATTTACTTCAAAATAAAGCATGTAAAGTACCTGTTTTCAGAAAGAAATGCTTTTCATAA 1052
Db 1811 ATTTACTTCAAAATAAAGCATGTAAAGTACCTGTTTTCAGAAAGAAATGCTTTTCATAA 1870

QY 1053 AAGGATATTATA 1065
Db 1871 AAGGATATTATA 1883

RESULT 11
US-09-099-041A-3
; Sequence 3, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-099-041A-3

Query Match 37.9%; Score 632; DB 4; Length 1620;
Best Local Similarity 99.9%; Pred. No. 3e-286; Mismatches 1; Indels 0; Gaps 0;
Matches 682; Conservative 0;

QY 333 AGTTACAGAGTGTTCACAGTGCATTACCTATGTGACAAAGAAATGGAATATATCTC 392
Db 938 AGTTACAGAGTGTTCACAGTGCATTACCTATGTGACAAAGAAATGGAATATATCTC 997

QY 393 TGAACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
Db 998 TGAACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1057

QY 453 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 512
Db 1058 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 1117

QY 513 TATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTGGAATCACA 572
Db 1118 TATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTGGAATCACA 1177

QY 573 GTTGGGATAGCACCATTCTGGATCTCAAAGGGCTGCACTTCTGTGATCAAGACCACTC 632
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QY 633 CATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACCTCTGCAGC 692
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; Sequence 3, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/09/245,281  
; EARLIER FILING DATE: 1998-02-05  
; EARLIER APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-245-281-3  
Query Match 37.9%; Score 632; DB 4; Length 1620;  
Best Local Similarity 99.9%; Pred. No. 3e-286;  
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCCTGAACTTCAAGTGCATTCACCTATGTGCAAGAGAAATGGAATTAATCTC 392  
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Db 1358 AAGCGTCCCTTAACCACTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGG 1417  
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RESULT 13  
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; Sequence 3, Application US/09207359B  
; Patent No. 6469140  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/207,359B  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-207-359B-3  
Query Match 37.9%; Score 632; DB 4; Length 1620;  
Best Local Similarity 99.9%; Pred. No. 3e-286;  
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCCTGAACTTCAAGTGCATTCACCTATGTGCAAGAGAAATGGAATTAATCTC 392  
Db 938 AGTTACAGAGTGTTCCTGAACTTCAAGTGCATTCACCTATGTGCAAGAGAAATGGAATTAATCTC 997  
QY 393 TGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGATCCTCTCAGTCCATG 452  
Db 998 TGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGATCCTCTCAGTCCATG 1057  
QY 453 AAAATAGTGGTCTCTCTGAACTTCAAGTGCCTGCCAGTCCCTCAAGACAATGATTTTT 512  
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QY 513 TAICTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCATCTGTCTGGAATACACA 572  
Db 1118 TAICTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCATCTGTCTGGAATACACA 1177  
QY 573 GTTGGGATAGCACCATTCTTGGATCTCAAGGGCTGCATTCCTGATCACAAGACCCTC 632  
Db 1178 GTTGGGATAGCACCATTCTTGGATCTCAAGGGCTGCATTCCTGATCACAAGACCCTC 1237  
QY 633 CATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGCTGTCAGC 692  
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QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGGAACCAAAATGACAG 752  
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QY 753 AAGCCTGCTTAAACCAAGTCGCTAGATGCGCTTCTGTCCAGGACCTGTGATCATGAAGAGG 812
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DB 1598 ATTTACTTCAAAATAAAGCATG 1620

RESULT 14
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; Sequence 3, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
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US-09-340-620A-3

Query Match 37.9%; Score 632; DB 4; Length 1620;
Best Local Similarity 99.9%; Pred. No. 3e-286;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 452
DB 938 AGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 997
QY 393 TGAACATACCTGTAATCATGTGTCACCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 452
DB 998 TGAACATACCTGTAATCATGTGTCACCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 1057
QY 453 AAAATAGTGGTCTCTCGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTTTT 512
DB 1058 AAAATAGTGGTCTCTCGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTTTT 1117
QY 513 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCAGGACAAATGATTTTTT 572
DB 1118 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCAGGACAAATGATTTTTT 1177
QY 573 GTTGGATAGCACCATTTCTGGATCTCAAAAGGCTCATTCTGTGATCAAGACCAATC 632
DB 1178 GTTGGATAGCACCATTTCTGGATCTCAAAAGGCTCATTCTGTGATCAAGACCAATC 1237
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RESULT 15
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; Sequence 3, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-865-364-3

Query Match 37.9%; Score 632; DB 4; Length 1620;
Best Local Similarity 99.9%; Pred. No. 3e-286;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 392
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Job time : 162 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_nus:\*

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25: em\_gss\_rod:\*

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27: em\_gss\_vrl:\*

28: gb\_gsl1:\*

29: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 11	599	35.9	744	14	CD365404
C 12	592	35.5	592	9	AI745575
C 13	591	35.4	624	14	CD368863
C 14	571	34.2	628	12	BQ000991
C 15	556	33.3	938	13	BQ670832
C 16	554	33.2	636	10	BE551615
C 17	554	33.2	660	12	BM840808
C 18	548	32.8	683	14	CB852764
C 19	538	32.2	852	12	BG757422
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C 22	528	31.6	811	12	BG170405
C 23	520	31.2	615	9	AI801150
C 24	518	31.0	546	12	BQ013098
C 25	511	30.6	738	10	AW978568
C 26	510	30.6	641	10	AW150819
C 27	505	30.3	505	13	EX280487
C 28	500	30.0	1623	29	AY415527
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C 35	464	27.8	1623	29	AY415528
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C 37	461	27.6	870	10	BE877822
C 38	457	27.4	476	14	CF528565
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C 40	451	27.0	616	9	AI307810
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#### ALIGNMENTS

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DEFINITION CDNA clone CS0DK011Y17 3-PRIME, mRNA sequence.  
ACCESSION BX401255  
VERSION BX401255.1 GI:30610587  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1. (bases 1 to 1201)  
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4797.f For more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DK011AE09NP1&cluster=4797.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DK011AB09NP1.

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/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 50.08; Score 835; DB 13; Length 1201;
Best Local Similarity 99.78; Pred. No. 0;
Matches 985; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1052 GATCTCAAGGGCTGCAATTCGTGATCAAGACCACTCCATGCTCTTCAGCAATATAA 993
QY 654 ATCCACTCTCACTGCAAGAACTCAGAACGCTCTGCAGCCTGGTATAGCCCGACAGTGA 713
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DB 212 CCAGGCTTAATTCGCTACAAAGGCTTATTAATTTAAACTCCATATAGGATTACAT 153
QY 1494 TTTAAAGTTTATTTATGAATTCCTTTTAAATATGATTTTCAAGGTAAACAAATACAA 1553
DB 152 TTTAAAGTTTATTTATGAATTCCTTTTAAATATGATTTTCAAGGTAAACAAATACAA 93
QY 1554 TATAAGAAAAAATAAATATAATATAA 1581
DB 92 TATAAGAAAAAATAAATATAATATAA 65

RESULT 2
CA413941/c
LOCUS
DEFINITION
709 bp mRNA linear EST 07-NOV-2002
UI-H-EZO-bau-f-07-0-UI.s1 NCI CGAP Ch1 Homo sapiens cDNA clone
UI-H-EZO-bau-f-07-0-UI 3', mRNA sequence.
CA413941
ACCESSION
CA413941
VERSION
CA413941.1 GI:24776592
KEYWORDS
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
REFERENCE
1 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-64, >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. .709
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZO-bau-f-07-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ch1"
/notes="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch1 is a cDNA library containing the following
tissue (s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(AT)18 tail. The sequence tag for this library is
TGATCAGCT.
TAG_TISSUE=grade-2-chondrosarcoma.
TAG_LIB=UI-H-EZO
TAG_SEQ=ATCTAATATG"
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ORIGIN

Query Match 41.5%; Score 692; DB 14; Length 709;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 AAAAGCTCAAGCTGTTATTTATGAAGCTGATCACTGCTCTGGAATCAAGTTGGGA 579  
 DB 709 AAAAGCTCAAGCTGTTATTTATGAAGCTGATCACTGCTCTGGAATCAAGTTGGGA 650

QY 580 TAGCACCATTCTGATCTCAAGGGCTGCTTCTGTGATCAAGACCACTCCATGCTC 639  
 DB 649 TAGCACCATTCTGATCTCAAGGGCTGCTTCTGTGATCAAGACCACTCCATGCTC 590

QY 640 TTCAGCAATAAATATCACTCTCAACTGCAGAACTCAGAACCTCTGCAGCTGGTAT 699  
 DB 589 TTCAGCAATAAATATCACTCTCAACTGCAGAACTCAGAACCTCTGCAGCTGGTAT 530

QY 700 AGCCAGAGCTGGATCCAGAGCAAGGAAGGAGACATTTGTGAACCAATGACAGAGCCTG 759  
 DB 529 AGCCAGAGCTGGATCCAGAGCAAGGAAGGAGACATTTGTGAACCAATGACAGAGCCTG 470

QY 760 CTTAACCACTGCTAGATGCTCTCTGTCAGAGGACTTGTATCATGAAGAGGACTATGA 819  
 DB 469 CTTAACCACTGCTAGATGCTCTCTGTCAGAGGACTTGTATCATGAAGAGGACTATGA 410

QY 820 ACTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGACATTTACTAGACACTACTGA 879  
 DB 409 ACTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGACATTTACTAGACACTACTGA 350

QY 880 CATCAAGAGGAAGATTGTCAGAGTTATAGTACAAATTTGAAGATAACAAACAAT 939  
 DB 349 CATCAAGAGGAAGATTGTCAGAGTTATAGTACAAATTTGAAGATAACAAACAAT 290

QY 940 GGTCTTCAAGCTTACCGGAAATCTGTGCTTTCTAGATCACTCTTTAAATTTACT 999  
 DB 289 GGTCTTCAAGCTTACCGGAAATCTGTGCTTTCTAGATCACTCTTTAAATTTACT 230

QY 1000 TCAAAATAAAGCATGTAAGTCACTGTTTTCAGAGAAATGTGTTTCATAAAAGGATA 1059  
 DB 229 TCAAAATAAAGCATGTAAGTCACTGTTTTCAGAGAAATGTGTTTCATAAAAGGATA 170

QY 1060 TTTATATCTCTGCTTTGACTTTTTTATATAAAATCCCGTGAATTTAAAGCTTTTAT 1119  
 DB 169 TTTATATCTCTGCTTTGACTTTTTTATATAAAATCCCGTGAATTTAAAGCTTTTAT 110

QY 1120 GAAGTTCTTTGGTAAATATTTAGTCTCCCTCCATGACACTGACATTTTTTAAATA 1179  
 DB 109 GAAGTTCTTTGGTAAATATTTAGTCTCCCTCCATGACACTGACATTTTTTAAATA 50

QY 1180 ATCAAGTAAAGTTTGAATTTTGTACATA 1211  
 DB 49 ATCAAGTAAAGTTTGAATTTTGTACATA 18

RESULT 3  
 LOCUS AI824070/c  
 DEFINITION wj3507.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2404860 3' similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. 1; RNA sequence.

ACCESSION AI824070  
 VERSION AI824070.1 GI:5444741  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 738)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Insert Length: 432 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 460.

FEATURES

source  
 1. 738  
 /location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2404860"  
 /tissue\_type="2 pooled tumors (clear cell type)"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Kid12"  
 /note="Torean: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 40.6%; Score 677; DB 9; Length 738;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 727; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 942 GTCCTTCAGCCTTACCGGAAATCTGTGTTCTTAGATCACCATCTTTAAATTTACTTC 1001  
 DB 728 GTCCTTCAGCCTTACCGGAAATCTGTGTTCTTAGATCACCATCTTTAAATTTACTTC 669

QY 1002 AAAATAAAGCATGTAAGTCACTGTTTTCAAGAGAAATGTGTTTCATAAAGGATATT 1061  
 DB 668 AAAATAAAGCATGTAAGTCACTGTTTTCAAGAGAAATGTGTTTCATAAAGGATATT 609

QY 1062 TATATCTCTGTTGCTTTGACCTTTTTTATATAAAATCCGTGAGTATTAAAGCTTTATTGA 1121  
 DB 608 TATATCTCTGTTGCTTTGACCTTTTTTATATAAAATCCGTGAGTATTAAAGCTTTATTGA 549

QY 1122 AGGTTCTTTGGTAAATATTTAGTCTCCCTCCATGACACTGAGTATTTTTTTAAATTAAT 1181  
 DB 548 AGGTTCTTTGGTAAATATTTAGTCTCCCTCCATGACACTGAGTATTTTTTTAAATTAAT 489

QY 1182 ACAAGTAAAGTTGAAATTTTGCTACATAGTTCAATTTTTTATGTCCTCTTTTGTGTAACAG 1241  
 DB 488 ACAAGTAAAGTTGAAATTTTGCTACATAGTTCAATTTTTTATGTCCTCTTTTGTGTAACAG 429

QY 1242 AAACCACTTTTAAAGGATAGTAATTTCTTTGTTTATTAACAGTGCCTTAAGTATGATGT 1301  
 DB 428 AAACCACTTTTAAAGGATAGTAATTTCTTTGTTTATTAACAGTGCCTTTAAGTATGATGT 369

QY 1302 ATTTCTGATGAAGCATTTTTCACATTCATGTTCTTCATGGATTATTTGTTACTTGTCTTA 1361  
 DB 368 ATTTCTGATGAAGCATTTTTCACATTCATGTTCTTCATGGATTATTTGTTACTTGTCTTA 309

QY 1362 AGATGCAATTTGATTTTATGAAGTATATACCTTTTACCCACAGACAGTACAGAAATCC 1421  
 DB 308 AGATGCAATTTGATTTTATGAAGTATATACCTTTTACCCACAGACAGTACAGAAATCC 249

QY 1422 CTGCCCTAAATCCAGGCTTAATTTGCCCTCAAGAGGTTTATTAATTTAAACTCCATTA 1481  
 DB 248 CTGCCCTAAATCCAGGCTTAATTTGCCCTCAAGAGGTTTATTAATTTAAACTCCATTA 189

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QY 1482 TTAGGATTACATTTTAAAGTTTATTTATGAAATTCCTTTTAAATAATGATATTTCAAAGGT 1541
Db 188 TTAGGATTACATTTTAAAGTTTATTTATGAAATTCCTTTTAAATAATGATATTTCAAAGGT 129
QY 1542 AAAACAATACAAATATAAAGAAAAAATAAATATATTAATACCGGCTTCCTGTGCCCATTT 1601
Db 128 AAAACAATACAAATATAAAGAAAAAATAAATATATTAATACCGGCTTCCTGTGCCCATTT 69
QY 1602 TTAACCTCAGCCTTCCTACTGTCAACCAACCAAGCTTAATAAAGTCAACGCTGTAT 1661
Db 68 TTAACCTCAGCCTTCCTACTGTCAACCAACCAAGCTTAATAAAGTCAACGCTGTAT 9
QY 1662 GTGTAAAA 1669
Db 8 GTGTAAAA 1

RESULT 4
BO008463/c
LOCUS
DEFINITION
BO008463
ACCESSION
VERSION
BO008463.1 GI:19733364
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 734)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Tissue Procurement: Dr. Jose Mercuende
Contact: Robert Strausberg, Ph.D.
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..734
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IWAG:5840010"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP ED1"
/notes="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C85. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an Ecor I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAGGCT.
TAG_LIB=UI-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAGGCT"
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```
Query Match 39.8%; Score 665; DB 12; Length 734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 GTTCTCTCAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAA 521
Db 683 GTTCTCTCAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAA 624
QY 522 AGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATCAAGTTGGATA 591
Db 623 AGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATCAAGTTGGATA 564
QY 582 GCACCAATTTCTGATCTCAAAAGGCTGCATTTCTGTGATCACAAGACCACTCCATGTCTTT 641
Db 563 GCACCAATTTCTGATCTCAAAAGGCTGCATTTCTGTGATCACAAGACCACTCCATGTCTTT 504
QY 642 CAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCGCAGCCCTGTTATAG 701
Db 503 CAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCGCAGCCCTGTTATAG 444
QY 702 CCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGAGCCTGCC 761
Db 443 CCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGAGCCTGCC 384
QY 762 TTAACCAAGTCGCTAGATGCCCTTTCTGTCCAGGGACTTTGATCATGAAGAGGACTATGAAC 821
Db 383 TTAACCAAGTCGCTAGATGCCCTTTCTGTCCAGGGACTTTGATCATGAAGAGGACTATGAAC 324
QY 822 TTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGCAATTAAGTCTAGACACTTACTGACA 891
Db 323 TTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGCAATTAAGTCTAGACACTTACTGACA 264
QY 882 TCCAAGGAGAGCAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAAACAATGG 941
Db 263 TCCAAGGAGAGCAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAAACAATGG 204
QY 942 GTCTTCAGCCTTACCCGGAAATACCTTGTGTTTCTAGATCACCATCTTTAAATTTACTTC 1001
Db 203 GTCTTCAGCCTTACCCGGAAATACCTTGTGTTTCTAGATCACCATCTTTAAATTTACTTC 144
QY 1002 AAATAAAGCATGTAAGTGCATGTTTTTCAAGAGAATATGTTTTCAATAAAGGATATT 1061
Db 143 AAATAAAGCATGTAAGTGCATGTTTTTCAAGAGAATATGTTTTTCAATAAAGGATATT 84
QY 1062 TATATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAGCTTTATTGA 1121
Db 83 TATATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAGCTTTATTGA 24
QY 1122 AGGTT 1126
Db 23 AGGTT 19

RESULT 5
BG393551
LOCUS
DEFINITION
BG393551
ACCESSION
VERSION
BG393551.1 GI:13286999
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 883)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
BG393551 883 bp mRNA linear EST 12-MAR-2001
602411943F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4540787 5',
mRNA sequence.
BG393551
EST.
GI:13286999
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 883)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
```



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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10471 row: e column: 12
High quality sequence stop: 767.

FEATURES
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            /clone="IMAGE:4540787"
            /tissue_type="embryonal carcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH MGC 92"
            /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
            Average insert size 2.5 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: this is a NIH_MGC Library."

ORIGIN
Query Match      38.9%; Score 650; DB 12; Length 883;
Best Local Similarity 100.0%; Pred. No. 8e-308;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 TGTAAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGG 462
DB 1 TGTAAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGG 60
QY 463 TTCTCTCTGAAACTTCAAGGTCCCTCCAGCTCCTCTCAAGCAATGATTTTATCTAGAAA 522
DB 61 TTCTCTCTGAAACTTCAAGGTCCCTCCAGCTCCTCTCAAGCAATGATTTTATCTAGAAA 120
QY 523 AGCTCAAGACTGTATTTATGAAGCTGCATCACTCTCTCGGAATCAAGTTGGGATAG 582
DB 121 AGCTCAAGACTGTATTTATGAAGCTGCATCACTCTCTCGGAATCAAGTTGGGATAG 180
QY 583 CACCATTTCTGGATCTCAAGGGCTGATTTCTGTGATCAAGACCACTCCATGCTCTTC 642
DB 181 CACCATTTCTGGATCTCAAGGGCTGATTTCTGTGATCAAGACCACTCCATGCTCTTC 240
QY 643 AGCAATAATAAATCAACTCTCAACTCGAGAACTCAGAACGCTCTCGAGCTGGTATAGC 702
DB 241 AGCAATAATAAATCAACTCTCAACTCGAGAACTCAGAACGCTCTCGAGCTGGTATAGC 300
QY 703 CCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGAGCCTGCCT 762
DB 301 CCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGAGCCTGCCT 360
QY 763 TAACCACTGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGCACTATGAATCT 822
DB 361 TAACCACTGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGCACTATGAATCT 420
QY 823 TGTAGTACCAAGCCTACAGAGCACTCAAAAGTTCAGACAAATCTAGACACTACTGCACAT 882
DB 421 TGTAGTACCAAGCCTACAGAGCACTCAAAAGTTCAGACAAATCTAGACACTACTGCACAT 480
QY 883 CCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGG 942
DB 481 CCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGG 540
QY 943 TCTTAGCCTTACCGGAATATCTGTGGTTCTAGATCACCATCTTTAAATTTACTTCA 1002
DB 541 TCTTAGCCTTACCGGAATATCTGTGGTTCTAGATCACCATCTTTAAATTTACTTCA 600
QY 1003 AAATAAAGCATCTAAGTCACTCTTTTCAAGAGAAATGTGTTTCATAA 1052
DB 601 AAATAAAGCATCTAAGTCACTCTTTTCAAGAGAAATGTGTTTCATAA 650
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## RESULT 6

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BM557041
LOCUS
DEFINITION
    BM557041
    AGENCOURT 6561869 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5547645
    5' mRNA sequence.
ACCESSION
    BM557041
VERSION
    BM557041.1 GI:18798748
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 1081)
    NIH-MGC http://mgc.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12255 row: e column: 22
High quality sequence stop: 662.

FEATURES
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            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_72"
            /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
            Average insert size 2 kb. Library constructed by Life
            Technologies."

ORIGIN
Query Match      38.1%; Score 636; DB 12; Length 1081;
Best Local Similarity 100.0%; Pred. No. 5.8e-301;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1031 CAAGAAGAAATGCTTTTCATAAAGGATTTATATCTCTGTTGCTTTCACATTTTAT 1090
DB 1 CAAGAAGAAATGCTTTTCATAAAGGATTTATATCTCTGTTGCTTTCACATTTTAT 60
QY 1091 ATAAATCCGTCAGTATTAAAGCTTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCT 1150
DB 61 ATAAATCCGTCAGTATTAAAGCTTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCT 120
QY 1151 CCATGACACTGTCAGTATTTTTAAATTAATCAAGTAAAAAGTTTGAATTTTGTACAT 1210
DB 121 CCATGACACTGTCAGTATTTTTAAATTAATCAAGTAAAAAGTTTGAATTTTGTACAT 180
QY 1211 AGTTCAATTTTATGTCCTCTTTTGTATACAGAAACCACTTTTAAAGGATAGTAATTATTC 1270
DB 181 AGTTCAATTTTATGTCCTCTTTTGTATACAGAAACCACTTTTAAAGGATAGTAATTATTC 240
QY 1271 TTGTTTATAACAGTCCTTAAAGGTATGATTTCTGTATGGAAGCACTTTTTCACATTCA 1330
DB 241 TTGTTTATAACAGTCCTTAAAGGTATGATTTCTGTATGGAAGCACTTTTTCACATTCA 300
QY 1331 TGTCTCTCATGGATTTATTGTTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATA 1390
DB 301 TGTCTCTCATGGATTTATTGTTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATA 360
QY 1391 CCCTTTACCCACAGACAGTACAGATCCCTGCCCTTAAATCCAGAGCTTAATTGCC 1450
DB 361 CCCTTTACCCACAGACAGTACAGATCCCTGCCCTTAAATCCAGAGCTTAATTGCC 420
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QY 1451 TACAAAGGGTTATTAATTTAAACCTCCATTATTAGGATTACATTTTAAAGTTTTTATTTAT 1510
Db 421 TACAAAGGGTTATTAATTTAAACTCCATTATTAGGATTACATTTTAAAGTTTTTATTTAT 480
QY 1511 GAATTCCTCTTAAATATGATTTTCAAGGTAAACCAATACATTAATTAAGAAAAATAAA 1570
Db 481 GAATTCCTCTTAAATATGATTTTCAAGGTAAACCAATACATTAATTAAGAAAAATAAA 540
QY 1571 ATATATTAATACCGGCTTCCTGCTCCCATTTTAACTCAGCTTCCCTACTGTCACCAA 1630
Db 541 ATATATTAATACCGGCTTCCTGCTCCCATTTTAACTCAGCTTCCCTACTGTCACCAA 600
QY 1631 CAACAAAGCTTAAATTAAGTCAACAGCCTGATGTGTA 1666
Db 601 CAACAAAGCTTAAATTAAGTCAACAGCCTGATGTGTA 636

RESULT 7
BQ773811/c
LOCUS BQ773811 667 bp mRNA linear EST 26-JUL-2002
DEFINITION UI-H-EZ1-bbz-f-10-0-UI.s1 NCI CGAP_Ch2 Homo sapiens cDNA clone
          UI-H-EZ1-bbz-f-10-0-UI 3', mRNA sequence.
ACCESSION BQ773811
VERSION BQ773811.1 GI:21982287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 667)
          NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapsb-x@mail.nih.gov
          Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
          Orthopedics
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Clone distribution information can be obtained
          from Dr. M. Bento Soares, bento-soares@uiowa.edu
          Seq primer: M13 FORWARD
          POLYA=Yes
FEATURES             Location/Qualifiers
     source            1..667
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ1-bbz-f-10-0-UI"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="NCI CGAP Ch2"
                     /clone_lib="NCI CGAP Ch2"
     note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
          with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
          NCI CGAP_Ch2 is a normalized cDNA library containing the
          following tissue(s): Chondrosarcoma Grade II. The library
          was constructed according to Bonaldo, Lennon and Soares,
          Genome Research, 6:791-806, 1996. First strand cDNA
          synthesis was primed with an oligo-dT primer containing a
          Not I site. Double stranded cDNA was ligated to an EcoR I
          adaptor, digested with Not I, and cloned directionally
          into pT73-Pac vector. The oligonucleotide used to prime
          the synthesis of first-strand cDNA contains a library tag
          sequence that is located between the Not I site and the
          (dT)18 tail. The sequence tag for this library is
          TGATCAGCT.
          TAG_TISSUE=grade-2-chondrosarcoma
          TAG_LIB=UI-H-EZ1
          TAG_SEQ=ATCTAATATG"

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ORIGIN
Query Match      36.7%; Score 613; DB 13; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.3e-289;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 514 ATCTAGAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTACTGCTCGTGAATACAG 573
Db 631 ATCTAGAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTACTGCTCGTGAATACAG 572
QY 574 TTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCC 633
Db 571 TTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCC 512
QY 634 ATGCTCTTTCAGCAATATAAATCCACTCTCAACTGCAGGAAACTCAGAACTGTCAGGCC 693
Db 511 ATGCTCTTTCAGCAATATAAATCCACTCTCAACTGCAGGAACTCAGAACTGTCAGGCC 452
QY 694 TGTATAGCCCTAGCTGGATCCAGAGCAAAAGGGAAGCAATTTGTGAACCAATATGACAGA 753
Db 451 TGTATAGCCCTAGCTGGATCCAGAGCAAAAGGGAAGCAATTTGTGAACCAATATGACAGA 392
QY 754 AGCTCGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAGAGGA 813
Db 391 AGCTCGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAGAGGA 332
QY 814 CTATGAATCTGTAGTACCAAGCCTCAAGGACTCAAGGACTCAAGGACTCAAGGACTCAAGC 873
Db 331 CTATGAATCTGTAGTACCAAGCCTCAAGGACTCAAGGACTCAAGGACTCAAGGACTCAAGC 272
QY 874 TACTGATCTCAAGAGGAAGAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAACAA 933
Db 271 TACTGATCTCAAGAGGAAGAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAACAA 212
QY 934 AGAAATGGGTCTTCAGCCTTACCGGAATACCTTGTGGTTCTTAGATCACCATCTTTAA 993
Db 211 AGAAATGGGTCTTCAGCCTTACCGGAATACCTTGTGGTTCTTAGATCACCATCTTTAA 152
QY 994 TTTACTTTCAAAATATAAGCATGTAAGTACTGTTTTTCAAGAGAAGAAATGTTTCATAAA 1053
Db 151 TTTACTTTCAAAATATAAGCATGTAAGTACTGTTTTTCAAGAGAAGAAATGTTTCATAAA 92
QY 1054 AGGATATTTATATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAGC 1113
Db 91 AGGATATTTATATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAGC 32
QY 1114 TTTATTGAAGGTT 1126
Db 31 TTTATTGAAGGTT 19

RESULT 8
BQ773770/c
LOCUS BQ773770 656 bp mRNA linear EST 20-FEB-2003
DEFINITION UI-CF-EC1-ach-1-07-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
          UI-CF-EC1-ach-1-07-0-UI 3', mRNA sequence.
ACCESSION BQ773770
VERSION BQ773770.1 GI:19591361
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 656)
          Bonaldo, M.F., Lennon, G. and Soares, M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
          Genome Res. 6 (9), 791-806 (1996)
JOURNAL MEDLINE
PUBMED 97044477
COMMENT 8889548
          Contact: McCray, PB
          University of Iowa

```

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171

Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=yes.

FEATURES  
source

Location/Qualifiers  
1. .656  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-EC1-ach-1-07-0-UI"  
/tissue\_type="Lung"  
/dev\_stage="Adult and Fetal"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EC1"  
/note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-EC1 is a normalized CDNA library containing the  
following tissue(s): Normal lung from adult and from fetal  
day 64, day 87, week 19 and week 42. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pTT3-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
AAGTCTTAC.  
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371  
and 380-383  
TAG LIB=UI-CF-EC1  
TAG\_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 36.5%; Score 609; DB 12; Length 656;  
Best Local Similarity 100.0%; Pred. No. 1.2e-287;  
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 GTTCTCTGAACTTCAGAGTCCCTCCAGCTCTCAGACAAATGATTTTATCTAGAA 521  
DB 627 GTTCTCTGAACTTCAGAGTCCCTCCAGCTCTCAGACAAATGATTTTATCTAGAA 568  
QY 522 AAGCTCAAGACTGTTATTTATGAAGTGCATCTGCTGATCACAAGACCACTCATCTCTT 581  
DB 567 AAGCTCAAGACTGTTATTTATGAAGTGCATCTGCTGATCACAAGACCACTCATCTCTT 508  
QY 582 GCACCATTTCTGGATCTCAAAGGGTGCATTTCTGATCACAAGACCACTCATCTCTT 641  
DB 507 GCACCATTTCTGGATCTCAAAGGGTGCATTTCTGATCACAAGACCACTCATCTCTT 448  
QY 642 CAGCAATAATAATCACTCTCACTGCAAGGAACTCAGAACTGCGAGCTGTGTATAG 701  
DB 447 CAGCAATAATAATCACTCTCACTGCAAGGAACTCAGAACTGCGAGCTGTGTATAG 388  
QY 702 CCCAGCTGGATCAGAGCAAAAGGGAGACATTTGTAACCAATGACAGAGCTGCC 761  
DB 387 CCCAGCTGGATCAGAGCAAAAGGGAGACATTTGTAACCAATGACAGAGCTGCC 328  
QY 762 TTAACCAAGCTCGTAGTGCCTTCTGTCAGGGACTTGTATCATGAAGAGGACTATGAAC 821  
DB 327 TTAACCAAGCTCGTAGTGCCTTCTGTCAGGGACTTGTATCATGAAGAGGACTATGAAC 268  
QY 822 TTGTTAGTACCAGGCTACAGGACCTCAAAGTCCAGACAAATTAAGTACTGACACTGAC 881

Db 267 TTGTTAGTACCAGGCTACAAAGGACCTCAAAGTCCAGACAAATTAAGTACTGACACTGAC 208  
QY 882 TCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTCGAAAGATACAAACAAATGG 941  
DB 207 TCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTCGAAAGATACAAACAAATGG 148  
QY 942 GTCTTCAGCTTACCCGGAATATCTGTGGTTCTAGATCACCACCTCTTTAAATTTACTTC 1001  
DB 147 GTCTTCAGCTTACCCGGAATATCTGTGGTTCTAGATCACCACCTCTTTAAATTTACTTC 88  
QY 1002 AAAATAAAGCATGTAGTACTGCTTTTCAAGAGAAATGCTTTCAATAAAGCATATT 1061  
DB 87 AAAATAAAGCATGTAGTACTGCTTTTCAAGAGAAATGCTTTTCAATAAAGCATATT 28  
QY 1062 TATATCTCT 1070  
DB 27 TATATCTCT 19  
RESULT 9  
CB851847/c  
LOCUS CB851847 715 bp mRNA linear EST 22-APR-2003  
DEFINITION UI-CF-FNO-aem-o-20-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
ACCESSION CB851847  
VERSION CB851847.1 GI:30046667  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 715)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: McCray, PB  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
The following repetitive elements were found in this cDNA  
sequence: 1-24, >AT-rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=yes.

FEATURES  
source

Location/Qualifiers  
1. .715  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-FNO-aem-o-20-0-UI"  
/tissue\_type="Human Lung Epithelial cells"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-FNO"  
/note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-FNO is a subtracted cDNA library derived from two  
normalized Human lung epithelial cell libraries (EN1 and  
DU1). The library was subtracted according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. For additional information, contact:

bento-soares@uiowa.edu  
TAG\_SEQ=None found"

ORIGIN

Query Match 36.2%; Score 604; DB 14; Length 715;  
Best Local Similarity 100.0%; Pred. No. 3.3e-285;  
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 GTTCTCTGAACTTCAAGGTCCTCGCAGCTCTCAAGCAATGATTTTATCTAGAA 521  
DB 619 GTTCTCTGAACTTCAAGGTCCTCGCAGCTCTCAAGCAATGATTTTATCTAGAA 560

QY 522 AAGCTCAAGCTGTTATTTATGAAGCTGCATCACTCTCTGGAATACACAGTTGGGATA 581  
DB 559 AAGCTCAAGCTGTTATTTATGAAGCTGCATCACTCTCTGGAATACACAGTTGGGATA 500

QY 582 GCACCATTTCTGATCTCAAGGCTGATTTCTGTGATCAAGACCACTCCATGCTCTT 641  
DB 499 GCACCATTTCTGATCTCAAGGCTGATTTCTGTGATCAAGACCACTCCATGCTCTT 440

QY 642 CAGCAATAATAAATCCACTCTCAACTCAGGAACTCAGAACTGCTGAGCTGGTATAG 701  
DB 439 CAGCAATAATAAATCCACTCTCAACTCAGGAACTCAGAACTGCTGAGCTGGTATAG 380

QY 702 CCCAGCAGTGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCCTGCC 761  
DB 379 CCCAGCAGTGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCCTGCC 320

QY 762 TTAACCACTGCTAGATGCTCTCTGCTGAGGACTTGATCATGAAAGGACTATGAAC 821  
DB 319 TTAACCACTGCTAGATGCTCTCTGCTGAGGACTTGATCATGAAAGGACTATGAAC 260

QY 822 TTGTTAGTACCAAGCTTACAGGACCTCAAAAGTACAGCAATTTACTAGACACTACTGACA 881  
DB 259 TTGTTAGTACCAAGCTTACAGGACCTCAAAAGTACAGCAATTTACTAGACACTACTGACA 200

QY 882 TCCAGAGAGAAGATTTGCCAAGTTATAGTACAAAATTTGAAGATAACAAATGG 941  
DB 199 TCCAGAGAGAAGATTTGCCAAGTTATAGTACAAAATTTGAAGATAACAAATGG 140

QY 942 GTCTTCAGCTTACCCGGAATCTGTGCTTTCTAGATCACCATCTTTAAATTTACTTC 1001  
DB 139 GTCTTCAGCTTACCCGGAATCTGTGCTTTCTAGATCACCATCTTTAAATTTACTTC 80

QY 1002 AAAATAAAGCATGTAGTGACTGTTTTCAGAGAAATGTTTTCATAAAGAGATAT 1061  
DB 79 AAAATAAAGCATGTAGTGACTGTTTTCAGAGAAATGTTTTCATAAAGAGATAT 20

QY 1062 TATA 1065  
DB 19 TATA 16

RESULT 10  
B0774940/c  
LOCUS  
DEFINITION  
UI-H-FHO-bcd-1-20-0-UI.s1 NCI CGAP FHO Homo sapiens cDNA clone  
UI-H-FHO-bcd-1-20-0-UI 3', mRNA sequence.  
B0774940  
VERSION  
B0774940.1 GI:21983416  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 721)  
REFERENCE  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: James Martin

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, bento-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 1-22, >AT rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

#### FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FHO-bcd-1-20-0-UI"  
/tissue\_type="Human Chondrosarcoma Cell Line"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP\_FHO"  
/note="Organ: Bone; Vector: p77T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP FHO is a cDNA library containing the following  
tissue(s): Human Grade 1 Chondrosarcoma Cell Line The  
library was constructed according to Bonaldo, Lennon and  
Soares, Genome Research, 6:791-806, 1996. First strand  
cDNA synthesis was primed with an oligo-dT primer  
containing a Not I site. Double stranded cDNA was ligated  
to an EcoR I adaptor, digested with Not I, and cloned  
directionally into p77T3-Pac vector. The oligonucleotide  
used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dT)18 tail. The sequence tag for this  
library is AGAATCCGGC. The cell line was provided by Dr  
James Martin from University of Iowa  
TAG\_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1  
Chondrosarcoma  
TAG\_LIB=UI-H-FHO  
TAG\_SEQ=AGAATCCGGC"

#### ORIGIN

Query Match 35.9%; Score 599; DB 13; Length 721;  
Best Local Similarity 99.8%; Pred. No. 9.4e-283;  
Matches 649; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 462 GTTCTCTGAACTTCAAGTCCCTCGCAGCTCTCAAGCAATGATTTTATCTAGAA 521  
DB 665 GTTCTCTGAACTTCAAGTCCCTCGCAGCTCTCAAGCAATGATTTTATCTAGAA 606

QY 522 AAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAATACACAGTTGGGATA 581  
DB 605 AAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAATACACAGTTGGGATA 546

QY 582 GCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTCCATGCTCTT 641  
DB 545 GCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTCCATGCTCTT 486

QY 642 CAGCAATAATAAATCCACTCTCAACTGAGGAACTCAGAACTGCTGAGCTGCTATAG 701  
DB 485 CAGCAATAATAAATCCACTCTCAACTGAGGAACTCAGAACTGCTGAGCTGCTATAG 426

QY 702 CCCAGCAGTGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCCTGCC 761  
DB 425 CCCAGCAGTGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCCTGCC 366

QY 762 TTAACCACTGCTAGATGCTCTCTGCTGAGGACTTGATCATGAAAGGACTATGAAC 821  
DB 365 TTAACCACTGCTAGATGCTCTCTGCTGAGGACTTGATCATGAAAGGACTATGAAC 306

QY 822 TTGTTAGTACCAAGCTTACAGGACCTCAAAAGTACAGCAATTTACTAGACACTACTGACA 881  
DB 305 TTGTTAGTACCAAGCTTACAGGACCTCAAAAGTACAGCAATTTACTAGACACTACTGACA 246

QY 882 TCCAGAGAGAAGATTTGCCAAGTTATAGTACAAAATTTGAAGATAACAAATGG 941

```

245 TCAAAGGAGAAATTTGCAAGTTATAGTACAAAATTTGAAGATACAAACAAATGG 186
942 GTCCTCAGCCTTACCCGGAATACTGTGGTTCTTAGATCACCATCTTTAAATTTACTTC 1001
185 GTCCTCAGCCTTACCCGGAATACTGTGGTTCTTAGATCACCATCTTTAAATTTACTTC 126
1002 AAAATAAAGCATGTAAAGTACGTGTTTTCAAGAGAAATGTGTTTCATPAAAGGATATT 1061
125 AAAATAAAGCATGTAAAGTACGTGTTTTCAAGAGAAATGTGTTTCATPAAAGGATATT 66
1062 TATATCTGTGCTTGTGCTTTTATATATAAATCCGTGAGTATATA 1111
65 TATATCTGTGCTTGTGCTTTTATATATAAATCCGTGAGTATATA 16

RESULT 11
LOCUS CD365404/c
DEFINITION UI-H-FT2-bj-j-h-03-0-UI.81 NCI CGAP FT2 Homo sapiens cDNA clone
ACCESSION CD365404
VERSION CD365404.1 GI:31149494
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES             Location/Qualifiers
     1..744
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         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="UI-H-FT2-bj-j-h-03-0-UI"
         /tissue_type="Aveolar Macrophage"
         /dev_stage="Adult"
         /lab_host="DH10B (Life Technologies)"
         /clone_lib="NCI CGAP FT2"
         /note="Organ: lung; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
subtracted according to Ronaldo, Lennon and Soares' Genome
Research, 6:791-806, 1996. The tissue was provided by Dr.
Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LTB=UI-H-FT2
TAG_SEQ=GGCCATCGCG"

ORIGIN
Query Match          35.9%; Score 599; DB 14; Length 744;
Best Local Similarity 99.8%; Pred. No. 9.3e-283;
Matches 649; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

387 TATCTCTGAACATACCTGTAAATCATGTGTCACAGAGCAATCATGTGGATCCTCTCAGC 446
664 TATCTCTGAACATACCTGTAAATCATGTGTCACAGAGCAATCATGTGGATCCTCTCAGC 605

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QY 447 TCCATGAAAAATAGTGGTTCTCCTGAAAATTCAAGTCCCTGCCAGCTCCTCAAGACAATG 506
Db 604 TCCATGAAAAATAGTGGTTCTCCTGAAAATTCAAGTCCCTGCCAGCTCCTCAAGACAATG 545
QY 507 ATTTTTCATCTAGAAAAGCTCAAGACTCTTATTTTATGAAGCTGCATCACTGCTCTGGAA 566
Db 544 ATTTTTCATCTAGAAAAGCTCAAGACTCTTATTTTATGAAGCTGCATCACTGCTCTGGAA 485
QY 567 ATCAGAGTTGGGATAGCACCATTCTTCGATCTCAAAAGGCTGCATTTCTGTGATCAACA 626
Db 484 ATCAGAGTTGGGATAGCACCATTCTTCGATCTCAAAAGGCTGCATTTCTGTGATCAACA 425
QY 627 CCATCTCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTC 686
Db 424 CCATCTCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTC 365
QY 687 TGCAGCCTGGTATAGCCCGCAGAGTGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAA 746
Db 364 TGCAGCCTGGTATAGCCCGCAGAGTGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAA 305
QY 747 TGACAGAAAGCCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGAGCTTGTGATCATGA 806
Db 304 TGACAGAAAGCCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGAGCTTGTGATCATGA 245
QY 807 AAGAGGACTATGAATCTGTTAGTACCAAGCCTTCAAGGACCTCAAAAGTTCAGACAATTAC 866
Db 244 AAGAGGACTATGAATCTGTTAGTACCAAGCCTTCAAGGACCTCAAAAGTTCAGACAATTAC 185
QY 867 TAGACACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAG 926
Db 184 TAGACACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAG 125
QY 927 ATAACAAAATAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTTAGATCACCAT 986
Db 124 ATAACAAAATAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTTAGATCACCAT 65
QY 987 CTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAA 1036
Db 64 CTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAA 15

RESULT 12
LOCUS AI745575/c
DEFINITION wc34f12.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2317103.3,
similar to TR:O43353 O43353 SERINE/THREONINE KINASE RICK. ;, mRNA
sequence.
ACCESSION AI745575
VERSION AI745575.1 GI:5113863
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 673 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 459.

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FEATURES  
source

Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:2317103"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Pr28"  
/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI\_CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones IDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

Query Match 35.5%; Score 592; DB 9; Length 592;  
Best Local Similarity 100.0%; Pred. No. 2.7e-279; Mismatches 0; Indels 0; Gaps 0;  
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 473 ACTTCAAGGTCCTCCAGAGCAATGATTTTATCTAGAAAAGCTCAAGAC 532  
Db 592 ACTTCAAGGTCCTCCAGAGCAATGATTTTATCTAGAAAAGCTCAAGAC 533  
Qy 533 TGTATTATTAGAGTCGATCATCTGCTGGAAATCACAGTGGGATAGACATTCT 592  
Db 532 TGTATTATTAGAGTCGATCATCTGCTGGAAATCACAGTGGGATAGACATTCT 473  
Qy 593 GGATCTCAAGGGCTGATCTTGATCAAGACCACTCCATGCTCTTCAAGAAATAA 652  
Db 472 GGATCTCAAGGGCTGATCTTGATCAAGACCACTCCATGCTCTTCAAGAAATAA 413  
Qy 653 AATCCACTCTCACTGAGGAAACTCAGAAAGCTGAGCTGGTATAGCCAGCTGG 712  
Db 412 AATCCACTCTCACTGAGGAAACTCAGAAAGCTGAGCTGGTATAGCCAGCTGG 353  
Qy 713 ATCCAGAGCAAAAGGAGACATTTGCAACCAATGACAGAGCTGCTTACCACTCG 772  
Db 352 ATCCAGAGCAAAAGGAGACATTTGCAACCAATGACAGAGCTGCTTACCACTCG 293  
Qy 773 CTAGATGCCCTTCTGTCCAGGACTTGTATGAAAGAGCACTATGAACTTTGTAGTACC 832  
Db 292 CTAGATGCCCTTCTGTCCAGGACTTGTATGAAAGAGCACTATGAACTTTGTAGTACC 233  
Qy 833 AAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACACTACTGATCCAGGAGAA 892  
Db 232 AAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACACTACTGATCCAGGAGAA 173  
Qy 893 GAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGTCTTCAGCCT 952  
Db 172 GAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGTCTTCAGCCT 113  
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Db 112 TACCCGAAATACATTGTGGTTTCTAGATCAACCTTTTAAATTTACTTCAAAATAAAGC 53  
Qy 1013 ATGTAAGTGAAGTCTTTTTCAGAGAAATGTTTTCATAAAGATATTTAT 1064  
Db 52 ATGTAAGTGAAGTCTTTTTCAGAGAAATGTTTTCATAAAGATATTTAT 1

## RESULT 13

CD368863/c  
LOCUS 624 bp mRNA linear EST 29-MAY-2003  
DEFINITION UI-H-Ftl1-bjx-o-04-0-UI.sl NCI\_CGAP\_Ftl1 Homo sapiens cDNA clone  
UI-H-Ftl1-bjx-o-04-0-UI 3', mRNA sequence.  
ACCESSION CD368863  
VERSION CD368863.1 GI:31152953

KEYWORDS  
SOURCE  
ORGANISM

EST.  
Homo sapiens (human)  
Homo sapiens

REFERENCE  
1 (bases 1 to 624)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS  
TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

Location/Qualifiers

1..624

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-H-Ftl1-bjx-o-04-0-UI"

/tissue\_type="Aveolar Macrophage"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI\_CGAP\_Ftl1"

/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI\_CGAP\_Ftl1 is a normalized cDNA library constructed from

a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The library was

normalized according to Bonaldo, Lennon and Soares, Genome

Research, 6:791-806, 1996. First strand cDNA synthesis was

performed with an oligo-dT primer containing a Not I site.

Doubled stranded cDNA was ligated to an EcoR I adaptor,

digested with Not I, and cloned directionally into

p7T3-Pac vector. The oligonucleotide used to prime the

synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

GGCCATGGCG. The tissue was provided by Dr. Gary W.

Hunninghake of the University of Iowa.

TAG\_TISSUE=Human Lung Aveolar Macrophage

TAG\_LIB=UI-H-Ftl1

TAG\_SEQ=GGCCATGGCG"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.2e-279; Mismatches 0; Indels 0; Gaps 0;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 624 GGGCTGCACTTGTGATCAACAAGACCACTCCATGCTCTTTCAGCAATAATAATCCACTCT 565

Qy 663 CAACTGCGAGAACTCAGAAAGCTGCGAGCTGGTATAGCCAGAGTGGATCCAGAGCA 722

Db 564 CAACTGCGAGAACTCAGAAAGCTGCGAGCTGGTATAGCCAGAGTGGATCCAGAGCA 505

Qy 723 AAAGGGAAGACATTGTGAACCAATGACAGAGCTGCTTAAACCAGTGCCTAGATGCC 782

Db 504 AAAGGGAAGACATTGTGAACCAATGACAGAGCTGCTTAAACCAGTGCCTAGATGCC 445

Qy 783 TTCTGTCCAGGACTTGTATCATGAAGAGGACTATGAACCTTGTAGTACCAAGCTACAA 842

Db 444 TTCTGTCCAGGACTTGTATCATGAAGAGGACTATGAACCTTGTAGTACCAAGCTACAA 385

Qy 843 GGACCTCAAAAGCTCAGACAAATTACTAGACACTTACTGACATCCCAAGGAGAAATTTGCCA 902

Db 384 GGACCTCAAAAGTCAGACAAATTAAGACACTACTGACATCCAGAGAGAAATTTGCCA 325

QY 903 AAGTTATAGTACAAAATTTAAAGATAACAAACAAATGGGTCTTCAGCCCTTACCCGGAAA 962

Db 324 AAGTTATAGTACAAAATTTAAAGATAACAAACAAATGGGTCTTCAGCCCTTACCCGGAAA 265

QY 963 TACTTGTGGTTTCTAGATCACCATCTTTTAAATTTACTTCAAAATTAAGAGATGTAAGTGA 1022

Db 264 TACTTGTGGTTTCTAGATCACCATCTTTTAAATTTACTTCAAAATTAAGAGATGTAAGTGA 205

QY 1023 CTGTTTTTCAAGAGAAATGTGTTTCATAAAAGGATATTTATATCTCTCTGCTTTGACT 1082

Db 204 CTGTTTTTCAAGAGAAATGTGTTTCATAAAAGGATATTTATATCTCTCTGCTTTGACT 145

QY 1083 TTTTTTATATAAAATCCCGTGTGATTTAAAGCTTTTATGAAGTCTCTTTGGGTAATATTA 1142

Db 144 TTTTTTATATAAAATCCCGTGTGATTTAAAGCTTTTATGAAGTCTCTTTGGGTAATATTA 85

QY 1143 GTCTCCCTCCATGACACTGACATCTTTTAAATTTAAATTAAGTAAGTAAGAAAG 1193

Db 84 GTCTCCCTCCATGACACTGACATCTTTTAAATTTAAATTAAGTAAGTAAGAAAG 34

RESULT 14

BQ000991/c

LOCUS

DEFINITION

UI-H-DH1-awt-c-10-0-UI.s1 NCI CGAP DH1 Homo sapiens cDNA clone

IMAGE:5823297 3', mRNA sequence.

ACCESSION

BQ000991

VERSION

Q000991.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1. (bases 1 to 628)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-r@mail.nih.gov

TISSUE PREPARATION: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

The following repetitive elements were found in this cDNA sequence: 1-60, >AT rich#Low complexity (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

1..628

/organism="Homo sapiens"

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/db\_xref="taxon:9606"

/clone="IMAGE:5823297"

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/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP DH1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR 1; Site\_2: Not I; NCI CGAP DH1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTTGC.

TAG\_TISSUE=lung

TAG\_LIB=UI-H-DH1

TAG\_SEQ=AGATCATTTGC"

ORIGIN

Query Match 34.2%; Score 571; DB 12; Length 628;

Best Local Similarity 100.0%; Pred. No. 5.5e-269;

Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 588 CTCCTTACCAATATAAATCCACTCTCAACTCCAGAGAACTCAGAACGCTCTGCAGCCTGG 529

QY 697 TATAGCCAGAGTGGATCCAGAGCAAAAGGAGGACATTTGTAACCAATGACAGAACG 756

Db 528 TATAGCCAGAGTGGATCCAGAGCAAAAGGAGGACATTTGTAACCAATGACAGAACG 469

QY 757 CTGCTTTAACCAAGTCCGCTAGATGCCCTTCTGTCCAGGAGCTTGTATGATGAAAGGACTA 816

Db 468 CTGCTTTAACCAAGTCCGCTAGATGCCCTTCTGTCCAGGAGCTTGTATGATGAAAGGACTA 409

QY 817 TGAATCTGTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCCAGACATTTACTAGACACTAC 876

Db 408 TGAATCTGTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCCAGACATTTACTAGACACTAC 349

QY 877 TGACATCCCAAGGAGAGAAATTTGCCAAAGTATATAGTACAAAATTTCAAGAGTAACAACA 936

Db 348 TGACATCCCAAGGAGAGAAATTTGCCAAAGTATATAGTACAAAATTTCAAGAGTAACAACA 289

QY 937 AATGGGTCTTACGCTTACCCGGAAATATCTGTGGTTCTAGATCACCATCTTTAAATTT 996

Db 288 AATGGGTCTTACGCTTACCCGGAAATATCTGTGGTTCTAGATCACCATCTTTAAATTT 229

QY 997 ACTTCAAAATAAAGCATGTAGTCACTGTGTTTTTCAAGAGAAATGTGTTTCAATAAAGG 1056

Db 228 ACTTCAAAATAAAGCATGTAGTCACTGTGTTTTTCAAGAGAAATGTGTTTCAATAAAGG 169

QY 1057 ATATTATATCTCTGCTTGTGCTTTTATATATAAATCCGTGAGTATTAAAGCTTT 1116

Db 168 ATATTATATCTCTGCTTGTGCTTTTATATATAAATCCGTGAGTATTAAAGCTTT 109

QY 1117 ATTGAAGTCTTCTTGGGTAATATTTAGTCTCCCTCCATGACACTGCAGTATTTTTTTAA 1176

Db 108 ATTGAAGTCTTCTTGGGTAATATTTAGTCTCCCTCCATGACACTGCAGTATTTTTTTAA 49

QY 1177 TTAATACAAAGTAAAGTTGAATTTTGCTA 1207

Db 48 TTAATACAAAGTAAAGTTGAATTTTGCTA 18

RESULT 15

BQ670832

LOCUS

DEFINITION

AGENCOURT 8191703 NIH\_MGC\_102 Homo sapiens cDNA clone IMAGE:6257019

5', mRNA sequence.

ACCESSION

BQ670832

VERSION

BQ670832.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1. (bases 1 to 938)

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory



cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM2410 row: k column: 04  
 High quality sequence spot: 659

## FEATURES

source

## ORIGIN

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Best local Similarity	.100.0%;	Prod. No. 1.2e-261;		
Matches 556;	Conservative 0;	Mismatches 261;	Indels 0;	Gaps 0;
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Qy	393	TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGTCCCATG	452	
Db	197	TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGTCCCATG	256	
Qy	453	AAAATAGTGGTTCCTCTGAAACTTCAAGGTCCTCGCCAGCTCCTCAAGACAATGATTTTT	512	
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Qy	513	TATCTAGAAAAGCTCAAGACTGTTATTTTTATGAAGCTGCATCAGCTCCTCGAAAATCACA	572	
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Qy	573	GTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCATCTC	632	
Db	377	GTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCATCTC	436	
Qy	633	CATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACTCTGCAGC	692	
Db	437	CATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACTCTGCAGC	496	
Qy	693	CTGTTATAGCCACGACGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAAACCAATGACAG	752	
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Qy	753	AAGCCTGCTTTAAACAGTCGCTAGTAGTGCCTTCTGTCCAGGGACTTGTATCATGAAGAGG	812	
Db	557	AAGCCTGCTTTAAACAGTCGCTAGTAGTGCCTTCTGTCCAGGGACTTGTATCATGAAGAGG	616	
Qy	813	ACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAAGTCAGACAATTTACTAGACA	872	
Db	617	ACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAAGTCAGACAATTTACTAGACA	676	
Qy	873	CTACTGACATCCAAGG	888	
Db	677	CTACTGACATCCAAGG	692	

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Job time : 4665 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:28:33 ; Search time 24 Seconds  
(without alignments)  
7180.312 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 531

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Word size: 20

Total number of hits satisfying chosen parameters: 25

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -CALIGN=200 -THR SCORE=quality -THR MIN=20  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	227	42.7	478	4	US-09-069-023-4
3	227	42.7	530	4	US-09-069-023-3
4	227	42.7	531	4	US-09-069-023-1
5	227	42.7	540	4	US-09-069-023-27
6	227	42.7	540	4	US-09-345-473E-28
7	167	31.5	167	4	US-09-069-023-6
8	128	24.1	540	3	US-09-019-942-1
9	128	24.1	540	4	US-09-099-041A-2
10	128	24.1	540	4	US-09-245-281-2
11	128	24.1	540	4	US-09-470-271-1
12	128	24.1	540	4	US-09-207-359B-2

ALIGNMENTS

RESULT 1

US-09-069-023-5  
; Sequence 5, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-5

Alignment Scores:

Pred. No.: 5,51e-232 Length: 284  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-5 (1-284)

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QY	395	AACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCATGAA	454	
DB	78	AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	97	
QY	455	AATAGTGGTTCCTGAAATTC	CAAGGTCCTTCAGAGCAATGATTTT	514
DB	98	AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	117	
QY	515	TCTAGAAAAGCTCAGACTGTATTTATGAAGCTGCATCAGTCTCTGGAATACAGT	574	
DB	118	SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer	137	
QY	575	TGGGATAGCACCATTTC	TGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCCTCCA	634
DB	138	trpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro	157	
QY	635	TGCTCTTCAGCAATATAATCACTCTCAACTGAGGAAACTCAGACGCTCTGACGCT	694	
DB	158	CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro	177	
QY	695	GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGACCAATGACAGAA	754	

Db 178 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 197  
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Db 198 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 217  
QY 815 TATCAACTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACAATTAAGTACAGACT 874  
Db 218 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 237  
QY 875 ACTGACATCCAAAGAGAAATTTGCCAAAGTTATAGTACAAAAATTAAGAGATAACAAA 934  
Db 238 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 257  
QY 935 CAATGGCTCTTACGCTTACCCGGAATCTTGGTTCTAGATCACCATCTTTAAAT 994  
Db 258 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 277  
QY 995 TTACTTCAAAATAAAGCATG 1015  
Db 278 LeuLeuGlnAsnLysSerMet 284

## RESULT 2

US-09-069-023-4  
; Sequence 4, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 478  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-4

Alignment Scores:  
Pred. No.: 5,3e-232 Length: 478  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-4 (1-478)

QY 335 TTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATATCTCTG 394  
Db 252 LeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 271  
QY 395 AACATACCTCTAAATCATGTGCACAGAGCAATCATGTGATCCTCTCAGCTCCATGAA 454  
Db 272 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 291  
QY 455 AATAGTGTTCCTGTAACCTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 514  
Db 292 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 311  
QY 515 TCTAGAAAAGCTCAAGACTGTATTTATGAGCTGCATCTGTCGATCACAAGACCACTCA 574  
Db 312 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 331  
QY 575 TGGGATAGCACCAATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTCA 634  
Db 332 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 351

QY 635 TGCTCTTCACCAATAATAATCCACTCTCACTGCAGGAAACTCAGAACTCTGCAGCCT 694  
Db 352 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 371  
QY 695 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTGTGAACCAATGACAGAA 754  
Db 372 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 391  
QY 755 GCCTGCCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGGAC 814  
Db 392 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 411  
QY 815 TATCAACTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACAATTAAGTACAGACT 874  
Db 412 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 431  
QY 875 ACTGACATCCAAAGAGAAATTTGCCAAAGTTATAGTACAAAAATTAAGAGATAACAAA 934  
Db 432 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 451  
QY 935 CAATGGCTCTTACGCTTACCCGGAATCTTGGTTCTAGATCACCATCTTTAAAT 994  
Db 452 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 471  
QY 995 TTACTTCAAAATAAAGCATG 1015  
Db 472 LeuLeuGlnAsnLysSerMet 478

## RESULT 3

US-09-069-023-3  
; Sequence 3, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-3

Alignment Scores:  
Pred. No.: 5,26e-232 Length: 530  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-3 (1-530)

QY 335 TTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATATCTCTG 394  
Db 304 LeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 323  
QY 395 AACATACCTCTAAATCATGTGCACAGAGCAATCATGTGATCCTCTCAGCTCCATGAA 454  
Db 324 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 343  
QY 455 AATAGTGTTCCTGTAACCTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 514  
Db 344 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 363  
QY 515 TCTAGAAAAGCTCAAGACTGTATTTATGAGCTGCATCTGTCGATCACAAGACCACTCA 574

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Db 364 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 383
Qy 575 TGGATAGACACCATTTCTGGATCTCAAGGGCTGCATCTTGTGATCACAAAGACCACTCCA 634
Db 384 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 403
Qy 635 TCCTCTTACGCAATATAAATCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCCT 694
Db 404 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 423
Qy 695 GGTATAGCCACAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACAGAA 754
Db 424 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 443
Qy 755 GCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAAGAGGAC 814
Db 444 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 463
Qy 815 TATGAACCTTGTAGTACCAAGCTCAAGGACTCAAAAGTCAAGCAATTAAGTACACT 874
Db 464 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 483
Qy 875 ACTGACATCCAAAGGAGAAATTTCGCAAGTTATAGTACAAAATTGAAAGATACACAA 934
Db 484 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 503
Qy 935 CAAATGGGTCTTTCAGCCTTTACCCGGAATPACTTGTGGTTTCTAGATCACCATCTTTAAAT 994
Db 504 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 523
Qy 995 TTACTTCAAAATAAAGCATG 1015
Db 524 LeuLeuGlnAsnLysSerMet 530

RESULT 4
US-09-069-023-1
; Sequence 1, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-1

Alignment Scores:
Pred. No.: 5,26e-232 Length: 531
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.75% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-1 (1-531)
Qy 335 TTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAAAATGAATATCTCTG 394
Db 305 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 324
Qy 395 ACATACCTGTAATCATCGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454
Db 325 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 344
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Qy 455 AATAGTGGTTCTCTGAAACTTCAAGGTCCCTGCAGCTCCTCAAGACAAATGATTTT 514
Db 345 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 364
Qy 515 TCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCACACT 574
Db 365 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 384
Qy 575 TGGATAGACACCATTTCTGGATCTCAAGGGCTGCATCTTGTGATCACAAAGACCACTCCA 634
Db 385 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 404
Qy 635 TCCTCTTACGCAATATAAATCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCCT 694
Db 405 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 424
Qy 695 GGTATAGCCACAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACAGAA 754
Db 425 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 444
Qy 755 GCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAAGAGGAC 814
Db 445 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 464
Qy 815 TATGAACCTTGTAGTACCAAGCTCAAGGACTCAAAAGTCAAGCAATTAAGTACACT 874
Db 465 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 484
Qy 875 ACTGACATCCAAAGGAGAAATTTCGCAAGTTATAGTACAAAATTGAAAGATACACAA 934
Db 485 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 504
Qy 935 CAAATGGGTCTTTCAGCCTTTACCCGGAATPACTTGTGGTTTCTAGATCACCATCTTTAAAT 994
Db 505 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 524
Qy 995 TTACTTCAAAATAAAGCATG 1015
Db 525 LeuLeuGlnAsnLysSerMet 531

RESULT 5
US-09-069-023-27
; Sequence 27, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-27

Alignment Scores:
Pred. No.: 5,26e-232 Length: 540
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.75% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-27 (1-540)
Qy 335 TTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAAAATGAATATCTCTG 394
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Db 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333
QY 395 AACATACCTGTAATCATGTCACAGAGAAATCATGTGGATCCTCTCAGCTCCATGAA 454
Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353
QY 455 AATAGTGGTCTCTCCTGAAACTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTAA 514
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCAAGACAATGATTTTAA 574
Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393
QY 575 TGGATAGCACCACTTTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCACTCCA 634
Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 413
QY 635 TGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGAACTCAGAACTCTGCAGCCT 694
Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433
QY 695 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACAGAA 754
Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453
QY 755 GCCTGCTTAAACCACTCGTAGTGCCTCTCTGCTCCAGGACTTGATCATGAAGAGGAC 814
Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473
QY 815 TATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAAGACAATTAAGTACACT 874
Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493
QY 875 ACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAATAAGTGAAGATAACAA 934
Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513
QY 935 CAATGGGTCTTACGCTTACCCTGGAATATCTGTGGTTCTAGATCACCACCTCTTAAAT 994
Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533
QY 995 TTAATCAAAATAAAGCATG 1015
Db 534 LeuLeuGlnAsnLysSerMet 540

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RESULT 6

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US-09-345-473E-28
; Sequence 28, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 3580/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-473E-28

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Alignment Scores: 5.26e-232 Length: 540  
Pred. No.: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 4 Gaps: 0

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US-09-771-161A-2 (1-1669) x US-09-345-473E-28 (1-540)
QY 335 TTACAGAGTGTTCCTCAAGTGCCTTCACTATGTGACAGAGAAATGGAATATCTCTG 394
Db 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333
QY 395 AACATACCTGTAATCATGTCACAGAGAAATCATGTGGATCCTCTCAGCTCCATGAA 454
Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353
QY 455 AATAGTGGTCTCTCCTGAAACTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTAA 514
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCAAGACAATGATTTTAA 574
Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393
QY 575 TGGATAGCACCACTTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTCCA 634
Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 413
QY 635 TGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGAACTCAGAACTCTGCAGCCT 694
Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433
QY 695 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACAGAA 754
Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453
QY 755 GCCTGCTTAAACCACTCGTAGTGCCTCTCTGCTCCAGGACTTGATCATGAAGAGGAC 814
Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473
QY 815 TATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAAGACAATTAAGTACACT 874
Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493
QY 875 ACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAATAAGTGAAGATAACAA 934
Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513
QY 935 CAATGGGTCTTACGCTTACCCTGGAATATCTGTGGTTCTAGATCACCACCTCTTAAAT 994
Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533
QY 995 TTAATCAAAATAAAGCATG 1015
Db 534 LeuLeuGlnAsnLysSerMet 540

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RESULT 7

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US-09-069-023-6
; Sequence 6, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-6

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Alignment Scores: 2.6e-168 Length: 167  
Pred. No.: 167

Score: 167.00 Matches: 167  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 31.45% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-6 (1-167)

QY 515 TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCTGGAATACACAGT 574  
Db 1 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 20  
QY 575 TGGGATAGACACCATTTCTGGATCTCAAGGGCTGCTCTCTGTGATCACAAGACCACTCCA 634  
Db 21 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 40  
QY 635 TCCTCTTCAAGCAATAATAATCACTCTCAACTGCAGGAAGCTCAGAACGCTGCGAGCT 694  
Db 41 CysSerSerAlaIleAlaLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 60  
QY 695 GGTATAGCCACGACGATCCAGACCAAAAGGGAAGACATTGTGAACCAATGACAGAA 754  
Db 61 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 80  
QY 755 GCCTGCTTAAACGACGCTAGATGCCCTTCTGTCCAGGACTTGCATGATGAAGAGGAC 814  
Db 81 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 100  
QY 815 TATGAACTGTGTAGTACCAAGCCTACAGGACCTCAAAAGTACAGAACTTACTACAGACT 874  
Db 101 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 120  
QY 875 ACTGACATCCAAAGGAGAAGAAATTGCAAAAGTTATAGTACAAAAATTGAAAGATAACAAA 934  
Db 121 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 140  
QY 935 CAAATGGGTCTTACGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATTCTTAAAT 994  
Db 141 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 160  
QY 995 TTACTTCAAAATAAAGCATG 1015  
Db 161 LeuLeuGlnAsnLysSerMet 167

RESULT 8

US-09-019-942-1  
; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-019-942-1

Alignment Scores:

Pred. No.: 5,696-127 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-019-942-1 (1-540)

QY 632 CCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 691  
Db 413 ProCysSerSerAlaIleAlaLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CCTGTATAGCCACGACGATCCAGACCAAAAGGGAAGACATTGTGAACCAATGACA 751  
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCTGCTTAAACGACGCTAGATGCCCTTCTGTCCAGGACTTGCATGATGAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAAGCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTACAGCAATTAAGAG 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGCATCCAAAGGAGAAGAAATTGCAAAAGTTATAGTACAAAAATTGAAAGATAAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAAATGGGTCTTCAAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATTCTTAA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTACTTCAAAATAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9

US-09-099-041A-2  
; Sequence 2, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-099-041A-2

Alignment Scores:  
 Pred. No.: 5.69e-127 Length: 540  
 Score: 128.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 24.11% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-099-041A-2 (1-540)

QY 632 CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGCATGAAAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAATCTTGTAGTACCAAGCCTCACAAGACCTCAAAAGCTCAGACAATTACTAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAAATGGTCTTCCAGCCTTACCCGGAATACTTGTGTTCTTAGATCACCATTCTTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerGlySerProSerLeu 532  
 QY 992 AATTACTTCAAAATAAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 10

US-09-245-281-2  
 ; Sequence 2, Application US/09245281  
 ; Patent No. 6369196  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; FILE REFERENCE: 07334/118001  
 ; CURRENT APPLICATION NUMBER: US/09/245,281  
 ; EARLIER FILING DATE: 1999-02-05  
 ; EARLIER FILING DATE: 1998-12-08  
 ; EARLIER FILING DATE: 1998-12-08  
 ; EARLIER FILING DATE: 1998-06-17  
 ; EARLIER FILING DATE: 1998-06-17  
 ; EARLIER FILING DATE: 1998-06-17  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-245-281-2

Alignment Scores:  
 Pred. No.: 5.69e-127 Length: 540  
 Score: 128.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 24.11% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-245-281-2 (1-540)

QY 632 CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGCATGAAAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAATCTTGTAGTACCAAGCCTCACAAGACCTCAAAAGCTCAGACAATTACTAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAAATGGTCTTCCAGCCTTACCCGGAATACTTGTGTTCTTAGATCACCATTCTTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerGlySerProSerLeu 532  
 QY 992 AATTACTTCAAAATAAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 11

US-09-470-271-1  
 ; Sequence 1, Application US/09470271  
 ; Patent No. 6410689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
 ; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/470,271  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/019,942  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meiklejohn, Ph.D., Anita L.  
 ; REGISTRATION NUMBER: 35,283  
 ; REFERENCE/DOCKET NUMBER: 07334/068001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617/542-5070  
 ; TELEFAX: 617/542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 540 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-09-470-271-1

Alignment Scores:  
 Pred. No.: 5.69e-127 Length: 540

Db 413 ProCysSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

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Db 473 AsptyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCCAAGAGAGATTGTCACAAAGTTATAGTACAAAATTGGAAGATAAC 931
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Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
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Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 14
US-09-865-364-2
; Sequence 2, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-364-2

Alignment Scores:
Pred. No.: 5.69e-127 Length: 540
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.11% Indels: 0
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US-09-771-161A-2 (1-1669) x US-09-865-364-2 (1-540)
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QY 692 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGCTTACCAAGTCGTAGATGCCCTTCTGTCAGGACCTGATCATCAAGAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTACTAGAC 871
Db 473 AsptyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCCAAGAGAGAAATTGTCACAAAGTTATAGTACAAAATTGGAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532

Search completed: March 29, 2004, 14:37:45
Job time : 35 secs

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QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 15
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; Sequence 1, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-537-1

Alignment Scores:
Pred. No.: 5.69e-127 Length: 540
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.11% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-748-537-1 (1-540)
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGAACTCAGAACGCTGTCAG 691
Db 413 ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGCTTAAACCAGTCGTAGATGCCCTTCTGTCAGGACCTGATCATCAAGAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTACTAGAC 871
Db 473 AsptyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCCAAGAGAGAAATTGTCACAAAGTTATAGTACAAAATTGGAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532

Search completed: March 29, 2004, 14:37:45
Job time : 35 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:20:43 ; Search time 81.5 Seconds

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11572.314 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Word size: 20

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=A\_Geneseq.25Jan04 -QFMT=fastan -SUFFIX=oli20n2p.rag -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=20  
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09711161 @CGN 1.1.81 @runat.29032004.124856.14304  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	227	42.7	478	3	Aay59405 Human RIC
3	227	42.7	531	3	Aay59404 Human RIC
4	227	42.7	540	2	Aaw52795 Human B1
5	227	42.7	540	3	Aay68774 Amino aci
6	227	42.7	540	4	Aam93621 Human pol
7	227	42.7	540	5	Aau80369 Human cel
8	227	42.7	540	5	Aae27882 Human rec
9	227	42.7	544	3	Aab43570 Human can
10	197	37.1	510	7	Adc99079 Human KPP

11 167 31.5 167 3 AAY59407  
12 128 24.1 540 2 AAY31140  
13 128 24.1 540 4 AAB20079  
14 128 24.1 540 5 ABG31075  
15 128 24.1 540 5 AAO22107  
16 128 24.1 540 6 ABUS6269  
17 128 24.1 540 7 ADB81362  
18 110 20.7 110 6 ABUS6272  
19 109 20.5 109 5 AAO22110  
20 98 18.5 131 5 AAO22109  
21 98 18.5 131 6 ABUS6271  
22 92 17.3 92 5 ABJ04754

#### ALIGNMENTS

RESULT 1  
AAV59406  
ID AAY59406 standard; protein; 284 AA.  
XX  
AC AAY59406;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Human RICK protein sequence residues 248-531.  
XX  
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
PN WO955134-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 27-APR-1999; 99WO-US009183.  
XX  
PR 27-APR-1998; 98US-00069023.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Nunez G, Inohara N, Koseki T;  
XX  
DR WPI; 2000-072163/06.  
XX  
PT Compositions for identifying apoptosis signaling pathway inhibitors  
XX  
PS Claim 6; Page; 93pp; English.  
XX  
CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening of assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.  
CC Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography

CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
 CC of an essential step in the biochemistry of apoptosis is needed. RICK  
 CC interaction with intracellular factors such as CLARP and FADD appears to  
 CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
 CC apoptosis factors are potential drug candidates. Note: This sequence was  
 CC created using information given in the specification  
 XX  
 SQ Sequence 284 AA;

Alignment Scores:  
 Pred. No.: 2,99e-237 Length: 284  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x AAY59405 (1-284)

QY	335	TTACAGAGTCTTTCAAGTGCATTACCTATGTGACAAAGAAATGGAATTTATCTCTG	394
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QY	395	AACATACCTTAATCATGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA	454
Db	78	AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	97
QY	455	AATAGTGGTCTCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACATGATTTTAA	514
Db	98	AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	117
QY	515	TCTAGAAAGCTCAAGACTGTATTTATCAAGCTGCATCACTGTCTCGAAATTCACAGT	574
Db	118	SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer	137
QY	575	TGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGATCAACAGACATCCA	634
Db	138	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro	157
QY	635	TGCTCTCAGCAATATATCACTCTCAACTGCAGGAACCTCAGAACCTCTGCAGCCT	694
Db	158	CysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro	177
QY	695	GGTATAGCCAGCAGTGGATCCAGAGCAAGAAAGGAGACATTTGTAACCAATGACAGAA	754
Db	178	GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu	197
QY	755	GCCTGCCTTAACGAGTCGCTAGATGCCCTTCTGTCAGGACTTGATCATGAAGAGGAC	814
Db	198	AlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAsp	217
QY	815	TATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAGGACCTCAAGCAATTTACTAGACCT	874
Db	218	TyrGlnLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr	237
QY	875	ACTGACATCCAAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA	934
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 ID AAY59405 standard; protein: 478 AA.  
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 AC AAY59405;  
 XX

DT 21-MAR-2000 (first entry)  
 XX Human RICK protein sequence residues 54-531.  
 DE  
 XX RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
 KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
 KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
 KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
 KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9555134-A2.  
 PN  
 XX  
 PD 04-NOV-1999.  
 XX  
 XX  
 PF 27-APR-1999; 99WO-US009183.  
 XX  
 PR 27-APR-1998; 98US-00069023.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Nunez G, Inohara N, Koseki T;  
 XX  
 DR WPI; 2000-072163/06.  
 XX  
 PT Compositions for identifying apoptosis signaling pathway inhibitors  
 PT useful for treating diseases.  
 PS  
 PS Claim 6; Page; 93pp; English.  
 XX  
 XX This sequence is a fragment of the human RICK (RIP-like interacting CLARP  
 CC kinase) protein of the invention. RICK acts as a positive regulator of  
 CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
 CC during CD95 signalling. The invention provides methods for identifying  
 CC apoptosis signalling pathway inhibitors and activators, and methods and  
 CC compositions for screening compounds which will modulate the interactions  
 CC of the various compositions identified: ARC, RICK, and the CIDE family of  
 CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening  
 CC assays for agents, useful in the diagnosis, prognosis or treatment of  
 CC disease associated with excess cell growth and dysregulation of  
 CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
 CC screening assays to identify inhibitor molecules blocking CD95-mediated  
 CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
 CC to identify inhibitors of the enzymatic activity of caspase-8.  
 CC Identification of ARC-like inhibitory compounds may be useful for gene  
 CC therapy treatment of disease with increased cell death in muscle tissue  
 CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
 CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
 CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
 CC can be used as reagents for the preparation or affinity chromatography  
 CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
 CC of an essential step in the biochemistry of apoptosis is needed. RICK  
 CC interaction with intracellular factors such as CLARP and FADD appears to  
 CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
 CC apoptosis factors are potential drug candidates. Note: This sequence was  
 CC created using information given in the specification  
 XX  
 SQ Sequence 478 AA;

Alignment Scores:  
 Pred. No.: 2,88e-237 Length: 478  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x AAY59405 (1-478)

QY	335	TTACAGAGTCTTTCAAGTGCATTACCTATGTGACAAAGAAATGGAATTTATCTCTG	394
Db	252	LeuGlnSerValSerSerAlaHisLeuHisCysAspLysLysMetGluLeuSerLeu	271

QY 395 AACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 454  
 DB 272 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 291  
 QY 455 AATAGTGGTCTCCCTGAAATCAAGCTCAAGGCTCCAGCTCCTCAAGACAAATGATTTTAA 514  
 DB 292 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 311  
 QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCTCACTGCTCGGAATCACAGT 574  
 DB 312 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 331  
 QY 575 TGGGTAGCACCATTTCTGGATCTCAAGGGCTGCTGATCTGTGATCAACAAGACCACTCCA 634  
 DB 332 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 351  
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 QY 875 ACTGATCCCAAGGAGAGAAATTCGCAAGTTATAGTACAAATTTGAAGATACAA 934  
 DB 432 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 451  
 QY 935 CAAATGGGTCTTACGCTTACCGGAAATACCTGTTGTTCTAGATCACCCTTTTAAAT 994  
 DB 452 GlnMetGlyLeuGlnProThrProGluIleLeuValValSerArgSerProSerLeuAsn 471  
 QY 995 TTACTTCAAAATAAAGCATG 1015  
 DB 472 LeuLeuGlnAsnLysSerMet 478

RESULT 3

AA59404  
 ID AAY59404 standard; protein; 531 AA.  
 AC AAY59404;  
 XX 21-MAR-2000 (first entry)  
 DT Human RICK protein sequence.  
 DE RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
 KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
 KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
 KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
 KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
 OS Homo sapiens.  
 PN WO955134-A2.  
 XX 04-NOV-1999.  
 PD 27-APR-1999; 99WO-US009183.  
 PF 27-APR-1998; 98US-00069023.  
 PR (UNMI ) UNIV MICHIGAN.

PI Nunez G, Inohara N, Koseki T;  
 DR WPI; 2000-072163/06.  
 DR N-PSDB; AAZ48762.  
 XX Compositions for identifying apoptosis signaling pathway inhibitors  
 PT useful for treating diseases.  
 PS Claim 1; Fig 7a; 93pp; English.  
 CC This sequence is the human RICK (RIP-like interacting CLARP kinase)  
 CC protein of the invention. The RICK protein acts as a positive regulator  
 CC of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
 CC during CD95 signalling. The invention provides methods for identifying  
 CC apoptosis signalling pathway inhibitors and activators, and methods and  
 CC compositions for screening compounds which will modulate the interactions  
 CC of the various compositions identified: ARC, RICK, and the CIDE family of  
 CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening of  
 CC assays for agents, useful in the diagnosis, prognosis or treatment of  
 CC disease associated with excess cell growth and dysregulation of  
 CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
 CC screening assays to identify inhibitor molecules blocking CD95-mediated  
 CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
 CC to identify inhibitors of the enzymatic activity of caspase-8.  
 CC Identification of ARC-like inhibitory compounds may be useful for gene  
 CC therapy treatment of disease with increased cell death in muscle tissue  
 CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
 CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
 CC ischaemic injury, and toxin-induced liver disease. Anti-RICK antibodies  
 CC can be used as reagents for the preparation or affinity chromatography  
 CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
 CC of an essential step in the biochemistry of apoptosis is needed. RICK  
 CC interaction with intracellular factors such as CLARP and FADD appears to  
 CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
 CC apoptosis factors are potential drug candidates  
 XX Sequence' 531 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 2,86e-237 Length: 531  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-771-161A-2 (1-1669) x AAY59404 (1-531)  
 QY 335 TTACAGAGTGTTCAGTGCCATTCACCTATGTGCAAGAGAAATGGAATTTATCTCTG 394  
 DB 305 LeuGlnSerValSerSerAlaIleHisLeuLysSerLysLysMetGluLeuSerLeu 324  
 QY 395 AACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 454  
 DB 305 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 344  
 QY 455 AATAGTGGTCTCCCTGAAATCAAGGCTCCCTGAGCTCCTCAAGACAAATGATTTTAA 514  
 DB 345 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 364  
 QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCTCACTGCTCGGAATCACAGT 574  
 DB 365 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 384  
 QY 575 TGGGTAGCACCATTTCTGGATCTCAAGGGCTGATCTCTGTGATCACAAGACCACTCCA 634  
 DB 385 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 404  
 QY 635 TGCTCTTCAGCAATTAATCACTCTCAACTGAGGAACTCAGAACGCTGAGCTT 694  
 DB 405 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 424  
 QY 695 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAA 754

Db 425 GlyileAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 444  
QY 755 GCCTGCCTTACCAAGTGCCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGAGGAC 814  
Db 445 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 464  
QY 815 TATGAACCTTGTAGTACCAAGCCTACCAAGGACCTCAAAAGTCACACAATTAAGACACT 874  
Db 465 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 484  
QY 875 ACTGACATCCCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTAAGAGATAACAAA 934  
Db 485 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 504  
QY 935 CAATGGGTCTTACGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTAAAT 994  
Db 505 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 524  
QY 995 TTACTTCAAAATAAAAGCATG 1015  
Db 525 LeuLeuGlnAsnLysSerMet 531

RESULT 4

AAW92795  
ID AAW92795 standard; protein; 540 AA.

AC AAW92795;

DT 07-MAY-1999 (first entry)

DE Human B1 protein.

KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
cell survival pathway; intracellular signalling; AIDS; cancer; human.

OS Homo sapiens.

PN W09855507-A2.

PD 10-DEC-1998.

PF 01-JUN-1998; 98WO-IL000255.

PR 05-JUN-1997; 97IL-00121011.

PR 30-JUN-1997; 97IL-00121199.

PR 11-SEP-1997; 97IL-00121746.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Wallach D, Boldin M, Malinin N;

PI WPI; 1999-070258/06.

DR N-PSDB; AAX02558.

XX New B1 protein regulates cell death and cell survival pathways -  
derivatives, DNA and antibodies, also regulate intracellular inflammation  
PT ; for treating AIDS, cancer.

PS Claim 4; Fig 3A; 90pp; English.

XX This invention describes the isolation of a novel human B1 protein which  
CC can interact with, intracellular mediators or modulators of inflammation,  
CC cell death and/or cell survival pathways, directly or indirectly. Cells  
CC can be modulated or mediated in inflammation, cell death or cell survival  
CC pathways or another intracellular signalling activity using B1.  
CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
CC oligonucleotides and ribozymes can also be used to regulate the above  
CC pathways

SQ Sequence 540 AA;

Alignment Scores:

Pred. No.: 2,86e-237 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 2 Gaps: 0

US-09-771-161A-2 (1-1669) x AAW92795 (1-540)

QY 335 TTACAGAGTGTTCCTCAAGTGCCTATTCACCTATGTGACAAGAAAAATGAATATCTCTG 394  
Db 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333  
QY 395 AACATACCTCTTAATCATGTCACAGAGGAAATCATCTGGATCTCTCAGCTCCATGAA 454  
Db 334 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHisGlu 353  
QY 455 AATAGTGGTTCCTCTCAAACTTCAAGTCCCTGCCAGCTCCCTCAAGACAAATGATTTTAA 514  
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
QY 515 TCTAGAAAAGCTCAAGACTGTATTTTATGAAGTGCATCCTGCTCTGGAATCAGT 574  
Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393  
QY 575 TGGGATAGCACCATTCTCGATCTCAAGGGCTGCTTCTGTGATCACAAGACCCTCCA 634  
Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 413  
QY 635 TGCTCTTACGCAATATAAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGAGCCT 694  
Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
QY 695 GGTATAGCCAGCAGTGGATCCAGACCAAGGAGAGACATTGTGAACCAATGACAGAA 754  
Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
QY 755 GCCTGCTTTAACCAAGTGCCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAAGAGGAC 814  
Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
QY 815 TATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAAGACACT 874  
Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
QY 875 ACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTAAGAGATAACAA 934  
Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
QY 935 CAAATGGGTCTTACGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTAAAT 994  
Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533  
QY 995 TTACTTCAAAATAAAAGCATG 1015  
Db 534 LeuLeuGlnAsnLysSerMet 540

RESULT 5

AAW68774  
ID AAY68774 standard; protein; 540 AA.

AC AAY68774;

DT 16-MAY-2000 (first entry)

XX Amino acid sequence of a human phosphorylation effector PHSP-6.  
XX Human; phosphorylation effector; PHSP; proliferative disorder;  
XX immune disorder; neuronal disorder.

OS Homo sapiens.

XX Key

Location/Qualifiers

FT Region 18. .287  
FT /note= "protein kinase family signature sequence"  
FT 23  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 34  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 58  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 100  
FT Modified-site  
FT /note= "potential glycosylation site"  
FT 102  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 180  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 183  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 207  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 224  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 267  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 296  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 301  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 360  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 374  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 391  
FT Modified-site  
FT /note= "potential glycosylation site"  
FT 401  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 428  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 442  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 457  
FT Modified-site  
FT /note= "potential glycosylation site"  
FT 478  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 478  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 484  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 537  
FT Modified-site  
FT /note= "potential glycosylation site"  
XX  
PN W0200006728-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 28-JUL-1999; 99WO-US017132.  
XX  
PR 28-JUL-1998; 98US-0155213P.  
PR 14-SEP-1998; 98US-0155196P.  
PR 14-OCT-1998; 98US-0155239P.  
PR 03-NOV-1998; 98US-0106889P.  
PR 19-NOV-1998; 98US-0109093P.  
PR 22-DEC-1998; 98US-0113796P.  
PR 12-JAN-1999; 99US-0155233P.  
XX  
PA (INCV-) INCVTE PHARM INC.  
XX  
PI Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX  
XX WPI; 2000-183125/16.  
DR N-PSDB; AA246143.  
DR  
XX New human phosphorylation effectors useful for the diagnosis, treatment

PT and prevention of proliferative, immune and neuronal disorders.  
XX Claim 1; Page 84-85; 142pp; English.  
XX  
CC AAY68769-95 and AAY68797-99 represent human phosphorylation effectors  
CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
CC given in the specification). The sequences were isolated from cDNA  
CC libraries prepared from various human tissues. The PHSP proteins are  
CC useful for the diagnosis, treatment and prevention of proliferative  
CC disorders, immune disorders and neuronal disorders. The PHSP proteins  
CC form pharmaceutical compositions which useful for treating or preventing  
CC disorders associated with decreased PHSP expression/activity. PHSP  
CC antagonists are useful for treating or preventing disorders associated  
CC with increased PHSP expression/activity  
XX  
SQ Sequence 540 AA;  
  
Alignment Scores:  
Pred. No.: 2,86e-237 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-771-161A-2 (1-1669) x AAY68774 (1-540)  
QY 335 TTACAGAGTGTTCCTCAAGTGCCATTCACCTATGTGACAAAGAAATGGAATTATCTCTG 394  
DB 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333  
QY 395 AACATACCTGTAAATCATGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454  
DB 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353  
QY 455 AATAGTGTTCTCTGAAACTTCAAGTCCCTCCAGCTCCCTCAAGACATGATTTTFA 514  
DB 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
QY 515 TCTAGAAAAGCTCAAGACTGTGTTATTTATGAAGTGCATCTGCTCTGGAATCACACT 574  
DB 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393  
QY 575 TGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAAGACCACTCA 634  
DB 394 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 413  
QY 635 TGCTCTTCAGCAATATAATCCACTCTCACTGAGGAACTCAGAACTCTGAGCTCTGAGCCT 694  
DB 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
QY 695 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAAAATGACAGAA 754  
DB 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
QY 755 GCCTGCCTTAACCACTCCCTAGATGCCCTTCTGTCCAGGACTTCGATCATGAAAGAGGAC 814  
DB 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
QY 815 TATGAACCTGTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTACTAGACACT 874  
DB 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
QY 875 ACTGACATCCCAAGGAGAAGATTTCGCAAGTTATAGTACAAAATTTGAAAGATACAA 934  
DB 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
QY 935 CAAATGGGTCTTCAGCCTTACCGGAAATACTTGTGGTTTCTAGATCAACCATCTTTAAAT 994  
DB 514 GlnMetGlyLeuGlnProtyr-ProGluIleLeuValSerArgSerProSerLeuAsn 533  
QY 995 TTACTTCAAAATAAAGCATG 1015  
|||||

Db	534	LeuLeuGlnAsnLysSerMet	540
Db	534	AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	379
RESULT 6			
AAM93621			
ID	AAM93621	standard; protein; 540 AA.	
XX			
AC	AAM93621;		
XX			
DT	06-NOV-2001	(first entry)	
XX			
DE	Human polypeptide, SEQ ID NO: 3454.		
XX			
KW	Human; full length cDNA; cDNA synthesis; oligo-capping.		
OS	Homo sapiens.		
XX			
PN	EP1130094-A2.		
XX			
PD	05-SEP-2001.		
XX			
PF	07-JUL-2000; 2000EP-00114089.		
XX			
PR	08-JUL-1999; 99JP-00194486.		
XX			
PR	11-JAN-2000; 2000JP-00118774.		
XX			
PR	02-MAY-2000; 2000JP-00183765.		
XX			
PA	(HELI-) HELIX RES INST.		
XX			
PI	Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;		
PI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;		
XX			
DR	WPI; 2001-524255/58.		
XX			
DR	N-PSDB; AAK94554.		
XX			
PT	830 Primers useful for synthesizing full length cDNA clones and their use		
PT	in genetic manipulation.		
XX			
PS	Claim 8; SEQ ID NO 3454; 1380pp + Sequence Listing; English.		
XX			
CC	The invention relates to primers for synthesising full length cDNA		
CC	clones. 830 cDNA molecules encoding a human protein have been isolated		
CC	and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have		
CC	been determined. Primers for synthesising the full length cDNA are useful		
CC	for clarifying the function of the protein encoded by the cDNA. The full		
CC	length clones were obtained by construction of full length enriched cDNA		
CC	libraries that were synthesised by the oligo-capping method. The primers		
CC	enable the production of the full length cDNA easily without any special		
CC	methods. The present sequence is a polypeptide encoded by a full length		
CC	human cDNA of the invention. Note: The sequence data for this patent did		
CC	not form part of the printed specification, but was obtained in CD-ROM		
XX	format directly from EPO		
SQ	Sequence 540 AA;		
Alignment Scores:			
Pred. No.:	2,868-237	Length:	540
Score:	227.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	42.75%	Indels:	0
DB:	4	Gaps:	0
US-09-771-161A-2 (1-1669) x AAM93621 (1-540)			
QY	335 TTACAGAGTGTTTCAAGTGCCATTACCCTGTATGCACGAAGAATAATTCCTCTG		394
Dd	314 LeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu		333
QY	395 AACATACCTGTAATCATGGTCCACAAGAGAAATCATGTGATCCTCTCGAGTCCATGAA		454
Dd	334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu		353
QY	455 AATAGTAGTGTTCTCCGAAACTTCAGGTGCCCTGTCAGAGCAATGATTTTITA		514

PS Disclosure; Page 23-24; 49pp; English.

XX The present invention relates to a new method for identifying compounds  
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
CC related diseases. The method of the invention comprises contacting a test  
CC compound with at least one of the cellular kinases RICK, RIP, Nck,  
CC interacting kinase, MKK3 and SHP-2 and detecting any change in kinase  
CC activity. The method of the invention can be used to treat and/or prevent  
CC CMV infections and related diseases. Oligonucleotides that can detect the  
CC specified kinases can also be used for diagnosis of infection. The  
CC present amino acid sequence represents the human cellular kinase RICK  
CC protein of the invention, as described above

XX Sequence 540 AA;

Alignment Scores:  
Pred. No.: 2,866-237 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 5 Gaps: 0

US-09-771-161A-2 (1-1669) x AAU80369 (1-540)

QY 335 TTACAGAGTGTTCAGTGCCTTCACTATGTGACAGAGAAATGGAATTATCTCTG 394  
DB 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333  
QY 395 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454  
DB 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353  
QY 455 AATAGTGGTTCCTGAACTTCAAGTCCCTGCAGCTCCTCAAGACAAATGATTTTGA 514  
DB 334 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCCTGCGAATACACAGT 574  
DB 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 393  
QY 575 TGGGATAGCACCATTCTCGGATCTCAAGGGCTGCATCTGTGATCACAGACCACTCCA 634  
DB 394 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrPro 413  
QY 635 TCCTCTTCAGCAATATAATCACTCTCAACTGCAGGAACTCAGAACTCTGCAGCT 694  
DB 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
QY 695 GGTATAGCCACAGCTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACAGAA 754  
DB 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
QY 755 GCCTGCTTAACAGCTCGTAGATGCCCTTCCTGTCAGGGACTTCATCATGAAAGAGNC 814  
DB 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
QY 815 TATGAACCTGTTAGTACCAAGCTTCAAGGACTCAAGGACTCAAGAACTTACTAGACACT 874  
DB 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
QY 875 ACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 934  
DB 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
QY 935 CAAATGGGTCTTCAGCTTACCGGAAATACCTTGGTTCTTAGATCACCATTCTTAAT 994  
DB 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 533  
QY 995 TTACTTCAAAATAAAGCATG 1015  
DB 534 LeuLeuGlnAsnLysSerMet 540

RESULT 8

AAE27882  
ID AAE27882 standard; protein; 540 AA.  
XX  
AC AAE27882;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human receptor interacting protein (RIP)2.  
XX  
KW Human; receptor interacting protein; RIP2; antisense; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US6426221-B1.  
XX  
PD 30-JUL-2002.  
XX  
PF 01-AUG-2001; 2001US-00920663.  
XX  
PR 01-AUG-2001; 2001US-00920663.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Ward DT, Cowser LM;  
XX  
DR WPI; 2002-673017/72.  
DR N-PSDB; AAD45172.  
XX  
PT New antisense oligonucleotide that targets regions of a nucleic acid  
PT encoding human receptor interacting protein (RIP)2, for treating diseases  
PT associated with RIP2 expression.  
XX  
PS Example 15; Col 49-54; 35pp; English.  
XX  
CC The invention relates to antisense compounds targetted to a nucleic acid  
CC encoding human receptor interacting protein (RIP)2 to inhibit its  
CC expression. Antisense compounds are used for treating diseases associated  
CC with RIP2 expression. They are also useful in antisense gene therapy. The  
CC present sequence is human RIP2 protein  
XX  
SQ Sequence 540 AA;

Alignment Scores:

Pred. No.: 2,866-237 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 5 Gaps: 0

US-09-771-161A-2 (1-1669) x AAE27882 (1-540)

QY 335 TTACAGAGTGTTCAGTGCCTTCACTATGTGACAGAGAAATGGAATTATCTCTG 394  
DB 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333  
QY 395 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454  
DB 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353  
QY 455 AATAGTGGTTCCTGAACTTCAAGGCTCCCTGCAGCTCCTCAAGACAAATGATTTTGA 514  
DB 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCAGCTCCATGACACT 574  
DB 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 393  
QY 575 TGGGATAGCACCATTCTCGGATCTCAAGGGCTGCATCTGTGATCACAGACCACTCCA 634  
DB 394 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrPro 413



QY 635 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACGCTCTCAGCCT 694  
 Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
 QY 695 GGTATAGCCAGCAGTGGATCCAGCAAAAGGGAAGACATTTGAAACCAATGACAGAA 754  
 Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
 QY 755 GCCTGCCTTACCACTGCCTAGATGCCCTCTGCTCCAGGACTTGATCATGAAAGGAC 814  
 Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
 QY 815 TATGAACCTTGTACTCAAGCCTTACAGGACCTCAAAAGCTCAGACAAATTAAGACACT 874  
 Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
 QY 875 ACTGACATCCAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAA 934  
 Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
 QY 935 CAAATGGGTCTTCAGCCTTACCCGGAAATCTTGTGGTTTCTAGATCACCATCTTTAAAT 994  
 Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533  
 QY 995 TTACTTCAAAATAAAGCATG 1015  
 Db 534 LeuLeuGlnAsnLysSerMet 540  
 RESULT 9  
 AAB43570  
 ID AAB43570 standard; protein; 544 AA.  
 XX  
 AC AAB43570;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human cancer associated protein sequence SEQ ID NO:1015.  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
 KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;  
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
 KW vasotropic; antipsoriatic; antidiabetic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055350-A1.  
 XX  
 FN 21-SEP-2000.  
 XX  
 PD 08-MAR-2000; 2000WO-US005882.  
 XX  
 PF 12-MAR-1999; 99US-0124270P.  
 XX  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PA Rosen CA, Ruben SM;  
 PI WPI; 2000-587533/55.  
 XX  
 DR N-PSDB; AAC77779.  
 XX  
 PT Novel isolated nucleic acids comprising sequences encoding peptides  
 XX useful for treating or diagnosing e.g. cancer.  
 XX  
 PS Claim 11; Page 1595-1597; 2352pp; English.  
 XX  
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB43398 to AAB44239. The proteins can have activities based on the

CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnery; immunomodulator;  
 CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC nootropic; vasotropic; antipsoriatic and angiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 544 AA;  
 Alignment Scores:  
 Pred. No.: 2,856-237 Length: 544  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-771-161A-2 (1-1669) x AAB43570 (1-544)  
 QY 335 TTACAGAGTGTTCAGTCCCATTCACCTATGTGACAGAAATGAATATCTCTG 394  
 Db 318 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 337  
 QY 395 AACATACCTGTAAATCATGTCCACAGAGGAATCATGTGGATCTCTCAGCTCATGAA 454  
 Db 338 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 357  
 QY 455 ATAGTGGTTCCTCGAAATTCAGGTCCTCCAGCTCCCTCAAGACATGATTTTAA 514  
 Db 358 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 377  
 QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGCTCGTGAATCAGACT 574  
 Db 378 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 397  
 QY 575 TGGATAGCACCATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCCTCCA 634  
 Db 398 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 417  
 QY 635 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACGCTCTCAGCCT 694  
 Db 418 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 437  
 QY 695 GGTATAGCCAGCAGTGGATCCAGCAAAAGGGAAGACATTTGAAACCAATGACAGAA 754  
 Db 438 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 457  
 QY 755 GCCTGCCTTACCACTGCCTAGATGCCCTCTGCTCCAGGACTTGATCATGAAAGGAC 814  
 Db 458 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 477  
 QY 815 TATGAACCTTGTACTCAAGCCTTACAGGACCTCAAAAGCTCAGACAAATTAAGACACT 874  
 Db 478 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 497  
 QY 875 ACTGACATCCAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAA 934  
 Db 498 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 517  
 QY 935 CAAATGGGTCTTCAGCCTTACCCGGAAATCTTGTGGTTTCTAGATCACCATCTTTAAAT 994



Db 518 GlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeuAsn 537  
 QY 995 TTACTTCAAAATAAAAGCATG 1015  
 Db 538 LeuLeuGlnAsnLysSerMet 544

RESULT 10  
 ADC99079  
 ID ADC99079 standard; protein; 510 AA.  
 AC ADC99079;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE .Human KPP protein - SEQ ID 32.  
 XX  
 KW anti-HIV; anti-allergic; anti-inflammatory; antianaemic; anti-parkinsonian;  
 KW immunosuppressive; anticonvulsant; antiarteriosclerotic; antiasthmatic;  
 KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;  
 KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;  
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
 KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;  
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
 KW cancer; developmental; mental retardation; neurological;  
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
 KW helminthic infection; transgenic; gene therapy; human; enzyme.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO2003033680-A2.  
 PN  
 PD 24-APR-2003.  
 XX  
 PF 17-OCT-2002; 2002WO-US033723.  
 XX  
 PR 19-OCT-2001; 2001US-0345474P.  
 PR 02-NOV-2001; 2001US-0343910P.  
 PR 13-NOV-2001; 2001US-0333098P.  
 PR 16-NOV-2001; 2001US-0332424P.  
 PR 30-NOV-2001; 2001US-0334289P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
 PI Emerling BM, Forsythe JJ, Gandhi AR, Gorvad AE, Griffin JA;  
 PI Gururajan R, Hafalia AUA, Khan FA, Lal PG, Lee EA, Lee SY;  
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
 PI Zebbarjadian Y;  
 XX  
 XX WPI; 2003-403214/38.  
 DR N-PSDB; ADC99131.  
 XX  
 PT New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX  
 PS Claim 1; SEQ ID NO 32; 424pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the

CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP protein of the  
 CC invention.  
 XX  
 SQ Sequence 510 AA;  
 Alignment Scores:  
 Pred. No.: 1.25e-204 Length: 510  
 Score: 197.00 Matches: 197  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 37.10% Indels: 0  
 DB: 7 Gaps: 0

US-09-771-161A-2 (1-1669) x ADC99079 (1-510)

QY 425 GAATCATGTCGATCCTCTCAGCTCCATCAAAATAGTGGTCTCTCCGAACTTCAAGGTCC 484  
 Db 314 GluSerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSer 333  
 QY 485 CTGCCAGCTCCTCAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTTATTTATG 544  
 Db 334 LeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMet 353  
 QY 545 AAGCTGCATCATCTGCTCGGAAATCACAGTGGGATAGCACCATTCTTGATCTCAAAGG 604  
 Db 354 LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArg 373  
 QY 605 GCTGCTATCTGTGATCACAGACCACTCCATGCTCTTCAGCAATTAATAATCACTCTCA 664  
 Db 374 AlaAlaPheCysAspHisLysThrThrProCysSerSerAlaIleAlaAsnProLeuSer 393  
 QY 665 ACTGCAGGAAACTCAGAACTCTGAGCTGTGTATAGCCAGCTGGATCCAGAGCAAA 724  
 Db 394 ThrAlaGlyAsnSerGluArgLeuGlnProGlyLleAlaGlnInTrpIleGlnSerLys 413  
 QY 725 AGGGAAGACATTGTGAACCAATATGACAGAGCTCCCTTAACCACTCGCTAGATGCCCTT 784  
 Db 414 ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeu 433  
 QY 785 CTGTCCAGGACTTGTATCATGAAAGAGCACTATGACTTGTAGTACCAAGCCTCAAGG 844  
 Db 434 LeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArg 453  
 QY 845 ACCTCAAAAGTCAGACAAATTAATCTAGACACTACTGATCCCAAGAGAGAAATTTGCCAA 904  
 Db 454 ThrSerLysValArgGlnLeuLeuAspThrThrAspLleGlnGlyGluGluPheAlaLys 473  
 QY 905 GTTATAGTACAAAATTCAAAAGATACAAACAAATGGGTCTTTCAGCCTTTACCCGAAATA 964  
 Db 474 ValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIle 493  
 QY 965 CTGTGGTCTTCTAGATCACCATCTTTAATTTACTTCAAAATAAAGCATG 1015  
 Db 494 LeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 510

RESULT 11  
 AAY59407  
 ID AAY59407 standard; protein; 167 AA.  
 XX  
 AC AAY59407;  
 XX  
 DT 21-MAR-2000 (first entry)  
 XX  
 DE Human RICK protein sequence residues 365-531.  
 XX  
 KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
 KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
 KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
 KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
 KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
 XX

OS Homo sapiens.  
 XX WO955134-A2.  
 XX  
 XX  
 PD 04-NOV-1999.  
 XX  
 XX 27-APR-1999; 99WO-US0009183.  
 XX 27-APR-1998; 98US-00069023.  
 XX (UNMI ) UNIV MICHIGAN.  
 XX  
 XX Nunez G, Inohara N, Koseki T;  
 XX WPI; 2000-072163/06.  
 XX  
 XX Compositions for identifying apoptosis signaling pathway inhibitors  
 PT useful for treating diseases.  
 XX  
 XX Claim 6; Page; 93pp; English.  
 XX  
 XX This sequence is a fragment of the human RICK (RIP-like interacting CLARP  
 CC kinase) protein of the invention. RICK acts as a positive regulator of  
 CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
 CC during CD95 signalling. The invention provides methods for identifying  
 CC apoptosis signalling pathway inhibitors and activators, and methods and  
 CC compositions for screening compounds which will modulate the interactions  
 CC of the various compositions identified: ARC, RICK, and the CIDE family of  
 CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening  
 CC assays for agents, useful in the diagnosis, prognosis or treatment of  
 CC disease associated with excess cell growth and dysregulation of  
 CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
 CC screening assays to identify inhibitor molecules blocking CD95-mediated  
 CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
 CC to identify inhibitors of the enzymatic activity of caspase-8.  
 CC Identification of ARC-like inhibitory compounds may be useful for gene  
 CC therapy treatment of disease with increased cell death in muscle tissue  
 CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
 CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
 CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
 CC can be used as reagents for the preparation or affinity chromatography  
 CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
 CC of an essential step in the biochemistry of apoptosis is needed. RICK  
 CC interaction with intracellular factors such as CLARP and FADD appears to  
 CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
 CC apoptosis factors are potential drug candidates. Note: This sequence was  
 CC created using information given in the specification  
 XX  
 XX SQ Sequence 167 AA;

Alignment Scores:  
 Pred. No.: 5,93e-172 Length: 167  
 Score: 167.00 Matches: 167  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 31.45% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-771-161A-2 (1-1669) x AAY59407 (1-167)

QY 515 TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTCGAAATCAAGT 574  
 Db 1 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisser 20  
 QY 575 TGGGATAGACCACTTTCTGCATCTCAAGGCTGCATCTCTGCATCAAGACCTCCA 634  
 Db 21 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 40  
 QY 635 TGCTCTTCAGCAATATAAATCAACTCTCAACTGCAGAAACTCAGAACCTCTGCAGCCT 694  
 Db 41 CysSerSerAlaIleIleAnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 60  
 QY 695 GGTTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAATGACAGAA 754

Db 61 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 80  
 QY 755 GCCTGCTTTAAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGGAC 814  
 Db 81 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 100  
 QY 815 TATGAACCTTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTTACTAGACACT 874  
 Db 101 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 120  
 QY 875 ACTGACATCAAGGAGGAAGAATTTGCCAAAGTTATAGTACAAAAATGAAAGATACAAA 934  
 Db 121 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 140  
 QY 935 CAAATCGGCTTTCAGCCTTACCCGGAATACCTTGCTGTTCTAGATCACCATCTTTAAAT 994  
 Db 141 GlnMetGlyLeuGlnProTyrProGluIleLeuValIleValSerArgSerProSerLeuAsn 160  
 QY 995 TTACTTTCAAAATAAAAGCATG 1015  
 Db 161 LeuLeuGlnAsnLysSerMet 167  
 RESULT 12  
 ID AAY31140 standard; protein; 540 AA.  
 XX  
 AC AAY31140;  
 XX  
 DT 25-OCT-1999 (first entry)  
 XX  
 DE Human CARD-3 protein.  
 XX  
 KW CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
 KW caspase activation; detection; screening; therapy; diagnosis; disease;  
 KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
 KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
 KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;  
 KW myelodysplastic syndrome; myocardial infarction; cell proliferation;  
 KW cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..300  
 FT /note= "predicted kinase domain"  
 FT Domain 301..431  
 FT /note= "predicted linker domain"  
 FT Domain 432..540  
 FT /note= "predicted CARD domain"  
 FT  
 XX WO9940102-A1.  
 PN  
 XX 12-AUG-1999.  
 PD  
 XX  
 XX 05-FEB-1999; 99WO-US002544.  
 PF  
 XX 06-FEB-1998; 98US-00019942.  
 PR  
 XX 17-JUN-1998; 98US-00099041.  
 PR  
 XX 08-DEC-1998; 98US-00207359.  
 PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Bertin J;  
 PI  
 XX WPI; 1999-494269/41.  
 XX N-PSDB; AA209246.  
 DR  
 XX Novel CARD-3 and CARD-4 genes and polypeptides used or treating

PT regulation of cellular proliferation and differentiation and cell survival.

XX

XX

CC This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial murine CARD-4L protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive medicine and therapeutic and prophylactic methods of treatment. The methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the TNF receptor complex, or abnormal activity of a caspase. Diseases that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p53 and hormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD-4L, a short transcript that encodes CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence represents the human CARD-3 protein described in the method of the invention

XX

SQ Sequence 540 AA;

Alignment Scores:  
Pred. No.: 1,478-129 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 2 Gaps: 0

US-09-771-161A-2 (1-1669) x ANY31140 (1-540)

QY 632 CCATGCTCTTTCAGCAATAATAATCACTCTCACTGCAGGAACCTCAGACGCTCTGCAG 691  
DB 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGACCAAGGAAGACATTGTGAACCAATGACA 751  
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCTGCCTTAACAGTGCCTAGATGCCCTCTCTCCAGGACTTGATCATGAAGAG 811  
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACCTTGTAGTACCAAGCCTACAAGACCTCAAAAGTCAGACAAATTACTAGAC 871  
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCAAGAGGAAGATTGTCGAAGTTATAGTCAAAAATTGAAGATAC 931  
DB 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGGCTTCAGCCTTACCGGAATCTGTGTTCTAGATCACCATCTTTA 991  
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTACTTCAAAATAAAGCATG 1015  
DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 13

AAB20079  
ID AAB20079 standard; protein; 540 AA.

XX

XX

DT 23-APR-2001 (first entry)

DE Human CARD-3 protein.

XX CARD-3; caspase recruitment domain; human; cancer; infection;

KW autoimmune disease; neurological disease; haematological disease;

KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;

XX antinflammatory; apoptosis; diagnosis; gene therapy.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..400

FT /note= "kinase domain"

FT Domain 401..431

FT /note= "linker domain"

FT Domain 432..540

FT /note= "CARD"

XX WO200100826-A2.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-US017691.

XX 28-JUN-1999; 99US-00340620.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J;

XX WPI; 2001-061973/07.

XX N-PSDB; AAF30001.

PT Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.

PS Claim 9; Fig 2; 208pp; English.

XX The present sequence is that of human caspase recruitment domain 3 (CARD-3), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAF30001). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using gene therapy methods. Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD-3, -4, -5 and -6 proteins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that modulate their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, -4, -5 or -6 protein, or production of an aberrant protein

Alignment Scores:  
Pred. No.: 1,478-129 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 4 Gaps: 0



AC	AAO22107;
XX	
DT	27-SEP-2002 (first entry)
DE	Protein of human CARD-3 SEQ ID No 2.
XX	
KW	Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;
KW	cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological;
KW	nootropic; antihaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;
KW	cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;
KW	hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;
KW	systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;
KW	anaemia; neutropenia; myelodysplastic syndrome; human.
XX	
OS	Homo sapiens.
PX	
NN	US6369196-B1.
XX	
PD	09-APR-2002.
XX	
PF	05-FEB-1999; 99US-00245281.
XX	
PR	06-FEB-1998; 98US-00019942.
PR	17-JUN-1998; 98US-0009041.
PR	08-DEC-1996; 98US-00207359.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Bertin J;
XX	
DR	WPI; 2002-391988/42.
DR	N-PSDB; AAL40752, AAL40753.
PT	Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD
PT	-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's
PT	disease, cancers and viral infections.
XX	
PS	Example 2; Fig 2; 116pp; English.
XX	
CC	The invention relates to novel isolated Caspase Recruitment Domain (CARD)
CC	polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may
CC	be used to treat disorders associated with decreased CARD expression by
CC	supplementing the patient's own production of CARD. Disorders associated
CC	with the expression and activity of CARD include cancers (particularly
CC	follicular lymphomas, carcinomas associated with mutations in p53, and
CC	hormone-dependent tumours such as breast cancer, prostate cancer, and
CC	ovarian cancer), autoimmune disorders (such as systemic lupus
CC	erythematosus, immune-mediated glomerulonephritis), viral infections
CC	(such as those caused by herpes viruses, poxviruses, and adenoviruses),
CC	neurological diseases (such as Alzheimer's disease, parkinson's disease,
CC	amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal
CC	muscular atrophy, and various forms of cerebellar degeneration), anaemia
CC	associated with chronic disease, aplastic anaemia, chronic neutropenia,
CC	and the myelodysplastic syndromes. This sequence represents a human CARD
CC	protein relating to the invention
XX	
SQ	Sequence 540 AA;
	Alignment Scores:
	Pred. No.: 1,47e-129 Length: 540
	Score: 128.00 Matches: 128
	Percent Similarity: 100.00% Conservative: 0
	Best Local Similarity: 100.00% Mismatches: 0
	Query Match: 24.11% Indels: 0
	DB: 5 Gaps: 0
US	09-771-161A-2 (1-1669) x RAO22107 (1-540)
QY	632 CCATGCTCTTTCAGCAATAATAATCCACTCTCACTGCAGGAACAACAGAACGTCTGCAG 691
Dd	
	413 ProcyseSerAlaAlleleasnProuserThrAlaGliAsnSerGliUArgLeuGln 432
QY	692 CCTGGTATAGCCCCAGCAGTGGAATCACAGAGCAAAAAGGGGAAGAACATTGTGAACCAANTGACA 751

Db	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	452
Qy	752	GAAGCCCTGCCTTAAACCAAGTCGCTAGATGCCCTTCTGTCACGGAGCTTGATCATGAAAGAG	811
Db	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472
Qy	812	GACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAAGTCAGACAAATTACTAGAC	871
Db	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492
Qy	872	ACTACTCACATCCCAAGGAGAGAAGATTGCCAAAAGTTATAGTACAAAATTTGAAAGATAAC	931
Db	493	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512
Qy	932	AAACAAATGGGTCTTCAGCCTTACC CGGAAATACTTGTGGTTCTTAGATCACCATCTTTA	991
Db	513	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	532
Qy	992	AATTTACTCATAATAAAGCATG	1015
Db	533	AsnLeuLeuGlnAsnLysSerMet	540

Search completed: March 29, 2004, 14:31:27  
Job time : 91.5 secs

Alignment Scores:	
Pred. No.:	1,478-129
Score:	128.00
Length:	540
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Matches:	128
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Indels:	0
DB:	5
Gaps:	0

US-09-771-161A-2 (1-1669) x AAO22107 (1-540)

Qy	632	CCATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGCAGGAARCTCAGAACGTCTGCAG	691
Db	413	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432
Qy	692	CTTGGTATAGCCGACGAGTGGATCCAGAGCAAAAGGGGAAGACATTTGTGAACCAAAATGACA	751

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 10:15:17 ; Search time 471 Seconds  
(without alignments)  
2092.531 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLQSQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: OLIGO  
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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 20

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:  
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=20  
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-LONGLOG -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
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3: Geneseqn2000s:.\*  
4: Geneseqn2001as:.\*  
5: Geneseqn2001bs:.\*  
6: Geneseqn2002s:.\*  
7: Geneseqn2003as:.\*  
8: Geneseqn2003bs:.\*  
9: Geneseqn2003cs:.\*  
10: Geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	2024	3	Aaz46143 CDNA sequ
2	227	97.8	2033	4	Aak94554 Human ful
3	227	97.8	2098	2	Aax02558 Human B1
4	227	97.8	2501	6	Abk51169 cDNA enco
5	227	97.8	2501	6	Aad45172 Human rec
6	227	97.8	2502	3	Aaz48762 Human RIC
7	227	97.8	2709	3	Aac77779 Human can
8	197	84.9	1959	9	Adc99131 Human KPP

9	128	55.2	1620	7	ABX75870	Abx75870 Human Cas
10	128	55.2	1931	2	Aaz09246	Aaz09246 Human CAR
11	128	55.2	1931	4	Aaf30001	Aaf30001 Human CAR
12	128	55.2	1931	6	ABK89280	Abk89280 Human CDN
13	128	55.2	1931	6	AA140752	AA140752 CDNA of h
14	128	55.2	1931	7	ABX75869	Abx75869 Human csn
15	128	55.2	1931	9	ADB81363	Adb81363 Human csn
16	120	51.7	491	8	ACH33353	Ach33353 Human end
17	110	47.4	1619	6	AA140753	AA140753 DNA of hu
18	44	19.0	762	7	ACD96414	Ac96414 Human col
c 19	40	17.2	575	4	AAK93010	Aak93010 Human CDN

ALIGNMENTS

RESULT 1  
AAZ46143  
ID AAZ46143 standard; CDNA; 2024 BP.  
AC AAZ46143;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE cDNA sequence encoding a human phosphorylation effector PHSP-6.  
XX  
KW Human; phosphorylation effector; PHSP; proliferative disorder;  
KW immune disorder; neuronal disorder; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 203..1825  
FT /\*tag= a  
FT /product= "phosphorylation effector"  
XX  
PN WO200006728-A2.  
XX  
PD 10-FEB-2000.  
XX  
28-JUL-1999; 99WO-US017132.  
PR 28-JUL-1998; 98US-0155213P.  
PR 14-SEP-1998; 98US-0155198P.  
PR 14-OCT-1998; 98US-0155239P.  
PR 03-NOV-1998; 98US-0106889P.  
PR 19-NOV-1998; 98US-0109093P.  
PR 22-DEC-1998; 98US-0113796P.  
PR 12-JAN-1999; 99US-0155233P.  
XX  
PA (INCY-) INCYTE PHARM INC.  
XX  
PI Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX  
DR WPI; 2000-183125/16.  
DR P-PSDB; AAY68774.  
XX  
PT New human phosphorylation effectors useful for the diagnosis, treatment  
PT and prevention of proliferative, immune and neuronal disorders.  
XX  
PS Claim 9; Page 121-122; 142pp; English.

XX  
CC AAZ46138-246168 encode human phosphorylation effectors (PHSP), designated  
CC PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the  
CC specification). The sequences were isolated from cDNA libraries prepared  
CC from various human tissues. The PHSP proteins are useful for the  
CC diagnosis, treatment and prevention of proliferative disorders, immune  
CC disorders and neuronal disorders. The PHSP proteins form pharmaceutical  
CC compositions which useful for treating or preventing disorders associated  
CC with decreased PHSP expression/activity. PHSP antagonists are useful for  
CC treating or preventing disorders associated with increased PHSP  
CC expression/activity

XX SQ Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.13e-218 Length: 2024  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 97.84% Indels: 0  
 DB: 3 Gaps: 0

US-09-771-161A-93 (1-232) x AAK46143 (1-2024)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 DB 1142 TTACAGAGTGTTCACAGTCCATTCACATATGTGACAAAGAAATGAATATCTCTG 1201  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 1202 AACATACCTGTAAATCATGTGTCCAAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1261  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1262 AATAGTGGTCTCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1321  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1322 TCTAGAAAGCTCAAGACTGTATTTATGAGCTGCATCTCTGGAATCAGT 1381  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 105  
 DB 1382 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 1441  
 QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 1442 TGTCTTCACAAATTAATATCCACTCTCACTGTCAGAAACTCAGAACTCTGCGACCT 1501  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 1502 GGTATAGCCCGAGCTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAA 1561  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 1562 GCCTGCCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 1621  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 DB 1622 TATGAACCTTGTAGTCAAGCCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACACT 1681  
 QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 DB 1682 ACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAAA 1741  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 DB 1742 CAAATGGGTCTTCCAGCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAAAT 1801  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 DB 1802 TTACTTCAAAATAAAGCATG 1822

RESULT 2  
 AAK94554  
 ID AAK94554 standard; cDNA; 2033 BP.  
 XX AC AAK94554;  
 XX 06-NOV-2001 (first entry)  
 XX Human full-length cDNA, SEQ ID NO: 3453.  
 XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.  
 PN EF1130094-A2.  
 XX 05-SEP-2001.  
 PD 07-JUL-2000; 2000BP-00114089.  
 XX 08-JUL-1999; 99JP-00194486.  
 XX 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.  
 DR P-PSDB; AAM93621.  
 XX 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.  
 XX Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.  
 PS The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesising the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a full length human cDNA of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in CD-ROM format directly  
 CC from EPO  
 XX SQ Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.13e-218 Length: 2033  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 97.84% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-771-161A-93 (1-232) x AAK94554 (1-2033)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 1158 TTACAGAGTGTTCACAGTCCATTCACATATGTGACAAAGAAATGAATATCTCTG 1217  
 QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 1218 AACATACCTGTAAATCATGTGTCCAAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1277  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1278 AATAGTGGTCTCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1337  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1338 TCTAGAAAGCTCAAGACTGTATTTATGAGCTGCATCTCTGCTGGAATCAGT 1397  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 105  
 DB 1398 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 1457  
 QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 1458 TGTCTTCTCAGCAATAATAAATCCACTCTCACTGCGAGAACTCAGAACGCTCTGCGACCT 1517



Qy	126	GlyIleAlaGlnGlnThrPilleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu	145
Db	1518	GGTATATGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGCAGAA	1577
Qy	146	AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp	165
Db	1578	GCTTGCCTTTAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCAAGAAGGAC	1637
Qy	166	TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr	185
Db	1638	TATGAACCTTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTTACTAGACACT	1697
Qy	186	ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys	205
Db	1698	ACTGCATCCAAAGGAGAAGAAATTTGCTAAAGTTTATAGTACAAAAAATTGAAAGATAACAAA	1757
Qy	206	GlnMetGlyLeuGlnProTyProGluIleLeuValSerArgSerProSerLeuAsn	225
Db	1758	CAATGGGCTTTAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT	1817
Qy	226	LeuLeuGlnAsnLysSerMet	232
Db	1818	TTACTTCAAAATAAAGCATG	1838
RESULT 3			
AAK02558	ID AAX02558 standard; cDNA; 2098 BP.		
XX	AC	AAK02558;	
XX	DT	07-MAY-1999 (first entry)	
XX	DE	Human B1 cDNA.	
XX	KW	B1 protein; intracellular mediator; modulator; inflammation; cell death;	
XX	KW	cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.	
XX	OS	Homo sapiens.	
XX	OS	WO9855507-A2.	
XX	PN	10-DEC-1998.	
XX	PD	01-JUN-1998; 98WO-IL000255.	
XX	PF	05-JUN-1997; 97IL-00121011.	
XX	PR	30-JUN-1997; 97IL-00121199.	
XX	PR	11-SEP-1997; 97IL-00121746.	
XX	XX	(YEDA ) YEDA RES & DEV CO LTD.	
XX	PA	Wallach D, Boldin M, Malinin N;	
XX	PI	WPI; 1999-070258/06.	
XX	PI	P-PSDB; AAW92795.	
XX	DR		
XX	XX		
PT	FT	New B1 protein regulates cell death and cell survival pathways -	
PT	PT	derivatives, DNA and antibodies, also regulate intracellular inflammation	
PT	PT	; for treating AIDS, cancer.	
XX	XX	Claim 4; Fig 3B; 90pp; English.	
XX	XX	This invention describes the isolation of a novel human B1 protein which	
XX	CC	can interact with, intracellular mediators or modulators of inflammation,	
XX	CC	cell death and/or cell survival pathways, directly or indirectly. Cells	
XX	CC	can be modulated or mediated in inflammation, cell death or cell survival	
XX	CC	pathways or another intracellular signalling activity using B1.	
XX	CC	Conditions such as AIDS and cancer can be treated using B1. Antibodies,	
XX	CC	oligonucleotides and ribozymes can also be used to regulate the above	
XX	XX	pathways	
XX	SO	Sequence 2098 BP; 649 A; 452 C; 449 G; 539 T; 0 U; 9 Other;	

Alignment Scores:		Length:	2098
Pred. No.:	1.17e-218	Matches:	227
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Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	97.84%	Gaps:	0
DB:	2		
US-09-771-161A-93 (1-232) x AAX02558 (1-2098)			
Qy	6	LeuGlnSerValSerSerAlaIleHisLeuCyAspLysLysLysMetGluLeuSerLeu	25
Db	1199	TTACAGAGTGTTTCAAGTGCATTCACCTATGTGACNAGAAGAAATGGAAATATCTCTG	1358
Qy	26	AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	45
Db	1259	AACATACCTGTAAATCATGTGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA	1318
Qy	46	AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	65
Db	1319	AAATAGTGGTTCTCTGAAACTTCAAGTGCCTGCCAGCTCCTCAAGACAAATGATTTTTTA	1378
Qy	66	SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer	85
Db	1379	TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTCTCTGGAAATCACAGT	1438
Qy	86	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro	105
Db	1439	TGGGATAGCACCATTTCTGGATCTCAAAAGGCTGCATTCGTGTATCAACAAGACCACCTCCA	1498
Qy	106	CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro	125
Db	1499	TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACTGTCGACCT	1558
Qy	126	GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu	145
Db	1559	GGTATATCCCGAGCTGATCCAGAGCAAAAGGGAGACATTTGTGAACCAATGACAGAA	1618
Qy	146	AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp	165
Db	1619	GCCTGCCCTTAACCAAGTCGCTAGATGCCCTTTCTGTCCAGGACATGTATCATGAAGAGGAC	1678
Qy	166	TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr	185
Db	1679	TATGAACCTTGTAGTACCAAGCCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACACT	1738
Qy	186	ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys	205
Db	1739	ACTGACATCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAACAAA	1798
Qy	206	GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn	225
Db	1799	CAAAATGGGTCTTCAGCCTTACCCGGAAATATCTTGTGGTTTCTAGATCACCATCTTTAAAT	1858
Qy	226	LeuLeuGlnAsnLysSerMet	232
Db	1859	TTACTTTCAAAATAAAGCATG	1879
RESULT 4			
ID	ABK51169		
ID	ABK51169	standard; cDNA; 2501 BP.	
XX	XX	ABK51169;	
XX	XX	30-JUL-2002 (first entry)	
XX	XX	cDNA encoding human cellular kinase RICK protein.	
XX	XX	Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;	
KW	KW	RIP; Nck-interacting kinase; MKK3; SRPK-2; gene; ss.	
XX	XX	Homo sapiens.	

XX FH Key Location/Qualifiers  
FT CDS 225..1847  
FT /\*tag= a  
FT /product= "Human cellular kinase RICK"  
XX  
XX EP1201765-A2.  
XX  
XX 02-MAY-2002.  
XX  
XX 15-OCT-2001; 2001EP-00124604.  
XX  
XX 16-OCT-2000; 2000US-0240750P.  
XX  
XX (AXXI-) AXIXIMA PHARM AG.  
XX  
XX Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;  
XX WPI; 2002-373930/41.  
DR P-PSDB; AAU80369.  
XX  
XX Identifying agents for treatment or prevention of cytomegalovirus  
PT infection, comprises contacting test compound with cellular kinase and  
PT detecting change in cellular kinase activity.  
XX  
XX Disclosure; Page 20-23; 49pp; English.  
XX  
XX The present invention relates to a new method for identifying compounds  
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
CC related diseases. The method of the invention comprises contacting a test  
CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
CC activity. The method of the invention can be used to treat and/or prevent  
CC CMV infections and related diseases. Oligonucleotides that can detect the  
CC specified kinases can also be used for diagnosis of infection. The  
CC present nucleic acid sequence encodes the human cellular kinase RICK  
CC protein of the invention, as described above  
XX  
XX Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
XX  
XX  
XX Alignment Scores:  
Pred. No.: 1.38e-218 Length: 2501  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
DB: 6 Gaps: 0  
XX  
XX US-09-771-161A-93 (1-232) x ABK51169 (1-2501)  
XX  
XX 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
DB 1164 TTACAGAGTGTTCACGTGCATTCACCTATGTGCACAGAGAAATGGATATCTCTG 1223  
XX  
XX 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1224 AACATACCTGTAATCATGTGTCACAGAGAGAAATCATGTGCATCTCCAGTCCATGAA 1283  
XX  
XX 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1284 AATAGTGGTTCCTCGAAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTTAA 1343  
XX  
XX 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
DB 1344 TCTAGAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTCGAATCACAGT 1403  
XX  
XX 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 105  
DB 1404 TGGGATAGCACCATTCTGGTTCCTCAAGGGCTGCATTCCTGATCACAGACCACTCCA 1463  
XX  
XX 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyValAsnSerGluArgLeuGlnPro 125  
DB 1464 TGCTCTTCAGCAATATATAATCCACTCTCACTGACGAGAAACTCAGAACTGCTGCAGCCT 1523

QY 126 GivileAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
DB 1524 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTGTGAACCAATGACAGAA 1583  
XX  
QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
DB 1584 GCGTGCCTTAACGACGTGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAGGAC 1643  
XX  
QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
DB 1644 TATGAACCTTGTGTAGTACCAGGCTCAAGAGCCTCAAAAGTCAGACAAATTACTAGACACT 1703  
XX  
QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
DB 1704 ACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAA 1763  
XX  
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225  
DB 1764 CAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGTTCTAGATCACCATCTTTAAAT 1823  
XX  
QY 226 LeuLeuGlnAsnLysSerMet 232  
DB 1824 TTACTTCAAAATAAAAGCATG 1844  
XX  
RESULT 5  
AAD45172  
ID AAD45172 standard; DNA; 2501 BP.  
XX  
AC AAD45172;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human receptor interacting protein (RIP) 2 DNA.  
XX  
KW Human; receptor interacting protein; RIP2; antisense; gene therapy; gene;  
XX ds.  
XX  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 225..1847  
FT /\*tag= a  
FT /product= "Human RIP2 protein"  
XX  
PN US6426221-B1.  
XX  
PD 30-JUL-2002.  
XX  
XX 01-AUG-2001; 2001US-00920663.  
XX  
XX 01-AUG-2001; 2001US-00920663.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Ward DT, Cowser LM;  
XX P-PSDB; AA27882.  
XX  
XX WPI; 2002-673017/72.  
XX  
XX P-PSDB; AA27882.  
XX  
XX New antisense oligonucleotide that targets regions of a nucleic acid  
PT encoding human receptor interacting protein (RIP) 2, for treating diseases  
PT associated with RIP2 expression.  
XX  
XX Claim 1; Col 49-54; 35pp; English.  
XX  
XX The invention relates to antisense compounds targetted to a nucleic acid  
CC encoding human receptor interacting protein (RIP) 2 to inhibit its  
CC expression. Antisense compounds are used for treating diseases associated  
CC with RIP2 expression. They are also useful in antisense gene therapy. The  
CC present sequence is human RIP2 DNA  
XX  
XX Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
XX

XX	OS	Homo sapiens.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1345 TCTAGAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTCTGGAAATCAGT 1404  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 DB 1405 TGGGATAGCAGCAATTTCTGGTTCTCAAGAGGCTGCATTTCTGTATCATCAAGACCACTCCA 1464  
 QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 1465 TGCTCTTCAGCAATAAATCAATCCACTCTCAACTGCAGAAACTCAGAAACGCTGCAGCCT 1524  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 1525 GGATATAGCCAGCAGCTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAGAA 1584  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 1585 GCCTGCCTTAAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 1644  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 DB 1645 TATGAACCTTGTTAGTACAGCCTTACAGGACCTCAAAAGTTCAGACAAATTAAGACACT 1704  
 QY 186 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 DB 1705 ACTGACATCCAAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1764  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 DB 1765 CAATGGGTCTTACAGCCTTACCCGAAATATCTGTGGTTTCTAGATCACCATCTTTAAAT 1824  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 DB 1825 TTACTTCAAAATAAAGCATG 1845

RESULT 7  
 AAC77779  
 ID AAC77779 standard; cDNA; 2709 BP.  
 AC AAC77779;  
 AT  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human cancer associated gene sequence SEQ ID NO:173.  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;  
 KW antidiabetic; antisthmatic; antirheumatic; antithyroid; antitumor;  
 KW antiinflammatory; antithyroid; antiallergic; antidiabetic; antitumor;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; neutropenic;  
 KW vasotrophic; antipsoriatic; antidiabetic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W0200055350-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 08-MAR-2000; 2000WO-US005882.  
 XX  
 XX 12-MAR-1999; 99US-0124270P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM;  
 XX  
 XX WPI; 2000-587533/55.

DR P-PSDB; AAB43570.

XX Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer.

XX Claim 1; Page 751-752; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC ABA43398 to ABA44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnary; immunomodulator;  
 CC antidiabetic; antisthmatic; antirheumatic; antithyroid; antitumor;  
 CC antiinflammatory; antithyroid; antiallergic; antidiabetic; antitumor;  
 CC dermatological; neuroprotective; thrombolytic; coagulant; neutropenic;  
 CC vasotrophic; antipsoriatic; antidiabetic; gene therapy; inflammation;  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease, and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological diseases and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and ABA44240 represent sequences used in the exemplification of  
 CC the present invention

SQ Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 0 U; 10 Other;

Alignment Scores:

Pred. No.:	1.49e-218	Length:	2709
Score:	227.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.84%	Indels:	0
DB:	3	Gaps:	0

US-09-771-161A-93 (1-232) x AAC77779 (1-2709)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 1206 TTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAGAGAAATGGAATTTATCTCTG 1265  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 1266 AACATACCTGTAAATCATGTGTCCACAGAGGAAATCATGTGGATCTCTCAGCTCCATGAA 1325  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1326 AATAGTGGTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAACACAATGATTTTTTA 1385  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1386 TCTAGAAAAGCTCAGACACTGTTATTTATGACAGTGCATCTGCTCTCGAATACAGT 1445  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 DB 1446 TGGGAYAGCACCATTCTGGATCTCAAGGGTGCATTTCTGTATCATCAAGACCACTCCA 1505  
 QY 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 1506 TGCTCTTCAGCAATAAATAATCACTCTCAACTGCAGGAAACTCAGACGCTCTGCAGCCT 1565  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 1566 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACAGAA 1625  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 1626 GCCTGCCTTAAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 1685

QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 Db 1686 TATGAACCTGTTAGTACCAAGGCTCAAGGACCTCAAAAGTCAGACAATTACTAGACACT 1745  
 QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 Db 1746 ACTGATCCCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATTAACAAA 1805  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 Db 1806 CAATGGGTCTTTCAGCTTACCCGGAATATCTGTGTTTCTAGATCACCCTCTTTAAAT 1865  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 Db 1866 TTACTTCAAAATAAAGCATG 1886

## RESULT 8

ADC99131  
 ID ADC99131 standard; cDNA; 1959 BP.

XX AC ADC99131;

XX DT 01-JAN-2004 (first entry)

XX DE Human KPP cDNA - SEQ ID 84.

XX anti-HIV; anti-allergic; anti-inflammatory; antianaemic; antiparkinsonian;  
 KW nootropic; anticonvulsant; antiarteriosclerotic; antidiabetic;  
 KW immunosuppressive; antichryoid; cytostatic; hepatotropic; dermatological;  
 KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;  
 KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoiatric;  
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
 KW viricide; protozoacide; fungicide; kinase; phosphatase; KPP;  
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
 KW cancer; developmental; mental retardation; neurological;  
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
 KW helminthic infection; transgenic; gene therapy; human; ss; gene.

XX Homo sapiens.

XX WO2003033680-A2.

XX 24-APR-2003.

XX 17-OCT-2002; 2002WO-US033723.

XX 19-OCT-2001; 2001US-0345474P.

XX 02-NOV-2001; 2001US-0343910P.

XX 13-NOV-2001; 2001US-0333098P.

XX 16-NOV-2001; 2001US-0332424P.

XX 30-NOV-2001; 2001US-0334288P.

XX (INCY-) INCYTE GENOMICS INC.

XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
 PI Emerling BN, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;  
 PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;  
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
 PI Zebarjadian Y;

XX WPI; 2003-403214/38.

DR P-PSDB; ADC99079.

XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.

XX Claim 5; SEQ ID NO 84; 424pp; English.

XX

CC The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP cDNA of the  
 CC invention.

XX Sequence 1959 BP; 597 A; 430 C; 420 G; 512 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 192e-188 Length: 1959  
 Score: 197.00 Matches: 197  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 84.91% Indels: 0  
 DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x ADC99131 (1-1959)

QY 36 GluSerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSer 55  
 Db 1160 GAATCATCTGGATCCTCTCAGCTCCATGAAATAGTGGTCTCTCTGAAACTTCAAGGTCC 1219  
 QY 56 LeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMet 75  
 Db 1220 CTGCCAGCTCTCTCAAGACAATGATTTTATCTAGAAAAGCTCAAGACTGTTTATTTATG 1279  
 QY 76 LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArg 95  
 Db 1280 AAGCTGCATCACTGTCTGGAAATCACAGTTGGGATAGCACCATTCTGGATCTCAAGG 1339  
 QY 96 AlaAlaPheCysAspHisLysThrThrProCysSerSerAlaIleAsnProLeuSer 115  
 Db 1340 GCTGCATTTCTGTGATCACAGACCACTCCATGCTCTTCAGCAATAATAATCCACTCTCA 1399  
 QY 116 ThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLys 135  
 Db 1400 ACTGCAGGAAACTCAGAACGCTGTCAGGCTGGTATAGCCCGCAGCTGGATCCAGAGCAA 1459  
 QY 136 ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeu 155  
 Db 1460 AGGGAAGACATTGTGAACCAATGACAGAAGCTCCCTTAACCACTGGCTAGATGCCCTT 1519  
 QY 156 LeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArg 175  
 Db 1520 CTGTCCAGGACTTGATCATGAAAGAGGACTATGAATTTGTTAGTACCAAGCTCAAGG 1579  
 QY 176 ThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLys 195  
 Db 1580 ACCTCAAAAGTCAGACAATTTACTAGACACTACTGACATCTCCAGAGAGAGAAATTTGCAAA 1639  
 QY 196 ValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIle 215  
 Db 1640 GTTATAGTACAAAATTGAAAGATTAACAAACAAATGGGTCTTCAGCCTTTACCCGGAAATA 1699  
 QY 216 LeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 232  
 Db 1700 CTTGTGGTTTCTAGATCACCATCTTTAAATTACTTTCAAAATAAAGCATG 1750

## RESULT 9

ABX75870

ID ABX75870 standard; cDNA; 1620 BP.

XX AC ABX75870;

XX DT 30-APR-2003 (first entry)



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FT FT          /*tag= a
PN PN          /product= "CARD-3"
XX XX
XX XX
XX XX
PD PD          WO9940102-A1.
XX XX          12-AUG-1999.
XX XX
XX XX          05-FEB-1999; 99WO-US002544.
XX XX          06-FEB-1998; 98US-00019942.
PR PR          17-JUN-1998; 98US-00099041.
PR PR          08-DEC-1998; 98US-00207359.
XX XX          (MILL-) MILLENNIUM PHARM INC.
PA PA
XX XX          Bertin J;
PI PI
XX XX          WPI: 1999-494269/41.
DR DR          P-PSDB; AAY31140.
XX XX
XX XX          Novel CARD-3 and CARD-4 genes and polypeptides used or treating
PT PT          regulation of cellular proliferation and differentiation and cell
PT PT          survival.
XX XX
XX XX          Example 2; Fig 1; 181pp; English.
XX XX
XX XX          This invention describes the isolation of novel human caspase recruitment
CC CC          domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial
CC CC          murine CARD-4L protein and genes. The genes and proteins of the invention
CC CC          are involved in the regulation of caspase activation. The caspase
CC CC          recruitment domain (CARD) polynucleotides, polypeptides, homologues and
CC CC          antibodies can be used in screening assays, detection assays, predictive
CC CC          medicine and therapeutic and prophylactic methods of treatment. The
CC CC          methods may be used to diagnose and treat patients which are suffering
CC CC          from a disorder associated with abnormal level or rate of apoptotic cell
CC CC          death, abnormal activity of the Fas/APO-1 receptor complex, abnormal
CC CC          activity of the TNF receptor complex, or abnormal activity of a caspase.
CC CC          Diseases that may be treated include cancer (particularly follicular
CC CC          lymphoma, carcinomas associated with mutations in p53 and hormone-
CC CC          dependent tumours), autoimmune disorders (e.g. systemic lupus
CC CC          erythematosus, immune-mediated glomerulonephritis), viral infections,
CC CC          Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC CC          retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,
CC CC          anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.
CC CC          CARD-3 protein interacts with other cellular proteins, and so can be used
CC CC          for regulation of cellular proliferation and differentiation and cell
CC CC          survival. The CARD proteins may also be used to for screen drugs or
CC CC          compounds which modulate their activity. The CARD-4 gene can express a
CC CC          long transcript that encodes CARD-4L, a short transcript that encodes
CC CC          CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence
CC CC          encodes the human CARD-3 protein described in the method of the invention
XX XX
XX XX          SQ Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          6.9e-119          Length:          1931
Score:          128.00          Matches:          226
Percent Similarity: 99.12%          Conservative: 0
Best Local Similarity: 99.12%          Mismatches: 1
Query Match:          55.17%          Indels: 2
DB:          2          Gaps: 0

US-09-771-161A-93 (1-232) x AAZ09246 (1-1931)

QY          6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
DB          1153 TTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGAATATCTCTG 1212
QY          26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHisGlu 45
DB          1213 AACATACCTGTAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272
QY          46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65

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Db          1273 AATAGTGGTTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCTCTCAAGACATGATTTTAA 1332
QY          66 SerArgLysAlaGlnAspCysTyzPheMetLysLeuHisHisCysProGlyAsnHisSer 85
DB          1333 TCTAGAAAAGCTCAAGACTGTTATTTATTAAGCTGTCATCACTGTCTCTGGAATCACAGT 1392
QY          86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPr 105
DB          1393 TGGGATAGCACCATTTCTGGATCTCAAAAGGGCTGCAITTTCTGTGATCACAAAGACCAT-TCC 1451
QY          105 oCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
DB          1452 ATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGAAACTCAGAACGTCTCGAGCC 1511
QY          125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
DB          1512 TGGTATAGCCCCAGCAGTGCATCCAGAGCAAAAGGGAAGACATTGTGAAACCAATCACAGA 1571
QY          145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
DB          1572 AGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAGA 1631
QY          165 pTyrgluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
DB          1632 CTATGAACCTTGTAGTCAAGCCTACAAAGGACCTCAAAAGTCACAAATTTACTAGACAC 1691
QY          185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205
DB          1692 TACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAA 1751
QY          205 sGlnMetGlyLeuGlnProTyProGluIleLeuValValSerArgSerProSerLeuAs 225
DB          1752 ACAATGGGTCTTCAGCCCTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1811
QY          225 nLeuLeuGlnAsnLysSerMet 232
DB          1812 TTTACTTCAAAATAAAAGCATG 1833

RESULT 11
AAF30001
ID AAF30001 standard; cDNA; 1931 BP.
XX
AC AAF30001;
XX
DT 23-APR-2001 (first entry)
XX
DE Human CARD-3 cDNA.
XX
KW CARD-3; caspase recruitment domain; human; cancer; infection;
KW autoimmune disease; neurological disease; haematological disease;
KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;
KW antiinflammatory; apoptosis; diagnosis; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 214..1826
FT /*tag= a
FT /note= "the open reading frame is also specifically
FT claimed in Claim 1(a)"
XX
PN WO200100826-A2.
XX
PD 04-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US017691.
XX
PR 28-JUN-1999; 99US-00340620.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Bertin J;

```



XX WPI; 2001-061973/07.  
 DR P-PSDB; AAB20079.  
 XX  
 PT Isolated intracellular proteins predicted to be involved in regulating  
 PT caspase activation are used for diagnosis and treatment of e.g. cancer,  
 PT viral infections, autoimmune diseases, neurological diseases and  
 PT hematological disorders.  
 XX  
 PS Claim 1(a); Fig 1; 208pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding human caspase recruitment  
 CC domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a  
 CC database search using known CARD sequences. Plasmid pXEL17A containing  
 CC CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular  
 CC protein predicted to be involved in regulating caspase activation. It is  
 CC useful as a modulating agent in regulating cellular processes include  
 CC cell growth and cell death. Methods of diagnosing and treating patients  
 CC suffering from a disorder associated with an abnormal level or rate of  
 CC apoptotic cell death, abnormal activity of the Fas/APO-1 receptor  
 CC complex, abnormal activity of the tumour necrosis factor receptor complex  
 CC or abnormal activity of a caspase involve administering a compound that  
 CC modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6  
 CC e.g. a small molecule, anticense nucleic acid, ribozyme or polypeptide.  
 CC Such disorders include cancer, viral infection, autoimmune disorders,  
 CC neurological diseases, haematological disorders, inflammatory disorders  
 CC and immune disorders. CARD nucleic acids can be used to express CARD  
 CC proteins in a host cell e.g. for gene therapy applications, to detect a  
 CC genetic lesion and to modulate CARD activity  
 XX  
 SQ Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6.9e-119 Length: 1931  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 4 Gaps: 0  
 US-09-771-161A-93 (1-232) x AAF30001 (1-1931)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 Db 1153 TTACAGAGTGTTCACAGTGCCTACCTATGTGACAAAGAAATGGAATATCTCTG 1212  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1213 AACATACCTGTAATATGATGTCACAGAGAAATCATGTGGATCCTCTCAGCTCCATGAA 1272  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1273 AATAGTGTTCCTGAACTTCAGGTCCCTGCCAGCTCTCAAGACATGATTTTTHA 1332  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 Db 1333 TCTAGAAAAGCTCAAGACTGTATTTATGAAGTGCATCACTGTCTCTGAAATACAGT 1392  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
 Db 1393 TGGATAGCACCATTCTGGATCTCAAGAGGCTGCTTCGTGATCACAAGACCAT -TCC 1451  
 QY 105 OCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1452 ATGCTCTTCAGCAATATAATCCACTCTCACTGCAGGAACTCAGACGCTCTGCAGCC 1511  
 QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
 Db 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATATGACAGA 1571  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 Db 1572 AGCCTGCCTTACACAGTCGCTAGTAGCCCTCTGTCCAGGACTTGTATCATGAAAGAGGA 1631

QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 Db 1632 CTATGACTTGTAGTACCAAGCTCAAGACCTCAAAAGTCAGACAAATTACTAGACAC 1691  
 QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
 Db 1692 TACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1751  
 QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225  
 Db 1752 ACAATGGGTCTTACCGGAAATACTTGTGGTTCTAGATCACCATCTTTTAA 1811  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 Db 1812 TTTACTTCAAAATATAAAGCATG 1833  
 RESULT 12  
 ABK89280  
 ID ABK89280 standard; cDNA; 1931 BP.  
 XX  
 AC ABK89280;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human cDNA encoding caspase recruitment domain protein CARD-3.  
 XX  
 KW Human; ss; gene; caspase recruitment domain; CARD-3; CARD-4; LRR;  
 KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;  
 KW nuclear factor kappa B; cancer; viral infection; autoimmune disorder;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis;  
 KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;  
 KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;  
 KW gastrointestinal allergy; insulin-dependent diabetes;  
 KW bacterial infection; tuberculosis; lepromatous leprosy;  
 KW cell signalling disorder; tissue disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 214..1836  
 FT /\*tag= a  
 FT /product= "CARD-3"  
 XX  
 PN WO200253765-A1.  
 XX  
 PD 11-JUL-2002.  
 XX  
 XX 20-DEC-2001; 2001WO-US049798.  
 XX  
 XX 29-DEC-2000; 2000US-0258724P.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Bertin J, Philpott D, Sansonetti P, Girardin S;  
 XX WPI; 2002-583627/62.  
 XX P-PSDB; ABG31075.  
 DR  
 XX Identifying modulators of long form of caspase recruitment domain, CARD-  
 PT 4L useful for treating cancer, infections, and immune disorders, by  
 PT contacting test compound with CARD-4L and determining effect of the  
 PT compound.  
 XX  
 XX Example 2; Fig 1; 139pp; English.  
 XX  
 CC The invention relates to identifying (M1) a compound which modulates a  
 CC human or murine caspase recruitment domain (CARD)-4L (long form)  
 CC polypeptide with a by contacting the polypeptide with a test compound and  
 CC determining the effect of the test compound on the activity of the  
 CC polypeptide to identify a compound which modulates the polypeptide. The  
 CC method may be adapted for identifying a compound which binds to the LRR  
 CC (leucine rich repeat) domain of CARD-4. Also included is a method of



CC identifying a candidate compound for modulating LPS (lipopolysaccharide)-  
 CC mediated activation of nuclear factor-kappa B (NF-kB), by providing a  
 CC cell expressing a polypeptide comprising the LRR domain of CARD-4 and  
 CC harbouring LPS, exposing the cell to a test compound and measuring NF-kB  
 CC activation, where altered NF-kB activation polypeptide in the presence of  
 CC the test compound compared to the binding in the absence of the test  
 CC compound indicates that the test compound is a candidate compound for  
 CC modulating LPS-mediated activation of NF-kB. Modulators identified by  
 CC (M1) are useful for treating a disorder characterised by aberrant CARD-4  
 CC protein or nucleic acid. Compounds that modulate the activity of CARD-4L  
 CC are useful to treat or diagnose disorders such as cancer, viral  
 CC infections, autoimmune disorders e.g. systemic lupus erythematosus,  
 CC immune-mediated glomerulonephritis and arthritis, immune disorders, such  
 CC as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as  
 CC asthma, allergy, psoriasis, contact dermatitis, gastrointestinal  
 CC allergies, insulin-dependent diabetes, bacterial infections, including  
 CC tuberculosis, and lepromatous leprosy, disorders of cell signalling and  
 CC disorders of tissues. The present sequence is the human cDNA encoding  
 CC CARD-3  
 XX  
 SQ Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6.9e-119 Length: 1931  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservativity: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x ABK89280 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 1153 TTACAGAGTGTTCAGTCCATTCACCTATGTGACAGAGAAATGGAATATCTCTG 1212  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 1213 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1273 AATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAGACAAATGATTTTVA 1332  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 DB 1333 TCTAGAAAGCTCAGACTGTATTATTATGAGCTGCATCAGTCTCTGGAATCAGCT 1392  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
 DB 1393 TGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCGTGATCACAAGACCAT-TCC 1451  
 QY 105 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 DB 1452 ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAATCTCAGACGCTCGAGCC 1511  
 QY 125 OGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145  
 DB 1512 TGTATAGCCAGCAGTGGATCAGAGCAAAAGGGAAGCATTTGTGAACCAATGACAGA 1571  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 DB 1572 AGCTGCTTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGA 1631  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 DB 1632 CTATGAACCTGTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 1691  
 QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 DB 1692 TACTGATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATNACAA 1751  
 QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225

DB 1752 ACAATGGGTCTTACGCTTACCGGAATACTTGTTGGTTCTAGATCACCATCTTTAA 1811  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 DB 1812 TTTACTTCAAAATAAAGCATG 1833

RESULT 13  
 AAL40752  
 ID AAL40752 standard; cDNA; 1931 BP.  
 XX AAL40752;  
 AC AAL40752;  
 XX 27-SEP-2002 (first entry)  
 DE cDNA of human CARD-3 SEQ ID No 1.  
 KW Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimer's;  
 KW cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological;  
 KW neurotropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;  
 KW cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;  
 KW hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;  
 KW systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;  
 KW anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss.  
 XX Homo sapiens.  
 OS US6369196-B1.  
 PN 09-APR-2002.  
 PD 05-FEB-1999; 99US-00245281.  
 PF 06-FEB-1998; 98US-00019942.  
 PR 17-JUN-1998; 98US-00099041.  
 PR 08-DEC-1998; 98US-00207359.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Bertin J;  
 PI WPI: 2002-391988/42.  
 DR N-PSDB; AAO221107, AAO221108, AAO221109, AAO221110.  
 XX Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.  
 PT Example 2; Fig 1; 116pp; English.  
 PS The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and hormone-dependent tumours such as breast cancer, prostate cancer, and ovarian cancer), autoimmune disorders (such as systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections (such as those caused by herpes viruses, poxviruses, and adenoviruses), neurological diseases (such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, and the myelodysplastic syndromes. This polynucleotide sequence represents the cDNA of a human CARD relating to the invention  
 SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6.9e-119 Length: 1931  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservativity: 0

XX	Homo sapiens.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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Db	1333	TCAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTCTGGAATCACAGT	1392
Qy	86	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleValSerThrPr	105
Db	1393	TGGGATAGACCACTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAGACCAT-TCC	1451
Qy	105	oCysSerSerAlaIleAlaSerProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr	125
Db	1452	ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCC	1511
Qy	125	oGlyIleAlaGlnGlnTrpIleGlnSerIleValSerGluArgAlaValAsnGlnMetThrGl	145
Db	1512	TGATATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACAGA	1571
Qy	145	uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs	165
Db	1572	AGCTGCTTACCACTGCTAGATGCCCTCTGTCCAGGACTTGATCATGAAGAGA	1631
Qy	165	pTyrGluLeuValSerThrIleProThrArgThrSerIleValArgGlnLeuLeuAspTh	185
Db	1632	CTATGAACCTTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTACTAGACAC	1691
Qy	185	rThrAspIleGlnGlyGluGluPheAlaIleValIleValGlnIleValLeuLysAspAsnIy	205
Db	1692	TACTGACATCCCAAGGAGAGAATTTCCTCAAGGTTATAGTACAAAATTCGAAGATAACA	1751
Qy	205	sGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeuAs	225
Db	1752	ACAAATGGCTCTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA	1811
Qy	225	nLeuLeuGlnAsnLysSerMet	232
Db	1812	TTTACTTCAAAATAAAAGCATG	1833
RESULT 15			
ADB81363			
ID	ADB81363	standard; cDNA; 1931 BP.	
XX	AC	ADB81363;	
XX	DT	04-DEC-2003 (first entry)	
XX	DE	Human caspase recruitment domain 3 (CARD-3) cDNA.	
KW	XX	human; ss; gene; CARD-3; CARD-4; caspase recruitment domain; apoptosis;	
KW	KW	p75; tumour necrosis factor; TNF; neutrophin receptor; cancer;	
KW	KW	autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;	
KW	KW	viral infection; neurological; retinitis pigmentosa; haematologic;	
KW	KW	chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAX.	
OS	XX	Homo sapiens.	
PH	Key	Location/Qualifiers	
FT	CDS	214..1836	
FT	FT	/*tag= a	
FT	FT	/product= "CARD-3 protein"	
XX	XX	US2002061833-A1.	
PN	XX	23-MAY-2002.	
PD	XX	26-DEC-2000; 2000US-00748537.	
XX	XX	06-FEB-1998; 98US-00019942.	
PR	XX	17-JUN-1998; 98US-00099041.	
XX	XX	(BERT/) BERTIN J.	
PA	XX	(CHAO/) CHAO M V.	
XX	XX	Bertin J, Chao MV;	
XX	XX	WPI; 2003-657125/62.	

DR	P-PSDB; ADB81362.		
XX	Detecting compounds which alter binding of the caspase recruitment domain		
PT	(CARD)-3 polypeptide to the neutrophin receptor p75 is useful		
PT	to provide compounds for treating CARD-3 mediated disorders.		
XX	Disclosure; Fig 2; 40pp; English.		
PS	This invention relates to two novel genes CARD-3 and CARD-4 (caspase		
XX	recruitment domains), which are mediators of apoptosis and are useful in		
CC	the identification of compounds that modulate apoptosis. Specifically,		
CC	CARD-3 (also known as RLP2, RICK and CARDIAX) is known to be a mediator		
CC	of p75 (a member of the tumour necrosis factor (TNF) family), and is		
CC	believed to provide the switch for cell survival and cell death decisions		
CC	mediated by this p75 neutrophin receptor. Accordingly these genes, and		
CC	the proteins encoded thereof, are linked to certain disorders associated		
CC	with an increased number of cells surviving and proliferating when		
CC	apoptosis is inhibited. These include cancer, autoimmune disorders e.g.		
CC	systemic lupus and immune mediated glomerulonephritis, viral infections		
CC	such as those caused by the herpesvirus, neurological disorders such as		
CC	retinitis pigmentosa, haematologic diseases including chronic		
CC	neutropenia, as well as myocardial infarction and strokes. The present		
CC	invention further describes a novel method for determining whether a test		
CC	compound alters the binding of CARD-3 to p75, which comprises measuring		
CC	the binding of a polypeptide containing the CARD domain of CARD-3 to a		
CC	polypeptide comprising the death domain of p75 in the presence and		
CC	absence of the test compound, and determining if binding is altered. This		
CC	polynucleotide is the human CARD-3 cDNA sequence of the invention.		
XX	Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;		
SQ			
Alignment Scores:			
Pred. No.:	6.9e-119	Length:	1931
Score:	128.00	Matches:	226
Percent Similarity:	99.12%	Conservative:	0
Best Local Similarity:	99.12%	Mismatches:	1
Query Match:	55.17%	Indels:	2
DB:	9	Gaps:	0
US-09-771-161A-93 (1-232) x ADB81363 (1-1931)			
Qy	6	LeuGlnSerValSerSerAlaIleHisIleCysAspLysLysMetGluLeuSerLeu	25
Db	1153	TTACAGAGTGTTCAGGTGCCATTCACCTATGTGCAAGAGAAATGGAATATCTCTG	1212
Qy	26	AnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu	45
Db	1213	AACATCTCTTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGTCCATGAA	1272
Qy	46	AnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	65
Db	1273	AATAGTGGTCTCTCTGAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAATGATTTT	1332
Qy	66	SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer	85
Db	1333	CTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTCTGGAATCACAGT	1392
Qy	86	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleValSerThrPr	105
Db	1393	TGGGATAGACCACTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAGACCAT-TCC	1451
Qy	105	oCysSerSerAlaIleAlaSerProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr	125
Db	1452	ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCC	1511
Qy	125	oGlyIleAlaGlnGlnTrpIleGlnSerIleValSerGluArgAlaValAsnGlnMetThrGl	145
Db	1512	TGATATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACAGA	1571
Qy	145	uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs	165
Db	1572	AGCTGCTTACCACTGCTAGATGCCCTCTGTCCAGGACTTGATCATGAAGAGA	1631

Qy	165	pTyrGluLeuValSerThrIlysProThrArgThrSerLysValArgGlnLeuLeuAspTh	185
Db	1632	CTATGAACCTTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACAC	1691
Qy	185	rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy	205
Db	1692	TACTGACATCCAGGAGAGAAATTGGCAAAGTTATAGTACAAAAATTGAAAGATAACAA	1751
Qy	205	sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs	225
Db	1752	ACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCACTTTTAA	1811
Qy	225	nLeuLeuGlnAsnLysSerMet	232
Db	1812	TTTACTTCAAAATAAAAGCATG	1833

Search completed: April 1, 2004, 12:58:53  
Job time : 485 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 03:06:50 ; Search time 754 Seconds  
(without alignments)  
9403.505 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 1669

Sequence: 1 acctggtttataccagata.....caacagcctgtgtgtaaaa 1669

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 20

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002s:\*
- 7: geneseqn2003as:\*
- 8: geneseqn2003bs:\*
- 9: geneseqn2003cs:\*
- 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1079	64.6	2709	3	AAC77779	Human can	Aac77779 Human can
2	879	52.7	2024	3	Aaz46143	CDNA sequ	Aaz46143 CDNA sequ
3	827	49.6	2033	4	Aak94554	Human ful	Aak94554 Human ful
4	812	48.7	2501	6	Abk51169	CDNA enco	Abk51169 CDNA enco
5	812	48.7	2501	6	Aad45172	Human rec	Aad45172 Human rec
6	812	48.7	2502	3	Aaz48762	Human RIC	Aaz48762 Human RIC
7	785	47.0	1959	9	Adc99131	Human KPP	Adc99131 Human KPP
8	783	46.9	2098	2	Aax02558	Human BI	Aax02558 Human BI
9	682	40.9	1931	2	Aaz09246	Human CAR	Aaz09246 Human CAR
10	682	40.9	1931	4	Aaf30001	Human CAR	Aaf30001 Human CAR
11	682	40.9	1931	6	Abk89280	Human CDN	Abk89280 Human CDN
12	682	40.9	1931	6	Aal40752	CDNA of h	Aal40752 CDNA of h
13	682	40.9	1931	7	Abx75869	Human CDN	Abx75869 Human CDN
14	682	40.9	1931	9	Adb81363	Human cas	Adb81363 Human cas
15	682	37.9	1620	7	Abx75870	Human cas	Abx75870 Human cas
16	578	34.6	1619	6	Aal40753	DNA of hu	Aal40753 DNA of hu
17	363	21.7	491	8	Ach33353	Human end	Ach33353 Human end
18	220	13.2	299	6	Abk55074	Human col	Abk55074 Human col
19	179	10.7	575	4	Aak93010	Human CDN	Aak93010 Human CDN
20	130	7.8	762	7	AcD96414	Human col	AcD96414 Human col
21	60	3.6	60	6	Abm58531	Human spl	Abm58531 Human spl
22	60	3.6	60	6	Abn58793	Human spl	Abn58793 Human spl
23	60	3.6	60	6	Abn41051	Human spl	Abn41051 Human spl

24	50	3.0	50	6	ABZ04660	Human leu
25	49	2.9	108	2	AAT19776	Human gen
c 26	37	2.2	54	9	ADB81375	3' mutage
c 27	37	2.2	54	9	ADB81373	3' PCR pr
28	24	1.4	804	7	ACA47914	Prokaryot
29	23	1.4	32	9	ADB81372	5' PCR pr
30	22	1.3	30	2	AAX02614	Human BI
c 31	22	1.3	30	2	AAX02615	Human BI
c 32	22	1.3	1119	5	AAH6023	E. coli p
c 33	22	1.3	1119	5	AAH81375	Escherich
34	21	1.3	438	6	ABK16480	Gram posi
35	21	1.3	600	5	ABV53180	Human pro
c 36	21	1.3	712	4	AAH07021	Human CDN
c 37	21	1.3	761	4	AAH07379	Human CDN
c 38	21	1.3	1712	3	AAH07039	Human ORF
c 39	21	1.3	1805	4	AAH14699	Human CDN
c 40	21	1.3	1942	6	ABK35775	Human CDN
41	21	1.3	2648	4	ABL28950	Drosophill
42	21	1.3	2656	4	ABL28946	Drosophill
c 43	21	1.3	2674	2	AAZ42043	Human end
c 44	21	1.3	3034	4	AAZ03899	Human sec
c 45	21	1.3	3034	7	ABT16854	Human sec

#### ALIGNMENTS

RESULT 1  
AAC77779  
ID AAC77779 standard; cDNA; 2709 BP.  
XX  
AC AAC77779;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated gene sequence SEQ ID NO:173.  
XX

Human; cancer associated gene; cancer antigen; detection; cancer;  
diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;  
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;  
dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;  
immune disorder; haematopoietic cell disorder; autoimmune disorder;  
allergic reaction; graft versus host disease; organ rejection;  
haemostatic; thrombolytic; cardiovascular disorder; infection;  
neurological disease; drug screening; ss.

OS Homo sapiens.

XX WO200005350-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005882.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587533/55.

XX P-PSDB; AAB43570.

XX Novel isolated nucleic acids comprising sequences encoding peptides  
useful for treating or diagnosing e.g. cancer.

XX Claim 1; Page 751-752; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
AAB43398 to AAB44239. The proteins can have activities based on the  
tissues and cells the genes are expressed in. Example of activities

CC include: cytostatic; proliferative; vulnery; immunomodulator;  
 CC anti-diabetic; antiasthmatic; antirheumatic; antiarthritic;  
 CC anti-inflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB4240 represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 0 U; 10 Other;

Query Match 64.6%; Score 1079; DB 3; Length 2709;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1329; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

333 AGTTACAGAGTGTTCAGAGGCCATTCACCTATGTGACAGAGAGAGAAATGGAATATCTC 392  
 1204 AGTTACAGAGTGTTCAGAGGCCATTCACCTATGTGACAGAGAGAGAAATGGAATATCTC 1263  
 393 TGAACATACCTGTAATATCATGTCCTCAACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
 1264 TGAACATACCTGTAATATCATGTCCTCAACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1323  
 453 AAAATAGTGGTTCCTGAACTTCAAGGTCCTGCGAGCTCCCTCAAGACAAATGATTTT 512  
 1324 AAAATAGTGGTTCCTGAACTTCAAGGTCCTGCGAGCTCCCTCAAGACAAATGATTTT 1383  
 513 TATCTAGAAAGCTCAAGAGCTGTTATTTATGAAGCTGCACTACTGTCCTGGAATACACA 572  
 1384 TATCTAGAAAGCTCAAGAGCTGTTATTTATGAAGCTGCACTACTGTCCTGGAATACACA 1443  
 573 GTTGGGATAGCACCATTCTCGATCTCAAGAGGCTGCAATCTGTGATCAACAGACCACTC 632  
 1444 GTTGGGAYAGCACCATTCTCGATCTCAAGAGGCTGCAATCTGTGATCAACAGACCACTC 1503  
 633 CATGCTCTTACGCAATATTAATCCACTCTCACTCAGGAACTCAGAACGTCGAGC 692  
 1504 CATGCTCTTACGCAATATTAATCCACTCTCACTCAGGAACTCAGAACGTCGAGC 1563  
 693 CTGTTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGGAACCAATGACAG 752  
 1564 CTGTTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGGAACCAATGACAG 1623  
 753 AAGCCTCCCTTAAACAGTCGCTAGATCCCTTCTGTCCAGGACTTGTATCATGAAGAGG 812  
 1624 AAGCCTCCCTTAAACAGTCGCTAGATCCCTTCTGTCCAGGACTTGTATCATGAAGAGG 1683  
 813 ACTATGAAGTGTGTAGTACCAAGCTCAGAGGCTCAAAAGTCAGACAAATTTACTAGACA 872  
 1684 ACTATGAAGTGTGTAGTACCAAGCTCAGAGGCTCAAAAGTCAGACAAATTTACTAGACA 1743  
 873 CTACTGATCATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACA 932  
 1744 CTACTGATCATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACA 1803  
 933 AACAAATGGGTCTTTCAGCTTACCCGGAATATCTGTGGTTCCTAGATCAACCATCTTTAA 992  
 1804 AACAAATGGGTCTTTCAGCTTACCCGGAATATCTGTGGTTCCTAGATCAACCATCTTTAA 1863  
 993 ATTTTACTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGAGAAATGTGTTTCATAA 1052  
 1864 ATTTTACTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGAGAAATGTGTTTCATAA 1923

1053 AAGGATATTTATATCTCTCTGTTGACTTTTTTATATAAAATCCGTCAGTATTAAG 1112  
 1924 AAGGATATTTATATCTCTCTGTTGACTTTTTTATATAAAATCCGTCAGTATTAAG 1983  
 1113 CTTTATGAGGTTCTTTGGGTAATAATATAGTCTCCCTCCATGACACTGCGAGTATTTT 1172  
 1984 CTTTATGAGGTTCTTTGGGTAATAATATAGTCTCCCTCCATGACACTGCGAGTATTTT 2043  
 1173 TTAATTAATACAGTAAGTAAGTTTGAATTTTGTACATAGTTCAATTTTATGCTCTCTT 1232  
 2044 TTAATTAATACAGTAAGTAAGTTTGAATTTTGTACATAGTTCAATTTTATGCTCTCTT 2103  
 1233 TGTAAACAGAAACCACTTTTAAAGGATAGTAATATTTCTTTTATAACAGTCGCTTAAG 1292  
 2104 TGTAAACAGAAACCACTTTTAAAGGATAGTAATATTTCTTTTATAACAGTCGCTTAAG 2163  
 1293 GTAAGATGATTTTCTGATGGAAGCCATTTTCAATTCATGTTCTTTCATGATTTATTTGTT 1352  
 2164 GTATGATGATTTTCTGATGGAAGCCATTTTCAATTCATGTTCTTTCATGATTTATTTGTT 2223  
 1353 ACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTTACCCACGACAGACAGT 1412  
 2224 ACTTGTCTAARAWGCAATTTGATTTTATGAAGTATATACCTTTTACCCACGACAGACAGT 2283  
 1413 ACAGAAATCCCTGCTTAAATCCAGGCTTAATTTGCCCTACAAAGGGTTATTAATTTAA 1472  
 2284 ACAGAAATCCCTGCTTAAATCCAGGCTTAATTTGCCCTACAAAGGGTTATTAATTTAA 2343  
 1473 ACTCCATTTATAGGATACATTTTAAAGTTTATTTATGAATTCCTTTTAAATGATAT 1532  
 2344 ACTCCATTTATAGGATACATTTTAAAGTTTATTTATGAATTCCTTTTAAATGATAT 2403  
 1533 TTCAAAGGTAAGAAACAATACAAATAAAGAAAGAAATAATATATATACCGGCTTCCCTG 1592  
 2404 TTCAAAGGTAAGAAACAATACAAATAAAGAAAGAAATAATATATATATACCGGCTTCCCTG 2463  
 1593 TCCCAATTTTAACTCAGCCTTCCCTACTGTCCAAACCAACCAAGCTAAATAAGTCAA 1652  
 2464 TCCCAATTTTAACTCAGCCTTCCCTACTGTCCAAACCAACCAAGCTAAATAAGTCAA 2523  
 1653 CAGCTGATGTGTA 1666  
 2524 CAGCTGATGTGTA 2537

RESULT 2  
 AAZ46143  
 ID AAZ46143 standard; cDNA; 2024 BP.  
 XX  
 AC AAZ46143;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE cDNA sequence encoding a human phosphorylation effector PHSP-6.  
 XX  
 KW Human; phosphorylation effector; PHSP; proliferative disorder;  
 KW immune disorder; neuronal disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 203..1825  
 FT /\*tag= a  
 FT /product= "phosphorylation effector"  
 XX  
 PN WO200006728-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 PF 28-JUL-1999; 99WO-US017132.  
 XX  
 PR 28-JUL-1998; 98US-0155213P.  
 PR 14-SEP-1998; 98US-0155196P.

PR 14-OCT-1998; 98US-01552339P.  
PR 03-NOV-1998; 98US-0106889P.  
PR 19-NOV-1998; 98US-0109093P.  
PR 22-DEC-1998; 98US-0113796P.  
PR 12-JAN-1999; 99US-0155233P.  
XX (INCY-) INCYTE PHARM INC.  
PI Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX WPI; 2000-183125/16.  
DR P-PSDB; AAY68774.  
XX New human phosphorylation effectors useful for the diagnosis, treatment  
PT and prevention of proliferative, immune and neuronal disorders.  
XX Claim 9; Page 121-122; 142pp; English.  
XX AA246138-246168 encode human phosphorylation effectors (PHSP), designated  
CC PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the  
CC specification). The sequences were isolated from cDNA libraries prepared  
CC from various human tissues. The PHSP proteins are useful for the  
CC diagnosis, treatment and prevention of proliferative disorders, immune  
CC disorders and neuronal disorders. The PHSP proteins form pharmaceutical  
CC compositions which useful for treating or preventing disorders associated  
CC with decreased PHSP expression/activity. PHSP antagonists are useful for  
CC treating or preventing disorders associated with increased PHSP  
CC expression/activity  
XX  
SQ Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 U; 0 Other;  
Query Match 52.7%; Score 879; DB 3; Length 2024;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 879; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCAGGTGCCATTACCTATGTGACAGAGAAATGGAATTATCTC 392  
DB 1140 AGTTACAGAGTGTTCAGGTGCCATTACCTATGTGACAGAGAAATGGAATTATCTC 1199  
QY 393 TGAACATAGTGTAAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGTCCATG 452  
DB 1200 TGAACATAGTGTAAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGTCCATG 1259  
QY 453 AAAATAGTGTCTCTGAAACTTCAAGGTCCCTGCGAGTCTCTCAAGACAATGATTTT 512  
DB 1260 AAAATAGTGTCTCTGAAACTTCAAGGTCCCTGCGAGTCTCTCAAGACAATGATTTT 1319  
QY 513 TATCTAGAAAAGCTCAAGACTGTATTATTAAGAGTGCATCACTCTCTGGAAATCACA 572  
DB 1320 TATCTAGAAAAGCTCAAGACTGTATTATTAAGAGTGCATCACTCTCTGGAAATCACA 1379  
QY 573 GTTGGATAGCACCATTCTTGATCTCAAGGGCTGCATCTGTGATCAAGACCACTC 632  
DB 1380 GTTGGATAGCACCATTCTTGATCTCAAGGGCTGCATCTGTGATCAAGACCACTC 1439  
QY 633 CATGCTCTTCAGCAATAATAATCACTCTCAACTCAGAGAACTCAGAACGTCTGCAGC 692  
DB 1440 CATGCTCTTCAGCAATAATAATCACTCTCAACTCAGAGAACTCAGAACGTCTGCAGC 1499  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAATACAG 752  
DB 1500 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAATACAG 1559  
QY 753 AAGCCTGCTTAACAGTGCCTAGATGCCCTTCTGTCCAGGGACTGTGATCATGAAGAGG 812  
DB 1560 AAGCCTGCTTAACAGTGCCTAGATGCCCTTCTGTCCAGGGACTGTGATCATGAAGAGG 1619  
QY 813 ACTATGACTTGTAGTACCAAGCCCTACAGGACCTCAAAAGTCCAGCAATTAAGACA 872  
DB 1620 ACTATGACTTGTAGTACCAAGCCCTACAGGACCTCAAAAGTCCAGCAATTAAGACA 1679

QY 873 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932  
DB 1680 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1739  
QY 933 AACAAATGGTCTTCCAGCCTTACCCGGAATACTTTGGTGTCTAGATCACCATCTTTAA 992  
DB 1740 AACAAATGGTCTTCCAGCCTTACCCGGAATACTTTGGTGTCTAGATCACCATCTTTAA 1799  
QY 993 ATTTACTTCAAAATAAAAGCATGTAAAGTACCTTTTATATAAAATCCGAGATATAAG 1112  
DB 1800 ATTTACTTCAAAATAAAAGCATGTAAAGTACCTTTTATATAAAATCCGAGATATAAG 1859  
QY 1053 AAGGATATTTATATCTCTGTGCTTTGACTTTTATATAAAATCCGAGATATAAG 1112  
DB 1860 AAGGATATTTATATCTCTGTGCTTTGACTTTTATATAAAATCCGAGATATAAG 1919  
QY 1113 CTTTATGAAGTCTCTTTGGGTAATAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1172  
DB 1920 CTTTATGAAGTCTCTTTGGGTAATAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1979  
QY 1173 TTAATTAATACAAAGTAAAGTTTGAATTTTGCTACATA 1211  
DB 1980 TTAATTAATACAAAGTAAAGTTTGAATTTTGCTACATA 2018  
RESULT 3  
AAK94554  
ID AAK94554 standard; cDNA; 2033 BP.  
XX AAK94554;  
AC AAK94554;  
DT 06-NOV-2001 (first entry)  
DE Human full-length cDNA, SEQ ID NO: 3453.  
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX Homo sapiens.  
OS  
PN EP1130094-A2.  
XX  
PD 05-SEP-2001.  
PF 07-JUL-2000; 2000EP-00114089.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
DR WPI; 2001-524255/58.  
DR P-PSDB; AAM93621.  
XX  
PT 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX  
PS Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.  
XX  
CC The invention relates to primers for synthesising full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesising the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a full length human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in CD-ROM format directly

CC	from BPO
XX	
SQ	Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;
	Query Match            49.6%; Score 827; DB 4; Length 2033;
	Best Local Similarity   99.9%; Pred. No. 0;
	Matches   877; Conservative   0; Mismatches   1; Indels   0; Gaps   0;
QY	333 AGTTACAGAGTGTTCCTCAAGTGCCATTACCTATGTGACAAGAAGAAATGGAATTAATCTC 392
DB	
DB	1156 AGTTACAGAGTGTTCCTCAAGTGCCATTACCTATGTGACAAGAAGAAATGGAATTAATCTC 1215
QY	393 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
DB	
DB	1216 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCATG 1275
QY	453 AAAATAGTGGTCTCTCCCGAAACTTCAAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTT 512
DB	
DB	1276 AAAATAGTGGTCTCTCCCGAAACTTCAAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTT 1335
QY	513 TATCTAGAAAAGCTCAAGACTGTGTATTTTATGAAGCTGCATCACTGTCCTGGAAAAACACA 572
DB	
DB	1336 TATCTAGAAAAGCTCAAGACTGTGTATTTTATGAAGCTGCATCACTGTCCTGGAAAAACACA 1395
QY	573 GTTGGGATAGCACCATTTCTTGGATCTCAAAGGGCTGCATTTCTGTGATCAAGAACCACCTC 632
DB	
DB	1396 GTTGGGATAGCACCATTTCTTGGATCTCAAAGGGCTGCATTTCTGTGATCAAGAACCACCTC 1455
QY	633 CATGCTCTTCAGCAATAAATAACCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGC 692
DB	
DB	1456 CATGCTCTTCAGCAATAAATAACCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGC 1515
QY	693 CTGGTATAGCCCAGCAGTGGATCAGAGCAAAAAGGGGAAGACATTGTGAAACCAATGACAG 752
DB	
DB	1516 CTGGTATAGCCCAGCAGTGGATCAGAGCAAAAAGGGGAAGACATTGTGAAACCAATGACAG 1575
QY	753 AAGCCTGCCCTTAAACAGCTCGCTAGATGCCCTTCTGTCCAGGACTTCATCATGAAAGAGG 812
DB	
DB	1576 AAGCCTGCCCTTAAACAGCTCGCTAGATGCCCTTCTGTCCAGGACTTCATCATGAAAGAGG 1635
QY	813 ACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGTAGACA 872
DB	
DB	1636 ACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGTAGACA 1695
QY	873 CTACTGCATCCAAGGAGAAGAAATTCGCAAGTTATAGTACAAAAATTGAAGATGAACA 932
DB	
DB	1696 CTACTGCATCCAAGGAGAAGAAATTCGCTAAAGTTATAGTACAAAAATTGAAGATGAACA 1755
QY	933 AACAAATGGGTCTTCAGCCTTTACCCGGAATACCTTGTGGTTCTCTAGATCACCATCTTTAA 992
DB	
DB	1756 AACAAATGGGTCTTCAGCCTTTACCCGGAATACCTTGTGGTTCTCTAGATCACCATCTTTAA 1815
QY	993 ATTTACTTCAAAATAAAGCATGTAAGTGAATGTGTTCCTCAAGAGAAATGTGTTTCATAA 1052
DB	
DB	1816 ATTTACTTCAAAATAAAGCATGTAAGTGAATGTGTTCCTCAAGAGAAATGTGTTTCATAA 1875
QY	1053 AAGGATATTTATATCTCTGTGTGCTTTGACATTTTTTTATATATAAATCCGTGAGTATTAAG 1112
DB	
DB	1876 AAGGATATTTATATCTCTGTGTGCTTTGACATTTTTTTATATAAATCCGTGAGTATTAAG 1935
QY	1113 CTTTATTTGAAGGTTCTTTGGGTAAATATTAAGTCTCCCTCCATGACACTGCAGTATTTTTT 1172
DB	
DB	1936 CTTTATTTGAAGGTTCTTTGGGTAAATATTAAGTCTCCCTCCATGACACTGCAGTATTTTTT 1995
QY	1173 TTAAATTAATACAAGTAAAAAGTTTGGAAATTTTGCTACAT 1210
DB	
DB	1996 TTAAATTAATACAAGTAAAAAGTTTGGAAATTTTGCTACAT 2033

RESULT 4  
ABK51169  
ID ABK51169 standard; cDNA; 2501 BP

AC	ABK51169;
XX	30-JUL-2002 (first entry)
XX	cDNA encoding human cellular kinase RICK protein.
DE	Human, virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;
KW	RIP; Nck-Interacting Kinase; MKK3; SRPK-2; gene; ss.
KW	Homo sapiens.
OS	
XX	Key Location/Qualifiers
FH	CDS 225..1847
FT	/Cag= a
FT	/product= "Human cellular kinase RICK"
XX	EPI201765-A2.
PN	
XX	02-MAY-2002.
PD	
XX	15-OCT-2001; 2001EP-00124604.
PF	
XX	16-OCT-2000; 2000US-0240750P.
PR	(AXXI-) AXXIMA PHARM AG.
XX	Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
DI	
XX	WPI; 2002-373930/41..
DR	P-PSDB; AAU80369.
DR	
XX	Identifying agents for treatment or prevention of cytomegalovirus
PT	infection, comprises contacting test compound with cellular kinase and
PT	detecting change in cellular kinase activity.
XX	Disclosure; Page 20-23; 49pp; English.
PS	
XX	The present invention relates to a new method for identifying compounds
CC	for treating and/or preventing cytomegalovirus (CMV) infection and/or
CC	related diseases. The method of the invention comprises contacting a test
CC	compound with at least one of the cellular kinases RICK, RIP, Nck-
CC	interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase
CC	activity. The method of the invention can be used to treat and/or prevent
CC	CMV infections and related diseases. Oligonucleotides that can detect the
CC	specified kinases can also be used for diagnosis of infection. The
CC	present nucleic acid sequence encodes the human cellular kinase RICK
CC	protein of the invention, as described above
XX	
SQ	Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;
	Query Match 48.7%; Score 812; DB 6; Length 2501;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	333 AGTTACAGAGTGTTCGAAGTGCCATTCACCTATGTCACAAGAGAATAATGGATTATCTC 392
Dd	1162 AGTTACAGAGTGTTCGAAGTGCCATTCACCTATGTCACAAGAGAATAATGGATTATCTC 1221
Qy	393 TGAACATACCTGTAATCATGGTGCACAAGAGAAATCATGTGGATCCTCTCACGCTCCATG 452
Dd	1222 TGAACATACCTGTAATCATGGTGCACAAGAGAAATCATGTGGATCCTCTCACGCTCCATG 1281
Qy	453 AAAATAGTGGTTCTCTGAAAACCTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTT 512
Dd	1282 AAAATAGTGGTTCTCTGAAAACCTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTT 1341
Qy	513 TAATCTGAAAAGCTCAAGACTGTTATTTTATGAAGCTGGATCACTGCTCGGAAAAATCACA 572
Dd	1342 TAATCTGAAAAGCTCAAGACTGTTATTTTATGAAGCTGGATCACTGCTCGGAAAAATCACA 1401
Qy	573 GTTGGGATAGCACCATTCTTGGATCTCAAAGGCGTCATTTCTGTGATCAAGAACCACTC 632
Dd	1402 GTTGGGATAGCACCATTCTTGGTCTCAAAGGCGTCATTTCTGTGATCAAGAACCACTC 1461



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QY 633 CATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACTCTGCAGC 692
Db 1462 CATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACTCTGCAGC 1521
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 752
Db 1522 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 1581
QY 753 AAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 812
Db 1582 AAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 1641
QY 813 ACTATGAACCTTGTATGATACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 872
Db 1642 ACTATGAACCTTGTATGATACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 1701
QY 873 CTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932
Db 1702 CTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1761
QY 933 AACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAA 992
Db 1762 AACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAA 1821
QY 993 ATTTACTTCAAAATAAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1052
Db 1822 ATTTACTTCAAAATAAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1881
QY 1053 AAGGATATTTATATCTCTGCTTGTGACTTTTTTATATAAAATCCGAGATATAAG 1112
Db 1882 AAGGATATTTATATCTCTGCTTGTGACTTTTTTATATAAAATCCGAGATATAAG 1941
QY 1113 CTTTATTGAAGTCTTTCGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTT 1172
Db 1942 CTTTATTGAAGTCTTTCGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTT 2001
QY 1173 TTAATTAATACAAAGTAAAGTT 1195
Db 2002 TTAATTAATACAAAGTAAAGTT 2024

RESULT 5
AAD45172
ID AAD45172 standard; DNA; 2501 BP.
XX AC AAD45172;
XX DT 27-DEC-2002 (first entry)
XX DE Human receptor interacting protein (RIP)2 DNA.
XX KW Human; receptor interacting protein; RIP2; antisense; gene therapy; gene
XX ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT 225..1847
XX FT /*tag= a
XX FT /product= "Human RIP2 protein"
XX PN US6426221-B1.
XX PP 30-JUL-2002.
XX PR 01-AUG-2001; 2001US-00920663.
XX PR 01-AUG-2001; 2001US-00920663.
XX PR (ISIS-) ISIS PHARM INC.
XX PA Ward DT, Cowser LM;
XX PI

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XX WPI; 2002-673017/72.
DR P-PSDB; AAE27882.
XX PT New antisense oligonucleotide that targets regions of a nucleic acid
PT encoding human receptor interacting protein (RIP)2, for treating diseases
PT associated with RIP2 expression.
XX PS Claim 1; Col 49-54; 35pp; English.
XX CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding human receptor interacting protein (RIP)2 to inhibit its
CC expression. Antisense compounds are used for treating diseases associated
CC with RIP2 expression. They are also useful in antisense gene therapy. The
CC present sequence is human RIP2 DNA
XX SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;

Query Match 48.7%; Score 812; DB 6; Length 2501;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTGCCTTCACTATGTGACAAAGAGAAATGGAAATTTATCTC 392
Db 1162 AGTTACAGAGTGTTCCTCAAGTGCCTTCACTATGTGACAAAGAGAAATGGAAATTTATCTC 1221
QY 393 TGAACATACCTGTAAATCATGTCTCCAAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
Db 1222 TGAACATACCTGTAAATCATGTCTCCAAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1281
QY 453 AAAATAGTGGTCTCTGAAACTTCAAGTCTCCAGGTCCTCAAGCAATGATTTTT 512
Db 1282 AAAATAGTGGTCTCTGAAACTTCAAGTCTCCAGGTCCTCAAGCAATGATTTTT 1341
QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAGTCTGCTGAAATCACA 572
Db 1342 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAGTCTGCTGAAATCACA 1401
QY 573 GTTGGGATAGCACCATTCTTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCCTC 632
Db 1402 GTTGGGATAGCACCATTCTTGGTCTCAAAGGGCTGCATTTCTGTGATCACAAGACCCTC 1461
QY 633 CATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACCTCTGCAGC 692
Db 1462 CATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACCTCTGCAGC 1521
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 752
Db 1522 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 1581
QY 753 AAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 812
Db 1582 AAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 1641
QY 813 ACTATGAACCTTGTATGATACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 872
Db 1642 ACTATGAACCTTGTATGATACCAAGCCTCAAAAGTCAGACAATTTACTAGACA 1701
QY 873 CTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932
Db 1702 CTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1761
QY 933 AACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAA 992
Db 1762 AACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAA 1821
QY 993 ATTTACTTCAAAATAAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1052
Db 1822 ATTTACTTCAAAATAAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1881
QY 1053 AAGGATATTTATATCTCTGCTTGTGACTTTTTTATATAAAATCCGAGATATAAG 1112
Db 1882 AAGGATATTTATATCTCTGCTTGTGACTTTTTTATATAAAATCCGAGATATAAG 1941

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QY 1113 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTT 1172  
 Db 1942 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTT 2001  
 QY 1173 TTAATTAATCAAGTAAAGTT 1195  
 Db 2002 TTAATTAATCAAGTAAAGTT 2024

RESULT 6  
 AAZ48762  
 ID AAZ48762 standard; cDNA; 2502 BP.

XX AC AAZ48762;  
 XX DT 21-MAR-2000 (first entry)  
 XX DE Human RICK coding sequence.

XX RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
 KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
 KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
 KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
 KW aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.

XX OS Homo sapiens.

XX PN WO995134-A2.

XX PD 04-NOV-1999.

XX PF 27-APR-1999; 99WO-US009183.

XX PR 27-APR-1998; 98US-00069023.

XX PA (UNMI ) UNIV MICHIGAN.

XX PI Nunez G, Inohara N, Koseki T;

XX DR WPI; 2000-072163/06.

XX DR P-PSDE; AAY59404.

XX PT Compositions for identifying apoptosis signaling pathway inhibitors  
 useful for treating diseases.

XX PS Claim 8; Fig 7b; 93pp; English.

XX This sequence encodes the human RICK (RIP-like interacting CLARP kinase)  
 protein of the invention. The RICK protein acts as a positive regulator  
 of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
 during CD95 signalling. The invention provides methods for identifying  
 apoptosis signalling pathway inhibitors and activators, and methods and  
 compositions for screening compounds which will modulate the interactions  
 of the various compositions identified: ARC, RICK, and the CIDE family of  
 activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening  
 assays for agents, useful in the diagnosis, prognosis or treatment of  
 disease associated with excess cell growth and dysregulation of  
 apoptosis. Complexes containing RICK and CLARP can be used in drug  
 screening assays to identify inhibitor molecules blocking CD95-mediated  
 apoptosis. Overexpression of ARC in an in vitro cell system can be used  
 to identify inhibitors of the enzymatic activity of caspase-8.  
 Identification of ARC-like inhibitory compounds may be useful for gene  
 therapy treatment of disease with increased cell death in muscle tissue  
 and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
 treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
 ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
 can be used as reagents for the preparation or affinity chromatography  
 media, and for diagnostically measuring RICK levels. A specific inhibitor  
 of an essential step in the biochemistry of apoptosis is needed. RICK  
 interaction with intracellular factors such as CLARP and FADD appears to  
 be essential for apoptosis, inhibitors of RICK binding to intracellular  
 apoptosis factors are potential drug candidates

XX SQ Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other;.  
 Query Match 48.7%; Score 812; DB 3; Length 2502;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 333 AGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAGAGAAATGGAATATCTC 392  
 Db 1163 AGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAGAGAAATGGAATATCTC 1222  
 QY 393 TGAACATACCTGTAAATCATGGTCCACAGAGAGAAATCATGTGATCCTCTCAGCTCCATG 452  
 Db 1223 TGAACATACCTGTAAATCATGGTCCACAGAGAGAAATCATGTGATCCTCTCAGCTCCATG 1282  
 QY 453 AAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTT 512  
 Db 1283 AAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTT 1342  
 QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTCTCTGGAAATCACA 572  
 Db 1343 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTCTCTGGAAATCACA 1402  
 QY 573 GTTGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCAAGACCACTC 632  
 Db 1403 GTTGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCAAGACCACTC 1462  
 QY 633 CATGCTCTTCAGCAATAAATCACTCTCAACTCAGAGAAACTCAGAACGTCGAGC 692  
 Db 1463 CATGCTCTTCAGCAATAAATCACTCTCAACTCAGAGAAACTCAGAACGTCGAGC 1522  
 QY 693 CTGCTATAGCCAGCAGTGCATCCAGAGCAAAAGGAGACATTTGGAACCAATCAGAG 752  
 Db 1523 CTGCTATAGCCAGCAGTGCATCCAGAGCAAAAGGAGACATTTGGAACCAATCAGAG 1582  
 QY 753 AAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTTGATCATGAAAGAGG 812  
 Db 1583 AAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTTGATCATGAAAGAGG 1642  
 QY 813 ACTATGAACCTTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAAATTAAGACA 872  
 Db 1643 ACTATGAACCTTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAAATTAAGACA 1702  
 QY 873 CTACTCACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
 Db 1703 CTACTCACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1762  
 QY 933 AACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAA 992  
 Db 1763 AACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAA 1822  
 QY 993 ATTACTTCAAATAAAGCATGTAGTCACTGTTTTTCAAGAGAAATGTGTTTCATAA 1052  
 Db 1823 ATTACTTCAAATAAAGCATGTAGTCACTGTTTTTCAAGAGAAATGTGTTTCATAA 1882  
 QY 1053 AAGGATATTATATCTCTGTGCTTTGACTTTTTTATATAAATCCGTGAGTATTAAG 1112  
 Db 1883 AAGGATATTATATCTCTGTGCTTTGACTTTTTTATATAAATCCGTGAGTATTAAG 1942  
 QY 1113 CTTTATGAGGTTCTTTGGTAAATATTAGTCTCCCTCATGACACTCGAGTATTTTT 1172  
 Db 1943 CTTTATGAGGTTCTTTGGTAAATATTAGTCTCCCTCATGACACTCGAGTATTTTT 2002  
 QY 1173 TTAATTAATCAAGTAAAGTT 1195  
 Db 2003 TTAATTAATCAAGTAAAGTT 2025

RESULT 7

ADC99131

ID ADC99131 standard; cDNA; 1959 BP.

XX AC ADC99131;

XX	01-JAN-2004 (first entry)	Db	1158	AGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCCTCTGAACTTCAAGGT	1217
XX	Human KPP CDNA - SEQ ID 84.	QY	483	CCCTGCCAGCTCCTCAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTATTATTTA	542
XX	anti-HIV; anti-allergic; anti-inflammatory; antianaemic; antiparkinsonian;	Db	1218	CCCTGCCAGCTCCTCAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTATTATTTA	1277
XX	nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;	QY	543	TGAAGCTGCATCCTCTCTGGAAATCAAGTTGGATAGCACCATTCTTGGATCTCAAA	602
XX	immunosuppressive; antithyroid; cytosstatic; hepatotropic; dermatological;	Db	1278	TGAAGCTGCATCCTCTCTGGAAATCAAGTTGGATAGCACCATTCTTGGATCTCAAA	1337
XX	antidiabetic; nephrotropic; angiot; thyromimetic; neuroprotective;	QY	603	GGGCTGCATCTCTGATCACAAGACCACTCCATGCTCTTCAGCAATATAAATCAACTCT	662
XX	osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoiatric;	Db	1338	GGGCTGCATCTCTGATCACAAGACCACTCCATGCTCTTCAGCAATATAAATCAACTCT	1397
XX	uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;	QY	663	CAACTGCAGGAACTCAGAACCTCTGCAGCTGGTATAGCCAGCAGTGGATCCAGAGCA	722
XX	virucide; protozoacide; fungicide; kinase; phosphatase; KPP;	Db	1398	CAACTGCAGGAACTCAGAACCTCTGCAGCTGGTATAGCCAGCAGTGGATCCAGAGCA	1457
XX	cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;	QY	723	AAAGGGAAGACATTTGTGAACCAATGACAGAGCTGCTTAAACCAAGTCGCTAGATGCC	782
XX	cancer; developmental; mental retardation; neurological;	Db	1458	AAAGGGAAGACATTTGTGAACCAATGACAGAGCTGCTTAAACCAAGTCGCTAGATGCC	1517
XX	Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;	QY	783	TTCTGTCCAGGACTTGTATGAAAGGAGGACTATGAACCTTGTAGTACCAAGCTTACAA	842
XX	diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;	Db	1518	TTCTGTCCAGGACTTGTATGAAAGGAGGACTATGAACCTTGTAGTACCAAGCTTACAA	1577
XX	helminthic infection; transgenic; gene therapy; human; ss; gene.	QY	843	GGACCTCAAAAGTCAAGCAATTTACTAGACACTACTGACATCCAAAGAGAGAAATTTGCCA	902
OS	Homo sapiens.	Db	1578	GGACCTCAAAAGTCAAGCAATTTACTAGACACTACTGACATCCAAAGAGAGAAATTTGCCA	1637
XX	WO2003033680-A2.	QY	903	AAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAA	962
XX	24-APR-2003.	Db	1638	AAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAA	1697
XX	17-OCT-2002; 2002WO-US033723.	QY	963	TACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAATGA	1022
XX	19-OCT-2001; 2001US-0345474P.	Db	1698	TACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAATGA	1757
XX	02-NOV-2001; 2001US-0343910P.	QY	1023	CTGTTTTCACAAAGAAATGTGTTTTCATAAAAGGATATTTATATCTCTGCTGCTTGACT	1082
XX	13-NOV-2001; 2001US-0333098P.	Db	1758	CTGTTTTCACAAAGAAATGTGTTTTCATAAAAGGATATTTATATCTCTGCTGCTTGACT	1817
XX	16-NOV-2001; 2001US-0332424P.	QY	1083	TTTTTATATAAAATCCGTGAGTATTTAAAGCTTTTATGAAGCTTTCTTTGGGTAAATATTA	1142
XX	30-NOV-2001; 2001US-0334288P.	Db	1818	TTTTTATATAAAATCCGTGAGTATTTAAAGCTTTTATGAAGCTTTCTTTGGGTAAATATTA	1877
XX	(INCY-) INCYTE GENOMICS INC.	QY	1143	GTCTCCCTCCATGACACTGCAGTATTTTAAATTAATACAAAGTAAAGTTTGAATTT	1202
XX	Bandnan O, Baughn MR, Becha SD, Borowsky M, Duggan BM;	Db	1878	GTCTCCCTCCATGACACTGCAGTATTTTAAATTAATACAAAGTAAAGTTTGAATTT	1937
XX	Emerling BM, Forsythe IU, Gandhi AR, Gorvad AE, Griffin JA;	QY	1203	TGCTA 1207	
XX	Gururajan R, Hafalia AJA, Khandi FA, Lal PG, Lee EA, Lee SJ;	Db	1938	TGCTA 1942	
XX	Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;	QY	102558	AAAX02558 standard; cDNA; 2098 BP.	
XX	Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;	Db	102558	AAAX02558;	
XX	Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;	QY	07-MAY-1999 (first entry)	07-MAY-1999 (first entry)	
XX	Zebbarjadian Y;	Db	Human B1 CDNA.	Human B1 CDNA.	
XX	WPI; 2003-403214/38.	QY	BI protein; intracellular mediator; modulator; inflammation; cell death;	BI protein; intracellular mediator; modulator; inflammation; cell death;	
XX	P-PSDB; ADC99079.	Db	cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.	cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.	
XX	New human kinases and phosphatases and polynucleotides, useful for	QY	Homo sapiens.	Homo sapiens.	
XX	diagnosing, treating or preventing autoimmune or inflammatory disorders	Db	WO9855507-A2.	WO9855507-A2.	
XX	(e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,	QY			
XX	cancer or hepatitis.	Db			
XX	Claim 5; SEQ ID NO 84; 424pp; English.	QY			
XX	The invention relates to a novel isolated polypeptide which is a human	Db			
XX	kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,	QY			
XX	agonists and antagonists are useful for diagnosing, treating or	Db			
XX	preventing cell proliferative disorders such as atherosclerosis,	QY			
XX	cirrhosis, hepatitis and cancer, developmental disorders e.g. mental	Db			
XX	retardation, neurological disorders including Alzheimer's disease and	QY			
XX	Parkinson's disease, autoimmune and inflammatory disorders such as	Db			
XX	Crohn's disease and diabetes mellitus and finally, viral, bacterial,	QY			
XX	fungal, parasitic, protozoan or helminthic infections. Furthermore, the	Db			
XX	polynucleotides encoding KPP may be useful for creating transgenic	QY			
XX	animals to model human disease, as well as during gene therapy	Db			
XX	procedures. The current sequence is that of the human KPP CDNA of the	QY			
XX	invention.	Db			
XX	Sequence 1959 BP; 597 A; 430 C; 420 G; 512 T; 0 U; 0 Other;	QY			
XX	Query Match 47.0%; Score 785; DB 9; Length 1959;	Db			
XX	Best Local Similarity 100.0%; Pred. No. 0;	QY			
XX	Matches 785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db			
XX	423 AGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCCTCTGAACTTCAAGGT	QY			

1020



CC domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial  
CC murine CARD-4L protein and genes. The genes and proteins of the invention  
CC are involved in the regulation of caspase activation. The caspase  
CC recruitment domain (CARD) polynucleotides, polypeptides, homologues and  
CC antibodies can be used in screening assays, detection assays, predictive  
CC medicine and therapeutic and prophylactic methods of treatment. The  
CC methods may be used to diagnose and treat patients which are suffering  
CC from a disorder associated with abnormal level or rate of apoptotic cell  
CC death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
CC activity of the TNF receptor complex, or abnormal activity of a caspase.  
CC Diseases that may be treated include cancer (particularly follicular  
CC lymphoma, carcinomas associated with mutations in p53 and hormone-  
CC dependent tumours), autoimmune disorders (e.g. systemic lupus  
CC erythematosus, immune-mediated glomerulonephritis), viral infections,  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,  
CC anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.  
CC CARD-3 protein interacts with other cellular proteins, and so can be used  
CC for regulation of cellular proliferation and differentiation and cell  
CC survival. The CARD proteins may also be used to for screen drugs or  
CC compounds which modulate their activity. The CARD-4 gene can express a  
CC long transcript that encodes CARD-4L, a short transcript that encodes  
CC CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence  
CC encodes the human CARD-3 protein described in the method of the invention  
XX  
SQ Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Query Match 40.9%; Score 682; DB 2; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTC 392  
DB 1151 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTC 1210

QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTAGCTCCATG 452  
DB 1211 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTAGCTCCATG 1270

QY 453 AAATAGTGGTCTCTCTGAAGTCTCAAGTCCCTGCGAGCTCTCAAGCAATGATTTTT 512  
DB 1271 AAATAGTGGTCTCTCTGAAGTCTCAAGTCCCTGCGAGCTCTCAAGCAATGATTTTT 1330

QY 513 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGCTCGAAATCACA 572  
DB 1331 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGCTCGAAATCACA 1390

QY 573 GTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCATTC 632  
DB 1391 GTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCATTC 1450

QY 633 CATGCTCTTCAGCAATAAATATCACTCTCACTGCAGGAACCTCAGAACCTCTGCAGC 692  
DB 1451 CATGCTCTTCAGCAATAAATATCACTCTCACTGCAGGAACCTCAGAACCTCTGCAGC 1510

QY 693 CTGGTATAGCCAGCAGTGGATCCAGCAAGGAAGACATTTGGAACCAATGACAG 752  
DB 1511 CTGGTATAGCCAGCAGTGGATCCAGCAAGGAAGACATTTGGAACCAATGACAG 1570

QY 753 AAGCCTGCTTTAACCAAGTGCAGTGCCTCTCTGTCCAGGGACTTGATCATGAAGAGG 812  
DB 1571 AAGCCTGCTTTAACCAAGTGCAGTGCCTCTCTGTCCAGGGACTTGATCATGAAGAGG 1630

QY 813 ACTATGAACCTTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAACTACTAGACA 872  
DB 1631 ACTATGAACCTTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAACTACTAGACA 1690

QY 873 CTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932  
DB 1691 CTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1750

QY 933 AACAAATGGGTCTTTCAGCCTTACCCGGAATATCTTGTGGTTTCTAGATCACCATCTTTAA 992

Db 1751 AACAAATGGGTCTTACGCCCTTACCCGGAATATCTTGTGGTTTCTAGATCACCATCTTTAA 1810  
QY 993 ATTTACTTTCAAAATAAAAGCATGTAAAGTGACTGTTTTTCAAGAAAGAAATGTTTTCATAA 1052  
DB 1811 ATTTACTTTCAAAATAAAAGCATGTAAAGTGACTGTTTTTCAAGAAAGAAATGTTTTCATAA 1870

QY 1053 AAGGATATTATA 1065  
DB 1871 AAGGATATTATA 1883

RESULT 10  
AAF30001  
ID AAF30001 standard; cDNA; 1931 BP.  
XX  
AC AAF30001;  
XX  
DT 23-APR-2001 (first entry)  
DE Human CARD-3 cDNA.  
XX  
KW CARD-3; caspase recruitment domain; human; cancer; infection;  
KW autoimmune disease; neurological disease; haematological disease;  
KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
KW antinflammatory; apoptosis; diagnosis; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 214..1826  
FT /\*tag= a  
FT /note= "the open reading frame is also specifically  
FT claimed in Claim 1(a)"  
XX  
PN WO200100826-A2.  
XX  
PD 04-JAN-2001.  
XX  
PF 28-JUN-2000; 2000WO-US017691.  
XX  
PR 28-JUN-1999; 99US-00340620.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Bertin J;  
XX  
DR WPI; 2001-061973/07.  
DR P-PSDB; AAB20079.  
XX  
PT Isolated intracellular proteins predicted to be involved in regulating  
PT caspase activation are used for diagnosis and treatment of e.g. cancer,  
PT viral infections, autoimmune diseases, neurological diseases and  
PT hematological disorders.  
XX  
PS Claim 1(a); Fig 1; 208pp; English.  
XX  
CC The present sequence is that of cDNA encoding human caspase recruitment  
CC domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a  
CC database search using known CARD sequences. Plasmid pXEL17A containing  
CC CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular  
CC protein predicted to be involved in regulating caspase activation. It is  
CC useful as a modulating agent in regulating cellular processes include  
CC cell growth and cell death. Methods of diagnosing and treating patients  
CC suffering from a disorder associated with an abnormal level or rate of  
CC apoptotic cell death, abnormal activity of the Fas/APO-1 receptor  
CC complex, abnormal activity of the tumour necrosis factor receptor complex  
CC or abnormal activity of a caspase involve administering a compound that  
CC modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6  
CC e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide.  
CC Such disorders include cancer, viral infection, autoimmune disorders,  
CC neurological diseases, haematological disorders, inflammatory disorders  
CC and immune disorders. CARD nucleic acids can be used to express CARD  
CC proteins in a host cell e.g. for gene therapy applications, to detect a

CC genetic lesion and to modulate CARD activity

XX Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;

Query Match 40.9%; Score 682; DB 4; Length 1931;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTC 392

DB 1151 AGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTC 1210

QY 393 TGAACATACCTGTAATATCAATGCTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 452

DB 1211 TGAACATACCTGTAATATCAATGCTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 1270

QY 453 AAAATAGTGTTCCTGAAACCTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTTT 512

DB 1271 AAAATAGTGTTCCTGAAACCTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTTT 1330

QY 513 TATCTAGAAAGCTCAAGAGCTGTTATTTATGAGCTGCATCTCTGCTGGAATCACA 572

DB 1331 TATCTAGAAAGCTCAAGAGCTGTTATTTATGAGCTGCATCTCTGCTGGAATCACA 1390

QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACTC 632

DB 1391 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACTC 1450

QY 633 CATGCTCTCAGCAATTAATATCACTCTCAACTGAGGAACTCAGAACGCTGCGAGC 692

DB 1451 CATGCTCTCAGCAATTAATATCACTCTCAACTGAGGAACTCAGAACGCTGCGAGC 1510

QY 693 CTGCTATAGCCAGCAGTGTGATCAGAGCAAAAGGGAAGACATGTGACCAATGACAG 752

DB 1511 CTGCTATAGCCAGCAGTGTGATCAGAGCAAAAGGGAAGACATGTGACCAATGACAG 1570

QY 753 AAGCCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG 812

DB 1571 AAGCCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG 1630

QY 813 ACTATGAACTTGTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAAGCAATTAAGACA 872

DB 1631 ACTATGAACTTGTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAAGCAATTAAGACA 1690

QY 873 CTACTGACATCCAGGAGAGAAATTTCCAAAGTTATAGTACAAAATTTCAAGAGATAACA 932

DB 1691 CTACTGACATCCAGGAGAGAAATTTCCAAAGTTATAGTACAAAATTTCAAGAGATAACA 1750

QY 933 AACAAATGGGTCTTACAGCTTACCCGAAATACCTGTGGTTCTAGATCAACATCTTTAA 992

DB 1751 AACAAATGGGTCTTACAGCTTACCCGAAATACCTGTGGTTCTAGATCAACATCTTTAA 1810

QY 993 ATTACTTCAAAATAAAGCATGTAGTACTGTTTTTCAAGAGAAATGTTTCAATA 1052

DB 1811 ATTACTTCAAAATAAAGCATGTAGTACTGTTTTTCAAGAGAAATGTTTCAATA 1870

QY 1053 AAGGATATTTATA 1065

DB 1871 AAGGATATTTATA 1883

RESULT 11

ABK89280

ID ABK89280 standard; cDNA; 1931 BP.

AC ABK89280;

XX 21-OCT-2002 (first entry)

DE Human cDNA encoding caspase recruitment domain protein CARD-3.

XX Human; ss; gene; caspase recruitment domain; CARD-3; CARD-4; LRR;

KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;

KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;

KW systemic lupus erythematosus; immune-mediated glomerulonephritis;

KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;

KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;

KW gastrointestinal allergy; insulin-dependent diabetes;

KW bacterial infection; tuberculosis; lepromatous leprosy;

KW cell signalling disorder; tissue disorder.

XX Homo sapiens.

OS Key Location/Qualifiers

XX CDS 214..1836

FT /\*tag= a

FT /product= "CARD-3"

XX WO200253765-A1.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-US049798.

XX 29-DEC-2000; 2000US-0258724P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J, Philpott D, Sansonetti P, Girardin S;

XX WPI; 2002-593627/62.

XX P-PSDB; ABG31075.

XX Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.

XX Example 2; Fig 1; 139pp; English.

XX The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, such as immune-mediated glomerulonephritis and arthritis, immune disorders, such as asthma, allergy, psoriasis, contact dermatitis, atopic conditions such as allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence is the human cDNA encoding CARD-3

XX Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Query Match 40.9%; Score 682; DB 6; Length 1931;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTC 392

DB 1151 AGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTC 1210

QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
DB 1211 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270  
QY 453 ABAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATTTT 512  
DB 1271 ABAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATTTT 1330  
QY 513 TATCTAGAAAAGCTCAAGACTGTATTTATTAAGCTGCATCACTCTCTGGAATCACA 572  
DB 1331 TATCTAGAAAAGCTCAAGACTGTATTTATTAAGCTGCATCACTCTCTGGAATCACA 1390  
QY 573 GTTGGATAGCACCATTTCTGATCTCAAGGGCTCATTTCTGTGATCAAGACCACTC 632  
DB 1391 GTTGGATAGCACCATTTCTGATCTCAAGGGCTCATTTCTGTGATCAAGACCACTC 1450  
QY 633 CATGCTCTTCAGCAATAAATAATCACTCACTCACTCAGGAACTCAGAACTGTGCAGC 692  
DB 1451 CATGCTCTTCAGCAATAAATAATCACTCACTCACTCAGGAACTCAGAACTGTGCAGC 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAG 752  
DB 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAG 1570  
QY 753 AAGCCTGCCTTAACCACTGCTAGATGCTCTTCTGTCCAGGACTTGTATCATGAAGAGG 812  
DB 1571 AAGCCTGCCTTAACCACTGCTAGATGCTCTTCTGTCCAGGACTTGTATCATGAAGAGG 1630  
QY 813 ACTATGAATCTGTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGGACCAATTAAGACA 872  
DB 1631 ACTATGAATCTGTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGGACCAATTAAGACA 1690  
QY 873 CTACTGACATCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
DB 1691 CTACTGACATCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750  
QY 933 AACAAATGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAA 992  
DB 1751 AACAAATGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAA 1810  
QY 993 ATTACTTCAAAATAAAGCATGTAGTACTGTTTTCAGAGAAATGTGTTTCATAA 1052  
DB 1811 ATTACTTCAAAATAAAGCATGTAGTACTGTTTTCAGAGAAATGTGTTTCATAA 1870  
QY 1053 AAGGATATTTATA 1065  
DB 1871 AAGGATATTTATA 1883  
RESULT 12  
ID AAL40752  
XX AAL40752 standard; cDNA; 1931 BP.  
AC AAL40752;  
XX  
XX 27-SEP-2002 (first entry)  
DT cDNA of human CARD-3 SEQ ID No 1.  
DE  
XX Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;  
KW cerebroprotective; antiparkinsonian; antischlerotic; ophthalmological;  
KW neotropic; antianemic; Caspase Recruitment Domain; CARD; CARD-41; p53;  
KW cancer; CARD-48; follicular lymphoma; carcinoma; autoimmune disorder;  
KW hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;  
KW systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;  
KW anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss.  
XX Homo sapiens.  
OS  
XX US6369196-B1.  
PN  
XX 09-APR-2002.  
PD

XX PF 05-FEB-1999; 99US-00245281.  
XX PR 06-FEB-1998; 98US-00019942.  
PR 17-JUN-1998; 98US-00090041.  
PR 08-DEC-1998; 98US-00207359.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Bertin J;  
XX WPI; 2002-391988/42.  
DR N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.  
XX Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.  
XX Example 2; Fig 1; 116pp; English.  
XX The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and hormone-dependent tumours such as breast cancer, prostate cancer, and ovarian cancer), autoimmune disorders (such as systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections (such as those caused by herpes viruses, poxviruses, and adenoviruses), neurological diseases (such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, and the myelodysplastic syndromes. This polynucleotide sequence represents the cDNA of a human CARD relating to the invention  
XX SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;  
Query Match 40.9%; Score 682; DB 6; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTC 392  
DB 1151 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTC 1210  
QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
DB 1211 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270  
QY 453 AAAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATTTT 512  
DB 1271 AAAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATTTT 1330  
QY 513 TATCTAGAAAAGCTCAAGACTGTATTTATTAAGCTGCATCACTCTCTGGAATCACA 572  
DB 1331 TATCTAGAAAAGCTCAAGACTGTATTTATTAAGCTGCATCACTCTCTGGAATCACA 1390  
QY 573 GTTGGATAGCACCATTTCTGATCTCAAGGGCTCATTTCTGTGATCAAGACCACTC 632  
DB 1391 GTTGGATAGCACCATTTCTGATCTCAAGGGCTCATTTCTGTGATCAAGACCACTC 1450  
QY 633 CATGCTCTTCAGCAATAAATAATCACTCACTCACTCAGGAACTCAGAACTGTGCAGC 692  
DB 1451 CATGCTCTTCAGCAATAAATAATCACTCACTCACTCAGGAACTCAGAACTGTGCAGC 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAG 752  
DB 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAG 1570  
QY 753 AAGCCTGCCTTAACCACTGCTAGATGCTCTTCTGTCCAGGACTTGTATCATGAAGAGG 812



Db 1571 AAGCCTGCCTTAACCAAGTCGCTAGATGCCCTCTCTGTCAGGAGCTTTCATCATGAAGAGG 1630  
 Qy 813 ACTATGAACCTTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTAAGTACAGACA 872  
 Db 1631 ACTATGAACCTTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTAAGTACAGACA 1690  
 Qy 873 CTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
 Db 1691 CTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750  
 Qy 933 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 992  
 Db 1751 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1810  
 Qy 993 ATTACTTCAAAATAAAGCATGTAGTGAAGTGTGTTTCAAGAGAAATGTGTTTCATAA 1052  
 Db 1811 ATTACTTCAAAATAAAGCATGTAGTGAAGTGTGTTTCAAGAGAAATGTGTTTCATAA 1870  
 Qy 1053 AAGGATATTTATA 1065  
 Db 1871 AAGGATATTTATA 1883  
 RESULT 13  
 ABX75869  
 ID ABX75869 standard; cDNA; 1931 BP.  
 XX  
 AC ABX75869;  
 XX  
 DT 30-APR-2003 (first entry)  
 XX  
 DE Human cDNA encoding Caspase recruitment domain protein, CARD-3.  
 XX  
 KW Human; ss; gene; caspase recruitment domain; CARD; CARD-3; CARD-4;  
 KW CARD-4L; CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS;  
 KW autoimmune disorder; systemic lupus erythematosus; viral infection;  
 KW immune related glomerulonephritis; acquired immunodeficiency syndrome;  
 KW neurological disease; Alzheimer's disease; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular atrophy; cerebellar degeneration; haematological disease;  
 KW anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;  
 KW stroke; chromosome 7.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US6469140-B1.  
 XX  
 XX 22-OCT-2002.  
 XX  
 XX 08-DEC-1998; 98US-00207359.  
 XX  
 XX 06-FEB-1998; 98US-00019942.  
 XX  
 XX 17-JUN-1998; 98US-00099041.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Bertin J;  
 XX  
 XX WPI; 2003-147109/14.  
 XX  
 XX P-PSDB; ABUS6269.  
 XX  
 XX Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z  
 XX polypeptide, or murine CARD-4L polypeptide, useful in screening assays,  
 XX detection assays, predictive medicine, and in therapeutic applications.  
 XX  
 XX Example 2; Fig 1; 99pp; English.  
 XX  
 XX The invention relates to an isolated polypeptide, comprising at least 25  
 XX contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,  
 XX human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)  
 XX polypeptide. Also included is an isolated fusion protein, comprising the  
 XX CARD polypeptide covalently linked by a peptide bond to a heterologous  
 XX polypeptide. The CARD polypeptide is useful in screening assays,

CC detection assays (e.g. chromosomal mapping, tissue typing and forensic  
 CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,  
 CC monitoring clinical trials and pharmacogenomics), and in therapeutic and  
 CC prophylactic treatments (in diseases associated with apoptotic cell death  
 CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and  
 CC immune related glomerulonephritis), viral infections, AIDS (acquired  
 CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
 CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),  
 CC haematological diseases (e.g. anaemia, neutropaenia and myelodysplastic  
 CC syndromes), myocardial infarction and stroke). The CARD polypeptide is  
 CC useful as bait protein in a two-hybrid assay or three hybrid assay to  
 CC identify other proteins, which bind to or interact with other CARD  
 CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
 CC human CARD-4 is located on chromosome 7. The present sequence is a human  
 CC CARD cDNA  
 XX  
 SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;  
 Query Match 40.9%; Score 682; DB 7; Length 1931;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 333 AGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTTATCTC 392  
 Db 1151 AGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTTATCTC 1210  
 Qy 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
 Db 1211 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270  
 Qy 453 AAAATAGTGGTCTCTCGAACTTCAAGGTCCCTGCGAGTCCCTCAAGACAATGATTTTT 512  
 Db 1271 AAAATAGTGGTCTCTCGAACTTCAAGGTCCCTGCGAGTCCCTCAAGACAATGATTTTT 1330  
 Qy 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTCTCTCGGAAATACACA 572  
 Db 1331 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTCTCTCGGAAATACACA 1390  
 Qy 573 GTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTC 632  
 Db 1391 GTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTC 1450  
 Qy 633 CATGCTCTTCAGCAATAATAATCCACTCTCACTGAGGAACTCAGAACGTCGAGC 692  
 Db 1451 CATGCTCTTCAGCAATAATAATCCACTCTCACTGAGGAACTCAGAACGTCGAGC 1510  
 Qy 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAG 752  
 Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAG 1570  
 Qy 753 AAGCCTGCCTTTAACCAAGTCGCTAGATGCCCTTCTGTCAGGGACTTTGATCATGAAGAGG 812  
 Db 1571 AAGCCTGCCTTTAACCAAGTCGCTAGATGCCCTTCTGTCAGGGACTTTGATCATGAAGAGG 1630  
 Qy 813 ACTATGAACCTTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGTACAGACA 872  
 Db 1631 ACTATGAACCTTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGTACAGACA 1690  
 Qy 873 CTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
 Db 1691 CTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750  
 Qy 933 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 992  
 Db 1751 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1810  
 Qy 993 ATTACTTCAAAATAAAGCATGTAGTGAAGTGTGTTTCAAGAGAAATGTGTTTCATAA 1052  
 Db 1811 ATTACTTCAAAATAAAGCATGTAGTGAAGTGTGTTTCAAGAGAAATGTGTTTCATAA 1870  
 Qy 1053 AAGGATATTTATA 1065





KW anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;  
KW stroke; chromosome 7.  
XX Homo sapiens.  
XX US6469140-B1.  
XX 22-OCT-2002.  
XX 08-DEC-1998; 98US-00207359.  
XX 06-FEB-1998; 98US-00019942.  
XX 17-JUN-1998; 98US-00099041.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Bertin J;  
XX WPI; 2003-147109/14.  
XX P-PSDB; ABUS6269.  
XX Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z  
XX polypeptide, or murine CARD-4L polypeptide, useful in screening assays,  
XX detection assays, predictive medicine, and in therapeutic applications.  
XX Disclosure; Col 71-74; 99pp; English.  
XX The invention relates to an isolated polypeptide, comprising at least 25  
XX contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,  
XX human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)  
XX polypeptide. Also included is an isolated fusion protein, comprising the  
XX CARD polypeptide covalently linked by a peptide bond to a heterologous  
XX polypeptide. The CARD polypeptide is useful in screening assays,  
XX detection assays (e.g. chromosomal mapping, tissue typing and forensic  
XX biology), predictive medicine (e.g. diagnostic assays, prognostic assays,  
XX monitoring clinical trials and pharmacogenomics), and in therapeutic and  
XX prophylactic treatments (in diseases associated with apoptotic cell death  
XX e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and  
XX immune related glomerulonephritis), viral infections, AIDS (acquired  
XX immunodeficiency syndrome), neurological disease (e.g. Alzheimer's  
XX disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
XX pigmentosa, spinal muscular atrophy and cerebellar degeneration),  
XX haematological diseases (e.g. anaemia, neutropaenia and myelodysplastic  
XX syndromes), myocardial infarction and stroke). The CARD polypeptide is  
XX useful as bait protein in a two-hybrid assay or three hybrid assay to  
XX identify other proteins, which bind to or interact with other CARD  
XX proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
XX human CARD-4 is located on chromosome 7. The present sequence is a human  
XX CARD cDNA

SQ Sequence 1620 BP; 517 A; 360 C; 320 G; 423 T; 0 U; 0 Other;

Query Match 37.9%; Score 632; DB 7; Length 1620;  
Best Local Similarity 99.9%; Pred. No. 4.4e-291;  
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAGAGAAATGGAATATCTC 392  
DB 938 AGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAGAGAAATGGAATATCTC 997  
QY 393 TGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCCTCAGCTCCATG 452  
DB 998 TGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCCTCAGCTCCATG 1057  
QY 453 AAAATAGTGGTTCCTGAACTTCAGAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 512  
DB 1058 AAAATAGTGGTTCCTGAACTTCAGAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1117  
QY 513 TATCTAGAAAAAGCTCAAGACTGTTATTTTATGAAGTGCATCACTGTCTGGAATCACA 572  
DB 1118 TATCTAGAAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGTCTGGAATCACA 1177  
QY 573 GTTGGGATAGCACCATTCTCGATCTCAAGGGGTGCATTTCTGTGATCAAGACCACCTC 632

Db	1178	GTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCATTTC	1237
QY	633	CATGCTCTTTCAGCAATAAATCCACTCTCACTGCGAGGAACTCAGAACTCTGCGACG	692
Db	1238	CATGCTCTTTCAGCAATAAATCCACTCTCACTGCGAGGAACTCAGAACTCTGCGACG	1297
QY	693	CTGGTATAGCCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAG	752
Db	1298	CTGGTATAGCCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAG	1357
QY	753	AAGCCTGCCTTAAACAGTGGTGTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAGG	812
Db	1358	AAGCCTGCCTTAAACAGTGGTGTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAGG	1417
QY	813	ACTATGAACCTTCTAGTACCAAGCCTACAAGGACCTCAAAAGCTCAGACAAATTTACTAGACA	872
Db	1418	ACTATGAACCTTCTAGTACCAAGCCTACAAGGACCTCAAAAGCTCAGACAAATTTACTAGACA	1477
QY	873	CTACTGACATCCCAAGGAGAAATTTGCCAAAGTTTATAGTACAAAAATTTGAAAGATAACA	932
Db	1478	CTACTGACATCCCAAGGAGAAATTTGCCAAAGTTTATAGTACAAAAATTTGAAAGATAACA	1537
QY	933	AACAAATGGTCTTCAAGCCTTACCGGAAATATCTGTGGTTTCTAGATCACCATCTTTAA	992
Db	1538	AACAAATGGTCTTCAAGCCTTACCGGAAATATCTGTGGTTTCTAGATCACCATCTTTAA	1597
QY	993	ATTACTTCAAAATAAAGCATG 1015	
Db	1598	ATTACTTCAAAATAAAGCATG 1620	

Search completed: April 1, 2004, 06:43:17  
Job time : 760 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 04:59:21 ; Search time 6741 Seconds  
(without alignments)  
10731.275 Million cell updates/sec

Title: US-09-771-161A-2  
Perfect score: 1669  
Sequence: 1 acctagttattaccagata.....caacagcctgatgtgtaaaa 1669

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 20

Total number of hits satisfying chosen parameters: 676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1333	79.9	2521	9	AY358814	AY358814 Homo sapi
2	990	59.3	116650	9	AC004003	AC004003 Homo sapi
3	990	59.3	320187	9	AF117829	AF117829 Homo sapi
4	879	52.7	2024	6	BD251808	BD251808 Phosphory
5	878	52.6	1886	9	AY358813	AY358813 Homo sapi
6	827	49.6	2033	6	BD127583	BD127583 Primer fo
7	827	49.6	2033	9	AK075213	AK075213 Homo sapi
8	812	48.7	2501	6	AR221453	AR221453 Sequence
9	812	48.7	2501	6	AX429236	AX429236 Sequence
10	812	48.7	2501	9	AF027706	AF027706 Homo sapi
11	812	48.7	2502	6	AR194318	AR194318 Sequence
12	783	46.9	2098	6	AB2777	AB2777 Sequence 2
13	783	46.9	2098	6	BD106658	BD106658 Modulator
14	733	43.9	1889	9	BC004553	BC004553 Homo sapi
15	727	43.6	61099	2	AC139421	AC139421 Homo sapi
16	708	42.4	1902	9	AF064824	AF064824 Homo sapi
17	684	41.0	1623	12	AY335645	AY335645 Synthetic
18	682	40.9	1931	6	AR183234	AR183234 Sequence
19	682	40.9	1931	6	AR205634	AR205634 Sequence
20	682	40.9	1931	6	AR216112	AR216112 Sequence
21	682	40.9	1931	6	AR241236	AR241236 Sequence
22	682	40.9	1931	6	AR256252	AR256252 Sequence
23	682	40.9	1931	6	AR391599	AR391599 Sequence
24	682	40.9	1931	6	AX082199	AX082199 Sequence
25	682	40.9	1931	6	BD123998	BD123998 Novel mol
26	635	38.0	1623	9	AF078530	AF078530 Homo sapi
27	632	37.9	1620	6	AR183235	AR183235 Sequence
28	632	37.9	1620	6	AR205635	AR205635 Sequence
29	632	37.9	1620	6	AR241237	AR241237 Sequence
30	632	37.9	1620	6	AR256253	AR256253 Sequence
31	632	37.9	1620	6	AR391600	AR391600 Sequence
32	632	37.9	1620	6	AX082201	AX082201 Sequence
33	632	37.9	1620	6	BD123999	BD123999 Novel mol
34	586	35.1	1060	6	AR380139	AR380139 Sequence
35	220	13.2	299	6	AX381606	AX381606 Sequence
36	179	10.7	575	6	BD126039	BD126039 Primer fo
37	26	1.6	1620	10	AF461040	AF461040 Mus muscu
38	26	1.6	1620	10	AF487539	AF487539 Mus muscu
39	26	1.6	186519	10	AL807379	AL807379 Mouse DNA
40	24	1.4	741	9	HSR341343	AJ341343 Homo sapi
41	24	1.4	80518	2	PFMAL13PA	AL109815 Plasmodiu
42	24	1.4	92300	10	AC119395	AC119395 Mus muscu
43	24	1.4	110000	2	PFMAL13_12	Continuation (13 o
44	24	1.4	148851	2	AC102277	AC102277 Mus muscu
45	24	1.4	211970	2	AC132407	AC132407 Mus muscu

ALIGNMENTS

RESULT 1	AY358814	Homo sapiens clone DNA3305 RIPK2 (UNQ277) mRNA, complete cds.	2521 bp	linear	PRI 03-OCT-2003
LOCUS	AY358814	Homo sapiens			
DEFINITION	AY358814	Homo sapiens			
ACCESSION	AY358814	Homo sapiens			
VERSION	AY358814.1	GI:37182745			
KEYWORDS	FLI_CDNA				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2521)	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,				

Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagstad, A., Vandien, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
12975309  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SUBMITTED (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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RESULT 2  
AC004003  
LOCUS  
DEFINITION Homo sapiens BAC clone CTA-437L15 from 8q21, complete sequence.  
AC004003  
AC004003  
VERSION 1 GI:272557

102a











[illegible]

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ACCESSION	AY358813					
VERSION	AY358813.1	GI:37182743				
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SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagstad, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.					
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment					
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)					
PUBMED	12975309					
REFERENCE	2 (bases 1 to 1886)					
AUTHORS	Clark, H.F.					
TITLE	Direct Submission					
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA					
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RESULT 6  
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 DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
 ACCESSION BD127583  
 VERSION BD127583.1 GI:23222528  
 KEYWORDS JP 2002017375-A/3014.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 2033)  
 Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
 Koga,H.  
 TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002017375-A 3014 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002017375-A/3014  
 PD 22-JAN-2002 JP 20020253172  
 PF 07-JUL-2000 JP 20020253172  
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 PI ISHII,  
 PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI  
 SHINICHI KOJIMA,  
 PI TETSUO OTSUKI,HISASHI KOGA  
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ACCESSION AK075213
VERSION AK075213.1 GI:22761157
KEYWORDS oligo capping, fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahara,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2033)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 877; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 333 AGTTACAGAGTGTTCAGATGCCATTCACCTATGTGACAGAGAAATGGAATTATCTC 392
DB 1156 AGTTACAGAGTGTTCAGATGCCATTCACCTATGTGACAGAGAGAAATGGAATTATCTC 1215
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ACCESSION AR221453
VERSION AR221453.1 GI:23328503
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2501)
AUTHORS Ward,D.T. and Cowser,L.M.
TITLE Antisense modulation of R1P2 expression
JOURNAL Patent: US 6426221-A 3 30-JUL-2002;
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DB	1402	GTGGATAGCACC	ATTCT	GGATCT	CAAGGGCT	CAATTCCTGATCAAGACCACTC 1461
QY	633	CATGCTCTTC	CAGCAAT	TAATTC	CACTCT	CAACTGAGGAACTCAGACGTCGAGC 692
DB	1462	CATGCTCTTC	CAGCAAT	TAATTC	CACTCT	CAACTGAGGAACTCAGACGTCGAGC 1521
QY	693	CTGCTATAGCC	CAGCAGT	GGATCC	AGAGCAAA	AGGAGACATTTGTGAACAAATGACAG 752
DB	1522	CTGCTATAGCC	CAGCAGT	GGATCC	AGAGCAAA	AGGAGACATTTGTGAACAAATGACAG 1581
QY	753	AAGCCTGCCTT	AAAGCAT	GTAGT	GAAGT	GTATTTTCAAGAGAAATGTTTTCATAA 812
DB	1582	AAGCCTGCCTT	AAAGCAT	GTAGT	GAAGT	GTATTTTCAAGAGAAATGTTTTCATAA 1641
QY	813	ACTATGAAC	TTGTTAGT	TACCAAG	CTCAAG	AGGAACTCAGACAAATTTACTAGACA 932
DB	1642	ACTATGAAC	TTGTTAGT	TACCAAG	CTCAAG	AGGAACTCAGACAAATTTACTAGACA 1701
QY	933	CTACTGACAT	CCAAAG	GAATTT	GGCCAA	AGTTATAGTACAAAATTTGAAAGATAACA 1761
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QY	993	ATTTACTT	CAAAAT	TAATTA	TTAGT	GTATTTTCAAGAGAAATGTTTTCATAA 1052
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QY	1053	AAGGATATTT	TATATCT	CTGTG	TTTAC	CTTGTGTTTCAAGAGAAATGTTTTCATAA 1112
DB	1882	AAGGATATTT	TATATCT	CTGTG	TTTAC	CTTGTGTTTCAAGAGAAATGTTTTCATAA 1941
QY	1113	CTTTATTT	GAAGGTT	CTTTT	GGTAAAT	TATAGTCTCCCTCCATGACACTGAGTATTTTT 1172
DB	1942	CTTTATTT	GAAGGTT	CTTTT	GGTAAAT	TATAGTCTCCCTCCATGACACTGAGTATTTTT 2001
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DB	2002	TTAATTAAT	CAAGT	AAAAAGTT	2024	

RESULT 9  
AX429236  
LOCUS  
DEFINITION Sequence 13 from Patent BP1201765.  
ACCESSION AX429236  
VERSION AX429236.1 GI:21540548  
KEYWORDS

SOURCE		synthetic construct
ORGANISM		synthetic construct
REFERENCE		artificial sequences.
AUTHORS		Schubart, D., Habenberger, P., Stein-Gerlach, M. and Bevec, D.
TITLE		Cellular kinases involved in cytomagalovirus infection and their inhibition
JOURNAL		Patent: EP 1201765-A 13 02-MAY-2002;
FEATURES		Axxima Pharmaceuticals Aktiengesellschaft (DE)
source		Location/Qualifiers
		1. .2501
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		/note="N/A"
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Best Local Similarity		99.9%; Pred. No. 0;
Matches 862;		Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	333	AGTTACAGAGTGTTC
DB	1162	AGTTACAGAGTGTTC
QY	393	TGAACATACCTGTA
DB	1222	TGAACATACCTGTA
QY	453	AAATAGTGGTTC
DB	1282	AAATAGTGGTTC
QY	513	TATCTAGAAAAGCT
DB	1342	TATCTAGAAAAGCT
QY	573	GTGGATAGCACC
DB	1402	GTGGATAGCACC
QY	633	CATGCTCTTC
DB	1462	CATGCTCTTC
QY	693	CTGCTATAGCC
DB	1522	CTGCTATAGCC
QY	753	AAGCCTGCCTT
DB	1582	AAGCCTGCCTT
QY	813	ACTATGAAC
DB	1642	ACTATGAAC
QY	933	CTACTGACAT
DB	1702	CTACTGACAT
QY	993	ATTTACTT
DB	1762	ATTTACTT
QY	1053	AAGGATATTT
DB	1882	AAGGATATTT



Unclassified.  
REFERENCE 1 (bases 1 to 2502)  
AUTHORS Nunez, G., Inohara, N. and Koseki, T.  
TITLE Compositions and methods for identifying apoptosis signaling pathway inhibitors and activators  
JOURNAL Patent: US 6348573-A 2 19-FEB-2002;  
FEATURES Location/Qualifiers  
source 1. .2502  
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Query Match 48.7%; Score 812; DB 6; Length 2502;  
Best Local Similarity 99.9%; Pred. No. 0;  
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QY 333 AGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAGAGAGAAAATGGAATATATCTC 392  
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QY 393 TGAACATACCTGTAATATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
Db 1223 TGAACATACCTGTAATATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1282

QY 453 AAAATAGTGGTTCCTCGAAATTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTT 512  
Db 1283 AAAATAGTGGTTCCTCGAAATTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTT 1342

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Db 1343 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCAATCACTGTCCTGGAATACACA 1402

QY 573 GTTGGGATAGCACCATTCTGGATCTCAAGAGGCTGATCTGTGATCAAGACCACTC 632  
Db 1403 GTTGGGATAGCACCATTCTGGTCTCAAGAGGCTGATCTGTGATCAAGACCACTC 1462

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QY 933 AACAAATGGGTCTTCAGCTTACCCGGAATATCTTGTGGTCTTAGATCACCATCTTTAA 992  
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Db 2003 TTAATTAATCAAGTAAAAAGTT 2025

RESULT 12  
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DEFINITION Sequence 2 from Patent WO9855507.  
ACCESSION A82777  
VERSION A82777.1 GI:6732464  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 2098)  
AUTHORS Boldin, M. and Wallach, D.  
TITLE MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL SURVIVAL PATHWAYS  
JOURNAL Patent: WO 9855507-A 2 10-DEC-1998;  
FEATURES Location/Qualifiers  
source 1. .2098  
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ORIGIN

Query Match 46.9%; Score 783; DB 6; Length 2098;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAGAGAAAATGGAATATATCTC 392  
Db 1197 AGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAGAGAAAATGGAATATATCTC 1256

QY 393 TGAACATACCTGTAATATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
Db 1257 TGAACATACCTGTAATATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1316

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QY 513 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTCTCTGGAATACACA 572  
Db 1377 TATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTCTCTGGAATACACA 1436

QY 573 GTTGGATAGCACCATTCTTGGATCTCAAGAGGCTGCATTTGTGATCAAGACCACTC 632  
Db 1437 GTTGGATAGCACCATTCTTGGATCTCAAGAGGCTGCATTTGTGATCAAGACCACTC 1496

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Db 1497 CATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTCGAGC 1556

QY 693 CTGTTATAGCCAGCAGTGCATGAGCAAGAGGGAAGACATGTGAACTGAATGACAG 752  
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Db 1617 AAGCTCCCTTAAACAGTGCATGAGTGCCTTCTGTCCAGGAGCTTGATCATGAAAGAGG 1676

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Qy 993 ATTACTCTCAAAATAAAGCATGTAGTGACCTGTTTTTCAAGAAGAAATGTGTTTCATAA 1052

Db 1857 ATTACTCTCAAAATAAAGCATGTAGTGACCTGTTTTTCAAGAAGAAATGTGTTTCATAA 1916

Qy 1053 AAGGATATTATATCTCTGCTGTTGACTTTTTTATATAAAATCCGCGAGTATTAAG 1112

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Qy 1113 CTT 1115

Db 1977 CTT 1979

BD106658 2098 bp DNA linear PAT 18-SEP-2002

BD106658 Modulators of intracellular inflammation, cell death and cell survival pathways.

DEFINITION

ACCESSION BD106658

VERSION BD106658.1 GI:23201476

KEYWORDS JP 2002502258-A/1.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 2098)

AUTHORS Wallach,D., Boldin,M. and Malinin,N.

TITLE Modulators of intracellular inflammation, cell death and cell survival pathways

JOURNAL Patent: JP 2002502258-A 1 22-JAN-2002;

YEDA RESEARCH AND DEVELOPMENT CO LTD

PN JP 2002502258-A/1

PD 22-JAN-2002

PF 01-JUN-1998 JP 1999501993

PR 05-JUN-1997 IL 121011,30-JUN-1997 IL 121199 PR 11-SEP-1997 IL 121746

PI DAVID WALLACH,MARK BOLDIN,NIKOLAI MALININ

PC C12N15/12,C07K14/47,C07K16/18,C12Q1/68,A61K38/17,G01N33/68 CC

Strandedness: Single;

CC Topology: Linear;

PH Key Location/Qualifiers.

source 1..2098

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/mol\_type="genomic DNA"

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ORIGIN

Query Match 46.9%; Score 783; DB 6; Length 2098;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 333 AGTTACAGAGTGTTCAGTGGCATTCACCTATGTGACAAAGAAATGGAATATCTC 392

Db 1197 AGTTACAGAGTGTTCAGTGGCATTCACCTATGTGACAAAGAAATGGAATATCTC 1256

Qy 393 TGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 452

Db 1257 TGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 1316

Qy 453 AAAATAGTGGTGTCTCCTGAAATCTCAAGGTCCTCGCAGCTCCTCAAGACAATGATTTT 512

Db 1317 AAAATAGTGGTGTCTCCTGAAATCTCAAGGTCCTCGCAGCTCCTCAAGACAATGATTTT 1376

Qy 513 TATCTAGAAAAGCTCAAGCTGTATTTATGAAGCTGCATCAGTCTCTCGAAATCACA 572

Db 1377 TATCTAGAAAAGCTCAAGCTGTATTTATGAAGCTGCATCAGTCTCTCGAAATCACA 1436

Qy 573 GTTGGATAGCACCATTTCTTGATCTCAAGGGTGCATTCTGTGATCACAAGACCCTC 632

Db 1437 GTTGGATAGCACCATTTCTTGATCTCAAGGGTGCATTCTGTGATCACAAGACCCTC 1496

Qy 633 CATGCTCTTCAGCAATAATAATCCACTCTCAACTGCGAGGAACTCAGAACTCTGCGAGC 692

Db 1497 CATGCTCTTCAGCAATAATAATCCACTCTCAACTGCGAGGAACTCAGAACTCTGCGAGC 1556

Qy 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 752

Db 1557 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 1616

Qy 753 AAGCCTGCCTTTAAACAGTCGCTAGATGCCCTTCTGCTCCAGGGACTTGTATCATGAAGAGG 812

Db 1617 AAGCCTGCCTTTAAACAGTCGCTAGATGCCCTTCTGCTCCAGGGACTTGTATCATGAAGAGG 1676

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Qy 993 ATTACTCTCAAAATAAAGCATGTAGTGACCTGTTTTTCAAGAAGAAATGTGTTTCATAA 1052

Db 1857 ATTACTCTCAAAATAAAGCATGTAGTGACCTGTTTTTCAAGAAGAAATGTGTTTCATAA 1916

Qy 1053 AAGGATATTATATCTCTGCTGTTGACTTTTTTATATAAAATCCGCGAGTATTAAG 1112

Db 1917 AAGGATATTATATCTCTGCTGTTGACTTTTTTATATAAAATCCGCGAGTATTAAG 1976

Qy 1113 CTT 1115

Db 1977 CTT 1979

RESULT 14

BC004553

LOCUS Homo sapiens receptor-interacting serine-threonine kinase 2, mRNA

DEFINITION (CDNA clone MGC:10684 IMAGE:4026156), complete cds.

ACCESSION BC004553

VERSION BC004553.2 GI:33871163

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1889)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerf,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22398257

PUBMED 12477932







JOURNAL  
REFERENCE  
AUTHORS

Unpublished  
2 (bases 1 to 61099)  
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
Anderson, S., Arachchi, H. M., Barna, N. A., Bastien, V., Bloom, T.,  
Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,  
Collimore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., K. Roepel, Y.,  
Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,  
Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,  
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,  
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,  
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,  
Meldrum, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J.,  
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,  
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C.,  
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,  
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,  
Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (03-FEB-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L29371  
Center clone name: 706\_H\_15  
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\* NOTE: This record contains 67 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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\* 821 920: gap of 100 bp  
\* 921 1725: contig of 805 bp in length  
\* 1726 1825: gap of 100 bp  
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\* 3589 3688: gap of 100 bp  
\* 3689 4491: contig of 803 bp in length  
\* 4492 4591: gap of 100 bp  
\* 4592 5412: contig of 821 bp in length  
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27548 28374: contig of 827 bp in length  
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28475 29297: contig of 823 bp in length  
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29398 30231: contig of 834 bp in length  
30232 30331: gap of 100 bp  
30332 31159: contig of 828 bp in length  
31160 31259: gap of 100 bp  
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36745 37572: contig of 828 bp in length  
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38476 38575: gap of 100 bp  
38576 39369: contig of 794 bp in length  
39370 39469: gap of 100 bp  
39470 40227: contig of 758 bp in length  
40228 40327: gap of 100 bp  
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41144 41243: gap of 100 bp  
41244 42067: contig of 824 bp in length  
42068 42167: gap of 100 bp  
42168 42986: contig of 819 bp in length  
42987 43086: gap of 100 bp  
43087 43894: contig of 808 bp in length  
43895 43994: gap of 100 bp  
43995 44818: contig of 824 bp in length  
44819 44918: gap of 100 bp

TITLE  
JOURNAL  
COMMENT

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* 45733 45832: gap of 100 bp
* 45835 46635: contig of 803 bp in length
* 46636 46735: gap of 100 bp
* 46736 47534: contig of 799 bp in length
* 47535 47634: gap of 100 bp
* 47635 48473: contig of 839 bp in length
* 48474 48573: gap of 100 bp
* 48574 49386: contig of 813 bp in length
* 49387 49486: gap of 100 bp
* 49487 50301: contig of 815 bp in length
* 50302 50401: gap of 100 bp
* 50402 51206: contig of 805 bp in length
* 51207 51306: gap of 100 bp
* 51307 52110: contig of 804 bp in length
* 52111 52210: gap of 100 bp
* 52211 53022: contig of 812 bp in length
* 53123 53122: gap of 100 bp
* 53123 53967: contig of 845 bp in length
* 53968 54067: gap of 100 bp
* 54068 54873: contig of 806 bp in length
* 54874 54973: gap of 100 bp
* 54974 55769: contig of 796 bp in length
* 55770 55869: gap of 100 bp
* 55870 56676: contig of 807 bp in length
* 56677 56776: gap of 100 bp
* 56777 57545: contig of 770 bp in length
* 57546 57645: gap of 100 bp
* 57647 58453: contig of 807 bp in length
* 58454 58553: gap of 100 bp
* 58554 59357: contig of 804 bp in length
* 59358 59457: gap of 100 bp
* 59458 60274: contig of 817 bp in length
* 60275 60374: gap of 100 bp
* 60375 61099: contig of 725 bp in length.
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## FEATURES

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source
1. 61099
   /organism="Homo sapiens"
   /mol_type="genomic DNA"
   /db_xref="taxon:9606"
   /chromosome="9"

Query Match      43.6%; Score 727; DB 2; Length 61099;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 727; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 789 CCAGGGACTTGATCAAGAGAGACTATGAACCTGTTAGTACCAAGCCTACAGGACCT 848
Db 32048 CCAGGGACTTGATCAAGAGAGACTATGAACCTGTTAGTACCAAGCCTACAGGACCT 31989

Qy 849 CAAAAGTCAGACATTAAGTACTAGACACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTA 908
Db 31988 CAAAAGTCAGACATTAAGTACTAGACACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTA 31929

Qy 909 TAGTACAAAATTAAGAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAATACTTG 968
Db 31928 TAGTACAAAATTAAGAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAATACTTG 31869

Qy 969 TGGTTTCTAGATCACCCTTTAAATTTACTTCAAAATAAAGCAATGTAAGTCACTGTTT 1028
Db 31868 TGGTTTCTAGATCACCCTTTAAATTTACTTCAAAATAAAGCAATGTAAGTCACTGTTT 31809

Qy 1029 TTCAGAAGAAATGTGTTTCATAAAAGGATATTATATCTCTGTTGCTTTGACTTTTTT 1088
Db 31808 TTCAGAAGAAATGTGTTTCATAAAAGGATATTATATCTCTGTTGCTTTGACTTTTTT 31749

Qy 1089 ATATAAATCCGTGAGPATTAAGCTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCC 1148
Db 31748 ATATAAATCCGTGAGPATTAAGCTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCC 31689

Qy 1149 CTCATGACACTGAGTATTTTAAATTAATACAGTAAAGTTGAATTTTGGTCTAC 1208
Db 31688 CTCATGACACTGAGTATTTTAAATTAATACAGTAAAGTTGAATTTTGGTCTAC 31629
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Qy 1209 ATAGTTCAATTTTATGTCTCTTTTGTAAACAGAAACCACTTTTAAAGGATAGTAATTAT 1268
Db 31628 ATAGTTCAATTTTATGTCTCTTTTGTAAACAGAAACCACTTTTAAAGGATAGTAATTAT 31569

Qy 1269 TCTTGTTTATAACAGTGCCTTAAAGGTATGATGTATTTCTGATGGAAGCCATTTTTCACATT 1328
Db 31568 TCTTGTTTATAACAGTGCCTTAAAGGTATGATGTATTTCTGATGGAAGCCATTTTTCACATT 31509

Qy 1329 CATGTTCTTCATGGATTTATTTGTACTGTCTAAGATGCAATTTGATTTATGGAAGTATA 1388
Db 31508 CATGTTCTTCATGGATTTATTTGTACTGTCTAAGATGCAATTTGATTTATGGAAGTATA 31449

Qy 1389 TACCCCTTTACCCACCAGAGACAGTACAGAAATCCCTGCCCTTAAATCCAGGCTTAATTGC 1448
Db 31448 TACCCCTTTACCCACCAGAGACAGTACAGAAATCCCTGCCCTTAAATCCAGGCTTAATTGC 31389

Qy 1449 CCTACAAAGGGTTTAAATTTTAAAACTCCATTTATAGGATTAACATTTTAAAGTTTATTT 1508
Db 31388 CCTACAAAGGGTTTAAATTTTAAAACTCCATTTATAGGATTAACATTTTAAAGTTTATTT 31329

Qy 1509 ATGAATTT 1515
Db 31328 ATGAATTT 31322
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Search completed: April 1, 2004, 08:35:46  
Job time : 6746 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:25:53 ; Search time 31.5 Seconds  
(without alignments)  
10193.248 Million cell updates/sec

Title: US-09-771-161A-2  
Perfect score: 531  
Sequence: 1 acctagttatccagata.....caacagcctgatgtgtaaaa 1669

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Word size: 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV=xlp  
-MODEL=frame\_n2p.model -Q=/cgn2\_1/USPTO\_spool\_p/US09771161/runat\_29032004\_124857\_14342/app.query.fasta\_1.1863  
-DB=PIR\_78 -QFMT=fastan -SUFFIX=oli20n2p.fpr -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=20 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161@CGN 1 1 44 @runat\_29032004\_124857\_14342 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : PIR\_78:  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description
-----		

No matches found

Search completed: March 29, 2004, 14:36:33  
Job time : 31.5 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:23:38 ; Search time 20.5 Seconds  
(without alignments)  
8478.545 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 531

Sequence: 1 acctagttatccagata.....caacagcctggtgtaaaa 1669

Scoring table:

OLIGO	
Xgapop 60.0 , Xgapext 60.0	
Ygapop 60.0 , Ygapext 60.0	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 141681 seqs, 52070155 residues

Word size: 20

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=SwissProt\_42 -OPMT=fastan -SUFFIX=oli20n2p.rsp -MINMATCH=0.1 -LOOFCU=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=quality -THR\_MIN=20 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CGN 1 1 19 @runat\_29032004\_124856\_14314 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	42.7	540	1 RIK2_HUMAN	O43353 h receptor-
2	27	5.1	539	1 RIK2_MOUSE	P58801 mus musculus

#### ALIGNMENTS

RESULT 1  
RIK2\_HUMAN  
ID RIK2\_HUMAN STANDARD; PRT; 540 AA.  
AC O43353;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)  
DE (RIP-like interacting CLARP kinase) (Receptor-interacting protein 2)  
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme  
DE associated kinase) (CARD-containing IL-1 beta ICE-Kinase).  
GN RIPK2 OR RICK OR RIP2 OR CARDIAK.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.  
RX MEDLINE=98241596; PubMed=9575181;  
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;  
RT "RICK, a novel protein kinase containing a caspase recruitment domain,  
interacts with CLARP and regulates CD95-mediated apoptosis.";  
RL J. Biol. Chem. 273:12296-12300(1998).  
RN [2]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.  
RX TISSUE=Endothelial cells;  
RA McCarthy J.V., Ni J., Dixit V.M.;  
RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing  
kinase";  
RL J. Biol. Chem. 273:16968-16975(1998).  
RN [3]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.  
RX MEDLINE=98381580; PubMed=9705938;  
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,  
RA Mattmann C., Tschopp J.;  
RT "Identification of CARDIAK, a RIP-like kinase that associates with  
caspase-1";  
RL Curr. Biol. 8:885-888(1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Ozersky P., Holmes A., Broy M.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Platzter M., Varon R.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [6]  
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RX TISSUE=Skin;  
RA MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Hous D.E.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
CASP-8-mediated apoptosis. Activates NF-kappaB.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.  
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and  
TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
receptor complex.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -!- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,  
peripheral blood leukocytes, spleen, kidney, testis, prostate,  
pancreas and lymph node.  
CC -!- PTM: Autophosphorylated.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -!- SIMILARITY: Contains 1 CARD domain.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; AF027706; AAC34970.1; -  
 DR EMBL; AF078530; AAC27722.1; -  
 DR EMBL; AF064824; AAC25668.1; -  
 DR EMBL; AF064003; AAC24561.1; -  
 DR EMBL; AF117829; AAD04634.1; -  
 DR EMBL; BC004553; AAH04553.1; -  
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 DR MIN; 603455; -  
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 DR GO; GO:0004871; F:signal transducer activity; TAS.  
 DR GO; GO:0006915; P:apoptosis; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00114; CARD; 1.  
 DR PROSITE; PS02029; CARD; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Apoptosis.  
 FT DOMAIN 18 294 PROTEIN\_KINASE.  
 FT DOMAIN 432 524 CARD.  
 FT NP\_BIND 24 32 ATP (BY SIMILARITY).  
 FT BINDING 47 47 ATP.  
 FT ACT\_SITE 146 146  
 FT MUTAGEN 47 47 K->A: ABOLISHES KINASE ACTIVITY.  
 FT MUTAGEN 47 47 K->M: REDUCES FAS-MEDIATED APOPTOSIS.  
 FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.  
 SQ SEQUENCE 540 AA; 61194 MW; 575A692239505792 CRC64;

Alignment Scores:  
 Pred. No.: 3,06e-235 Length: 540  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 1 Gaps: 0

US-09-771-161A-2 (1-1669) x RIK2\_HUMAN (1-540)

QY 335 TTACAGAGTGTTCACAGTGCCATTACCTATGTGACAGAGAAATGGAATTATCTCTG 394  
 Db 314 LeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333  
 QY 395 AACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCCATGAA 454  
 Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 353  
 QY 455 AATAGTGGTCTCTGAACTTCAGTCCCTGCCAGTCTCTCAAGCAATGATTTTTHA 514  
 Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
 QY 515 TCTAGAAAGCTCAAGACTGTATTATTAAGCTGCATCAGTCTCTCGAAATACAGT 574  
 Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393

QY 575 TGGCATAGACACCATTTCTGGATCTCAAGGGCTGCATCTTGTGATCACAAGACACATCCA 634  
 Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 413  
 QY 635 TGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACCTCTGCAGCCT 694  
 Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
 QY 695 GGTATAGCCAGCAGTGGATCCAGACGAAAGGAAGAGACATTGTGACCAATGACAGAA 754  
 Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
 QY 755 GCCTGCTTAAACAGTCGCTAGATGCCCTCTCTCCAGGAGCTTGATCATGAAGAGGAC 814  
 Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
 QY 815 TATGAATCTGTTAGTACCAAGCTCAAGAGCTCAAAAGCTCAGAACTTACTAGACACT 874  
 Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
 QY 875 ACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAATAATGAAAGATAACAA 934  
 Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 533  
 QY 935 CAAATGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTAAAT 994  
 Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533  
 QY 995 TTACTTCAAAATAAAAGCATG 1015  
 Db 534 LeuLeuGlnAsnLysSerMet 540

RESULT 2  
 RIK2\_MOUSE  
 ID\_RIK2\_MOUSE STANDARD; PRT; 539 AA.  
 AC P58801;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).  
 GN RIPK2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=21891093; PubMed=11894097;  
 RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;  
 RT "Involvement of receptor-interacting protein 2 in innate and adaptive  
 immune responses";  
 RL Nature 416:190-194(2002).  
 CC -|- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
 CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).  
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -|- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.  
 CC Binds to BIRC3/C-IAP1 and BIRC2/C-IAP2, TRAF1, TRAF2, TRAF5 and  
 CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
 CC receptor complex (By similarity).  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC -|- PTM: Autophosphorylated (By similarity).  
 CC -|- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
 CC -|- SIMILARITY: Contains 1 CARD domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; AF461040; AAL96436.1; -.  
 DR MGD; MGI:1891456; RPK2.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR000719; Prot Kinase.  
 DR InterPro; IPR008271; Ser Thr pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00699; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot Kinase; 1.  
 DR SMART; SM00114; CARD; 1.  
 DR PROSITE; PSS0209; CARD; 1.  
 DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PSS0107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PSS0108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Apoptosis.  
 FT DOMAIN 18 294 PROTEIN KINASE.  
 FT DOMAIN 431 523 CARD.  
 FT NP BIND 24 32 ATP (BY SIMILARITY).  
 FT BINDING 47 47 ATP (BY SIMILARITY).  
 FT ACT SITE 146 146 BY SIMILARITY.  
 SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;

Alignment Scores:  
 Pred. No.: 4.28e-20 Length: 539  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 5.08% Indels: 0  
 DB: 1 Gaps: 0

US-09-771-161A-2 (1-1669) x RIK2\_MOUSE (1-539)

Qy	743	CAAATGACAGAGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGATC	802
Db	449	GlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIle	468
Qy	803	ATGAAAGAGGACTATGAACCTT	823
Db	469	MetLysGluAspTyrGluLeu	475

Search completed: March 29, 2004, 14:32:12  
 Job time : 22.5 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.  
No matches found  
Search completed: March 29, 2004, 14:35:18  
Job time : 87.5 secs

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:24:58 ; Search time 87.5 Seconds  
(without alignments)  
12036.569 Million cell updates/sec

Title: US-09-771-161A-2  
Perfect score: 531  
Sequence: 1 acctagttataccagata.....caacagcctgatgtgtaaaa 1669

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Word size: 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV=xlp  
-O=/cn2 1/USPTO spool\_p/US09771161/runat 29032004 124857 14326/app query.fasta\_1.1863  
-DB=SPTREMBL\_25 -QWAT=fastcan -SUFFIX=oli20n2p.rspt -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=20 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CN 1 1.95 @runat 29032004 124857 14326 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : SPTREMBL 25: \*  
1: sp archaea: \*  
2: sp bacteria: \*  
3: sp fungi: \*  
4: sp human: \*  
5: sp invertebrate: \*  
6: sp mammal: \*  
7: sp mhc: \*  
8: sp organelle: \*  
9: sp phage: \*  
10: sp plant: \*  
11: sp rodent: \*  
12: sp virus: \*  
13: sp vertebrate: \*  
14: sp unclassified: \*  
15: sp rvirus: \*  
16: sp bacteriap: \*  
17: sp archaeap: \*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
-----					

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:08:46 ; Search time 59 Seconds  
(without alignments)  
1111.034 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLOQSVSAIHLCDKKK.....PEILVSRSPSLNLLQNKSM 232

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 20

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_29Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	284	3	AAY59406 Human RIC
2	227	97.8	478	3	AAY59405 Human RIC
3	227	97.8	531	3	AAY59404 Human RIC
4	227	97.8	540	2	AAY92795 Human B1
5	227	97.8	540	3	AAY68774 Amino aci
6	227	97.8	540	4	AAY93621 Human pol
7	227	97.8	540	5	AAY80369 Human cel
8	227	97.8	540	5	AAY827882 Human rec
9	227	97.8	544	3	AAB43570 Human can
10	197	84.9	510	7	Adc99079 Human KPP
11	167	72.0	167	3	AAY59407 Human RIC
12	128	55.2	540	2	AAY31140 Human CAR
13	128	55.2	540	4	AAB20079 Human CAR
14	128	55.2	540	5	ABG31075 Human cas
15	128	55.2	540	5	AAC22107 Protein o
16	128	55.2	540	6	ABU56269 Human Cas
17	128	55.2	540	7	ADB81362 Human cas
18	110	47.4	110	6	ABU56272 Human CAR
19	109	47.0	109	5	AAC22110 Protein o
20	98	42.2	131	5	AAC22109 Protein o
21	98	42.2	131	6	ABU56271 Human Cas
22	92	39.7	92	5	ABJ04754 RICK prot

ALIGNMENTS

RESULT 1  
AAY59406  
ID AAY59406 standard; protein; 284 AA.  
XX  
AC AAY59406;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Human RICK protein sequence residues 248-531.  
XX  
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DRP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
PN WO9955134-A2.  
XX  
PD 04-NOV-1999. (b)  
XX  
PF 27-APR-1999; 99WO-US0009183.  
XX  
PR 27-APR-1998; 98US-00069023.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Nunez G, Inohara N, Koseki T;  
XX  
DR WPI; 2000-072163/06.  
XX  
PT Compositions for identifying apoptosis signaling pathway inhibitors  
PT useful for treating diseases.  
XX  
PS Claim 6; Page; 93pp; English.  
XX  
CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP  
CC kinase) protein of the invention. RICK acts as a positive regulator of  
CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
CC during CD95 signalling. The invention provides methods for identifying  
CC apoptosis signalling pathway inhibitors and activators, and methods and  
CC compositions for screening compounds which will modulate the interactions  
CC of the various compositions identified: ARC, RICK, and the CIDE family of  
CC activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening of  
CC assays for agents, useful in the diagnosis, prognosis or treatment of  
CC disease associated with excess cell growth and dysregulation of  
CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
CC screening assays to identify inhibitor molecules blocking CD95-mediated  
CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
CC to identify inhibitors of the enzymatic activity of caspase-8.  
CC Identification of ARC-like inhibitory compounds may be useful for gene  
CC therapy treatment of disease with increased cell death in muscle tissue  
CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
CC can be used as reagents for the preparation or affinity chromatography  
CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
CC of an essential step in the biochemistry of apoptosis is needed. RICK  
CC interaction with intracellular factors such as CLARP and FADD appears to  
CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
CC apoptosis factors are potential drug candidates. Note: This sequence was  
CC created using information given in the specification  
XX  
SQ Sequence 284 AA;

Query Match 97.8%; Score 227; DB 3; Length 284;  
Best Local Similarity 100.0%; Pred. No. 5.5e-222;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC	media, and for diagnostically measuring RICK levels. A specific inhibitor
CC	of an essential step in the biochemistry of apoptosis is needed. RICK
CC	interaction with intracellular factors such as CLARP and FADD appears to
CC	be essential for apoptosis, inhibitors of RICK binding to intracellular
CC	apoptosis factors are potential drug candidates. Note: This sequence was
CC	created using information given in the specification
XX	
SQ	Sequence 478 AA;
QY	6
Db	252
QY	66
Db	312
QY	126
Db	372
QY	186
Db	432
QY	186
Db	432
QY	186
Db	432
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QY	1

compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking C95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8. Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates

XX Sequence 531 AA;

Query Match 97.8%; Score 227; DB 3; Length 531;  
Best Local Similarity 100.0%; Pred. No. 9.9e-222;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMWLSLNPVNHGQESCGSSQLHENSGETSRSLPAPQNDPL 65  
DB 305 LQSVSSAIHLCDKKKMWLSLNPVNHGQESCGSSQLHENSGETSRSLPAPQNDPL 364  
QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
DB 365 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 424  
QY 126 GIAQWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLD 185  
DB 425 GIAQWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLD 484  
QY 186 TDIQEEPAKVIQKLNKQKQGLQPYPEILVVSRSPLNLLQNKSM 232  
DB 485 TDIQEEPAKVIQKLNKQKQGLQPYPEILVVSRSPLNLLQNKSM 531

RESULT 4  
AAW92795  
ID AAW92795 standard; protein; 540 AA.

AC AAW92795;  
XX  
DT 07-MAY-1999 (first entry)  
XX  
DE Human B1 protein.  
XX  
KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
KW cell survival pathway; intracellular signalling; AIDS; cancer; human.  
XX  
OS Homo sapiens.

PN WO9855507-A2.  
XX  
PD 10-DEC-1998.  
XX  
PF 01-JUN-1998; 98WO-TL000255.  
XX  
PR 05-JUN-1997; 97IL-00121011.  
PR 30-JUN-1997; 97IL-00121199.  
PR 11-SEP-1997; 97IL-00121746.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Wallach D, Boldin M, Malinin N;

DR WPI; 1999-070258/06.  
DR N-PSDB; AAX02558.  
XX  
PT New B1 protein regulates cell death and cell survival pathways -  
PT derivatives, DNA and antibodies, also regulate intracellular inflammation  
PT ; for treating AIDS, cancer.  
XX  
PS Claim 4; Fig 3A; 90pp; English.  
XX  
CC This invention describes the isolation of a novel human B1 protein which  
CC can interact with, intracellular mediators or modulators of inflammation,  
CC cell death and/or cell survival pathways, directly or indirectly. Cells  
CC can be modulated or mediated in inflammation, cell death or cell survival  
CC pathways or another intracellular signalling activity using B1.  
CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
CC oligonucleotides and ribozymes can also be used to regulate the above  
CC pathways  
XX  
SQ Sequence 540 AA;

Query Match 97.8%; Score 227; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1e-221;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMWLSLNPVNHGQESCGSSQLHENSGETSRSLPAPQNDPL 65  
DB 314 LQSVSSAIHLCDKKKMWLSLNPVNHGQESCGSSQLHENSGETSRSLPAPQNDPL 373  
QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
DB 374 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 433  
QY 126 GIAQWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLD 185  
DB 434 GIAQWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLD 493  
QY 186 TDIQEEPAKVIQKLNKQKQGLQPYPEILVVSRSPLNLLQNKSM 232  
DB 494 TDIQEEPAKVIQKLNKQKQGLQPYPEILVVSRSPLNLLQNKSM 540

RESULT 5  
AAW68774  
ID AAW68774 standard; protein; 540 AA.  
XX  
AC AAW68774;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Amino acid sequence of a human phosphorylation effector PHSP-6.  
KW Human; phosphorylation effector; PHSP; proliferative disorder;  
KW immune disorder; neuronal disorder.  
XX

OS Homo sapiens.  
XX  
FT Key  
FT Region  
FT Location/Qualifiers  
FT 18..287  
FT /note= "protein kinase family signature sequence"  
FT Modified-site  
FT 23 /note= "potential phosphorylation site"  
FT Modified-site  
FT 34 /note= "potential phosphorylation site"  
FT Modified-site  
FT 58 /note= "potential phosphorylation site"  
FT Modified-site  
FT 100 /note= "potential glycosylation site"  
FT Modified-site  
FT 102 /note= "potential phosphorylation site"  
FT Modified-site  
FT 180 /note= "potential phosphorylation site"  
FT Modified-site  
FT 183 /note= "potential phosphorylation site"  
FT Modified-site  
FT /note= "potential phosphorylation site"

FT Modified-site 207 /note= "potential phosphorylation site"  
FT Modified-site 224 /note= "potential phosphorylation site"  
FT Modified-site 267 /note= "potential phosphorylation site"  
FT Modified-site 296 /note= "potential phosphorylation site"  
FT Modified-site 301 /note= "potential phosphorylation site"  
FT Modified-site 360 /note= "potential phosphorylation site"  
FT Modified-site 374 /note= "potential phosphorylation site"  
FT Modified-site 391 /note= "potential phosphorylation site"  
FT Modified-site 401 /note= "potential glycosylation site"  
FT Modified-site 428 /note= "potential phosphorylation site"  
FT Modified-site 442 /note= "potential phosphorylation site"  
FT Modified-site 457 /note= "potential glycosylation site"  
FT Modified-site 478 /note= "potential phosphorylation site"  
FT Modified-site 478 /note= "potential phosphorylation site"  
FT Modified-site 484 /note= "potential phosphorylation site"  
FT Modified-site 537 /note= "potential phosphorylation site"  
FT Modified-site /note= "potential glycosylation site"  
PN WO200006728-A2.  
XX  
XX  
PD 10-FEB-2000.  
XX  
XX 28-JUL-1999; 99WO-US017132.  
XX  
XX 28-JUL-1998; 98US-0155213P.  
PR 14-SEP-1998; 98US-0155196P.  
PR 14-OCT-1998; 98US-0155239P.  
PR 03-NOV-1998; 98US-0106889P.  
PR 19-NOV-1998; 98US-0109093P.  
PR 23-DEC-1998; 98US-0113796P.  
PR 12-JAN-1999; 99US-0155233P.  
XX  
XX (INCYTE PHARM INC.  
XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX  
XX WPI; 2000-183125/16.  
DR N-PSDB; AAZ46143.  
XX  
XX New human phosphorylation effectors useful for the diagnosis, treatment  
PT and prevention of proliferative, immune and neuronal disorders.  
PT  
XX  
PS Claim 1; Page 84-85; 142pp; English.  
XX  
XX AAY68769-95 and AAY68797-99 represent human phosphorylation effectors  
CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
CC given in the specification). The sequences were isolated from cDNA  
CC libraries prepared from various human tissues. The PHSP proteins are  
CC useful for the diagnosis, treatment and prevention of proliferative  
CC disorders, immune disorders and neuronal disorders. The PHSP proteins  
CC form pharmaceutical compositions which useful for treating or preventing  
CC disorders associated with decreased PHSP expression/activity. PHSP  
CC antagonists are useful for treating or preventing disorders associated  
CC with increased PHSP expression/activity  
XX  
XX Sequence 540 AA;

Query Match 97.8%; Score 227; DB 3; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1e-221;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 LOSVSAIHLCDKKMELSLNIPVNHGPOEESCGSQHNSGSPETSRLPAPQNDL 65  
DB 314 LQSVSAIHLCDKKMELSLNIPVNHGPOEESCGSQHNSGSPETSRLPAPQNDL 373  
QY 66 SRKAQDCYFMKLHHCPCGNSHSDSTISGSORAAFCDHKTTPCSAIINPLSTAGNSERLOP 125  
DB 374 SRKAQDCYFMKLHHCPCGNSHSDSTISGSORAAFCDHKTTPCSAIINPLSTAGNSERLOP 433  
QY 126 GIAQWIOQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLDDT 185  
DB 434 GIAQWIOQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLDDT 493  
QY 186 TDIQGEFAKIVQKLKDNKQMGLOPYPEILVVSRSPLNLLQNKSM 232  
DB 494 TDIQGEFAKIVQKLKDNKQMGLOPYPEILVVSRSPLNLLQNKSM 540  
RESULT 6  
AAM93621  
ID AAM93621 standard; protein; 540 AA.  
XX  
XX AAM93621;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human polypeptide, SEQ ID NO: 3454.  
XX  
DE Human; full length cDNA; cDNA synthesis; oligo-capping.  
XX  
XX Homo sapiens.  
XX  
XX EP1130094-A2.  
XX  
XX 05-SEP-2001.  
XX  
XX 07-JUL-2000; 2000EP-00114089.  
XX  
XX 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakanatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
XX WPI; 2001-524255/58.  
DR N-PSDB; AAK94554.  
XX  
XX  
PT 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX  
XX Claim 8; SEQ ID NO 3454; 1380pp + Sequence Listing; English.  
XX  
XX The invention relates to primers for synthesising full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have  
CC been determined. Primers for synthesising the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a polypeptide encoded by a full length  
CC human cDNA of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in CD-ROM  
CC format directly from EPO  
XX  
XX Sequence 540 AA;

Query Match 97.8%; Score 227; DB 4; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1e-221;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDFL 65  
DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDFL 373

QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125  
DB 374 SRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433

QY 126 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
DB 434 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 493

QY 186 TDIQGEFEFAKVIQKLDKQKMGLOPYPEILVWSRSPSLNLLQKSM 232  
DB 494 TDIQGEFEFAKVIQKLDKQKMGLOPYPEILVWSRSPSLNLLQKSM 540

RESULT 7  
AAU80369  
ID AAU80369 standard; protein; 540 AA.  
AC AAU80369;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE Human cellular kinase RICK protein.  
XX  
KW Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;  
KW RIP; Nck-interacting kinase; MKK3; SRPK-2.  
XX  
OS Homo sapiens.  
XX  
PN EP1201765-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 15-OCT-2001; 2001EP-00124604.  
XX  
PR 16-OCT-2000; 2000US-0240750P.  
XX  
PA (AXXI-) AXKIMA PHARM AG.  
XX  
PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;  
XX  
DR WPI; 2002-373930/41.  
DR N-PSDB; ABK51169.  
XX  
PT Identifying agents for treatment or prevention of cytomegalovirus  
PT infection, comprises contacting test compound with cellular kinase and  
PT detecting change in cellular kinase activity.  
XX  
PS Disclosure; Page 23-24; 49pp; English.  
XX  
CC The present invention relates to a new method for identifying compounds  
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
CC related diseases. The method of the invention comprises contacting a test  
CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
CC activity. The method of the invention can be used to treat and/or prevent  
CC CMV infections and related diseases. Oligonucleotides that can detect the  
CC specified kinases can also be used for diagnosis of infection. The  
CC present amino acid sequence represents the human cellular kinase RICK  
CC protein of the invention, as described above  
XX  
SQ Sequence 540 AA;

Query Match 97.8%; Score 227; DB 5; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1e-221;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDFL 65  
DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDFL 373

QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125  
DB 374 SRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433

QY 126 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
DB 434 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 493

QY 186 TDIQGEFEFAKVIQKLDKQKMGLOPYPEILVWSRSPSLNLLQKSM 232  
DB 494 TDIQGEFEFAKVIQKLDKQKMGLOPYPEILVWSRSPSLNLLQKSM 540

RESULT 8  
AAE27882  
ID AAE27882 standard; protein; 540 AA.  
XX  
AC AAE27882;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human receptor interacting protein (RIP)2.  
XX  
KW Human; receptor interacting protein; RIP2; antisense; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US6426221-B1.  
XX  
PD 30-JUL-2002.  
XX  
PF 01-AUG-2001; 2001US-00920663.  
XX  
PR 01-AUG-2001; 2001US-00920663.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Ward DT, Cowser LM;  
XX  
DR WPI; 2002-673017/72.  
DR N-PSDB; AAD45172.  
XX  
PT New antisense oligonucleotide that targets regions of a nucleic acid  
PT encoding human receptor interacting protein (RIP)2, for treating diseases  
PT associated with RIP2 expression.  
XX  
PS Example 15; Col 49-54; 35pp; English.  
XX  
CC The invention relates to antisense compounds targeted to a nucleic acid  
CC encoding human receptor interacting protein (RIP)2 to inhibit its  
CC expression. Antisense compounds are used for treating diseases associated  
CC with RIP2 expression. They are also useful in antisense gene therapy. The  
CC present sequence is human RIP2 protein  
XX  
SQ Sequence 540 AA;

Query Match 97.8%; Score 227; DB 5; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1e-221;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDFL 65  
DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDFL 373

QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125  
DB 374 SRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433

QY 126 GIAQWITQSKREDIVNQMTAECLNQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDIT 185  
DB 434 GIAQWITQSKREDIVNQMTAECLNQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDIT 493  
QY 186 TDIOGEEFAKVIQVOKLKDKNQMGLOPYPEILVVSRSFSLNLLQKSM 232  
DB 494 TDIOGEEFAKVIQVOKLKDKNQMGLOPYPEILVVSRSFSLNLLQKSM 540  
RESULT 9  
AAB43570  
ID AAB43570 standard; protein; 544 AA.  
AC AAB43570;  
XX  
XX 08-FEB-2001 (first entry)  
DE Human cancer associated protein sequence SEQ ID NO:1015.  
XX  
XX Human; cancer associated gene; cancer antigen; detection; cancer;  
KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;  
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;  
KW dermatological; neuroprotective; thrombolytic; coagulant; neutropic;  
KW vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;  
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.  
XX  
OS Homo sapiens.  
XX  
XX WO200055350-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 08-MAR-2000; 2000WO-US005882.  
XX  
XX 12-MAR-1999; 99US-0124270P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
PI  
XX WPI: 2000-587533/55.  
DR  
DR N-PSDB; AAC7779.  
XX  
XX Novel isolated nucleic acids comprising sequences encoding peptides  
PT useful for treating or diagnosing e.g. cancer.  
XX  
XX Claim 11; Page 1595-1597; 2352pp; English.  
XX  
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
CC AAB43398 to AAB44239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnery; immunomodulator;  
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
CC neutropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of

CC the present invention  
XX  
XX Sequence 544 AA;  
Query Match 97.8%; Score 227; DB 3; Length 544;  
Best Local Similarity 100.0%; Pred. No. 1e-221;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 LOSVSSAIHLCDKKKMWLSLNPVNHGPOBESGSSQLEHSGSPETSRLPAPQNDL 65  
DB 318 LOSVSSAIHLCDKKKMWLSLNPVNHGPOBESGSSQLEHSGSPETSRLPAPQNDL 377  
QY 66 SRKAQDCYFMKLHHCPCGNHSDSTTSGSQRAAFCDHKTTPCSSAIINPLSTAGNSRLQ 125  
DB 378 SRKAQDCYFMKLHHCPCGNHSDSTTSGSQRAAFCDHKTTPCSSAIINPLSTAGNSRLQ 437  
QY 126 GIAQWITQSKREDIVNQMTAECLNQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDIT 185  
DB 434 GIAQWITQSKREDIVNQMTAECLNQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDIT 497  
QY 186 TDIOGEEFAKVIQVOKLKDKNQMGLOPYPEILVVSRSFSLNLLQKSM 232  
DB 498 TDIOGEEFAKVIQVOKLKDKNQMGLOPYPEILVVSRSFSLNLLQKSM 544  
RESULT 10  
ADC99079  
ID ADC99079 standard; protein; 510 AA.  
XX  
XX ADC99079;  
AC  
XX  
XX 01-JAN-2004 (first entry)  
DE Human KPP protein - SEQ ID 32.  
XX  
XX anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;  
KW neutropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;  
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;  
KW antidiabetic; nephrotropic; antitumor; thyromimetic; neuroprotective;  
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;  
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
KW virucide; protozoicide; fungicide; kinase; phosphatase; KPP;  
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
KW cancer; developmental; mental retardation; neurological;  
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
KW helminthic infection; transgenic; gene therapy; human; enzyme.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003033680-A2.  
XX  
XX 24-APR-2003.  
XX  
XX 17-OCT-2002; 2002WO-US033723.  
XX  
XX 19-OCT-2001; 2001US-0345474P.  
PR 02-NOV-2001; 2001US-0343910P.  
PR 13-NOV-2001; 2001US-033098P.  
PR 16-NOV-2001; 2001US-033424P.  
PR 30-NOV-2001; 2001US-0334288P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
PI Emerling BM, Forsythe ID, Gandhi AR, Gorvad AE, Griffin JA;  
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;  
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
PI Zebbarjadian Y;  
XX  
XX WPI: 2003-403214/38.



DR N-PSDB; ADC99131.  
 PT New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX Claim 1; SEQ ID NO 32; 424pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP protein of the  
 CC invention.  
 XX Sequence 510 AA;  
 XX  
 Query Match 84.9%; Score 197; DB 7; Length 510;  
 Best Local Similarity 100.0%; Pred. No. 3e-191;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 ECGSSQLHSGSPETSLPAPQNDFLSRKAQDCYFMKLHCHGNSHSDTSGSOR 95  
 DB 314 ECGSSQLHSGSPETSLPAPQNDFLSRKAQDCYFMKLHCHGNSHSDTSGSOR 373  
 QY 96 AAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIOSKREDIVNQMTACINQSLDAL 155  
 DB 374 AAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIOSKREDIVNQMTACINQSLDAL 433  
 QY 156 LSRDLIMKEDYELVSTKPTRTSKVROLDDTTDIOGEEFAKIVQKLKDKNQMGLOPYPEI 215  
 DB 434 LSRDLIMKEDYELVSTKPTRTSKVROLDDTTDIOGEEFAKIVQKLKDKNQMGLOPYPEI 493  
 QY 216 LVVSRSPSLNLLQNSM 232  
 DB 494 LVVSRSPSLNLLQNSM 510  
 RESULT 11  
 AAY59407  
 XX ID AAY59407 standard; protein; 167 AA.  
 XX AC AAY59407;  
 XX 21-MAR-2000 (first entry)  
 XX  
 DE Human RICK protein sequence residues 365-531.  
 XX  
 KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
 KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
 KW CIDE-A; CIDE-B; DRP-1; diagnosis; cell growth; apoptosis dysregulation;  
 KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
 KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9955134-A2.  
 XX  
 PD 04-NOV-1999.  
 XX  
 XX 27-APR-1999; 99WO-US0009183.  
 PF  
 PR 27-APR-1998; 98US-00069023.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.

XX Nunez G, Inohara N, Koseki T;  
 XX WPI; 2000-072163/06.  
 XX Compositions for identifying apoptosis signaling pathway inhibitors  
 PT useful for treating diseases.  
 XX  
 PS Claim 6; Page; 93pp; English.  
 XX  
 CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP  
 CC kinase) protein of the invention. RICK acts as a positive regulator of  
 CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
 CC during CD95 signalling. The invention provides methods for identifying  
 CC apoptosis signalling pathway inhibitors and activators, and methods and  
 CC compositions for screening compounds which will modulate the interactions  
 CC of the various compositions identified: ARC, RICK, and the CIDE family of  
 CC activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening  
 CC assays for agents, useful in the diagnosis, prognosis or treatment of  
 CC disease associated with excess cell growth and dysregulation of  
 CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
 CC screening assays to identify inhibitor and molecules blocking CD95-mediated  
 CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
 CC to identify inhibitors of the enzymatic activity of caspase-8.  
 CC Identification of ARC-like inhibitory compounds may be useful for gene  
 CC therapy treatment of disease with increased cell death in muscle tissue  
 CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
 CC treat e.g. cancer, AIDS, neurodegenerative diseases, aplastic anaemia,  
 CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
 CC can be used as reagents for the preparation or affinity chromatography  
 CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
 CC of an essential step in the biochemistry of apoptosis is needed. RICK  
 CC interaction with intracellular factors such as CLARP and FADD appears to  
 CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
 CC apoptosis factors are potential drug candidates. Note: This sequence was  
 CC created using information given in the specification  
 XX  
 SQ Sequence 167 AA;  
 XX  
 Query Match 72.0%; Score 167; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-161;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 66 SRKAQDCYFMKLHCHGNSHSDTSGSORAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
 DB 1 SRKAQDCYFMKLHCHGNSHSDTSGSORAFCDHKTTPCSSAIINPLSTAGNSERLQ 60  
 QY 126 GIAQQWIOSKREDIVNQMTACINQSLDALSRDLIMKEDYELVSTKPTRTSKVROLDDT 185  
 DB 61 GIAQQWIOSKREDIVNQMTACINQSLDALSRDLIMKEDYELVSTKPTRTSKVROLDDT 120  
 QY 186 TDIQGEFAKIVQKLKDKNQMGLOPYPEILVVSRSPSLNLLQNSM 232  
 DB 121 TDIQGEFAKIVQKLKDKNQMGLOPYPEILVVSRSPSLNLLQNSM 167  
 RESULT 12  
 AAY31140  
 ID AAY31140 standard; protein; 540 AA.  
 XX  
 AC AAY31140;  
 XX  
 XX 25-OCT-1999 (first entry)  
 DT  
 XX Human CARD-3 protein.  
 XX  
 KW CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
 KW caspase activation; detection; screening; therapy; diagnosis; disease;  
 KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
 KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
 KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;



CC with insufficient or excessive production of CARD-3, -4, -5 or -6  
 CC protein, or production of an aberrant protein  
 CC  
 SQ Sequence 540 AA;

Query Match 55.2%; Score 128; DB 4; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-121; Indels 0; Gaps 0;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SQ Sequence 540 AA;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQWQIQSKREDIVNQMTACLNQSLDALLSRDLINKE 164  
 DB 413 PCSSAIINPLSTAGNSERLQPGIAQWQIQSKREDIVNQMTACLNQSLDALLSRDLINKE 472

QY 165 DYELVSTKPTSTSKVRQLLDTTIOGEEFAKVIQKLDKDKQMGLOPYPEILVWSRPSL 224  
 DB 473 DYELVSTKPTSTSKVRQLLDTTIOGEEFAKVIQKLDKDKQMGLOPYPEILVWSRPSL 532

QY 225 NLLQNKSM 232  
 DB 533 NLLQNKSM 540

RESULT 14  
 ABG31075  
 ID ABG31075 standard; protein; 540 AA.

AC ABG31075;  
 DT 21-OCT-2002 (first entry)  
 DE Human caspase recruitment domain protein CARD-3.

KW Human; caspase recruitment domain; CARD-3; CARD-4; LRR;  
 KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;  
 KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis;  
 KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;  
 KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;  
 KW gastrointestinal allergy; insulin-dependent diabetes;  
 KW bacterial infection; tuberculosis; lepromatous leprosy;  
 KW cell signalling disorder; tissue disorder.

XX Homo sapiens.  
 OS WO200253765-A1.  
 FN 11-JUL-2002.  
 PD 20-DEC-2001; 2001WO-US049798.  
 PF 29-DEC-2000; 2000US-0258724P.  
 PR (MILL-) MILLENNIUM PHARM INC.  
 PA Bertin J, Philpott D, Sansonetti P, Girardin S;  
 PI WPI; 2002-583627/62.  
 DR N-PSDB; ABK89280.

XX Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.

XX Example 2; Fig 2; 139pp; English.  
 CC The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of

CC identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB); by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4 are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence represents human CARD-3 protein

XX SQ Sequence 540 AA;

Query Match 55.2%; Score 128; DB 5; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-121; Indels 0; Gaps 0;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQWQIQSKREDIVNQMTACLNQSLDALLSRDLINKE 164  
 DB 413 PCSSAIINPLSTAGNSERLQPGIAQWQIQSKREDIVNQMTACLNQSLDALLSRDLINKE 472

QY 165 DYELVSTKPTSTSKVRQLLDTTIOGEEFAKVIQKLDKDKQMGLOPYPEILVWSRPSL 224  
 DB 473 DYELVSTKPTSTSKVRQLLDTTIOGEEFAKVIQKLDKDKQMGLOPYPEILVWSRPSL 532

QY 225 NLLQNKSM 232  
 DB 533 NLLQNKSM 540

RESULT 15  
 AA022107  
 ID AA022107 standard; protein; 540 AA.

AC AA022107;  
 DT 27-SEP-2002 (first entry)  
 DE Protein of human CARD-3 SEQ ID No 2.

XX Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimer's; cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human.

XX Homo sapiens.  
 FN US6369196-B1.  
 XX 09-APR-2002.

XX 05-FEB-1999; 99US-00245281.  
 XX 06-FEB-1998; 98US-00019942.  
 PR 17-JUN-1998; 98US-00039041.  
 PR 08-DEC-1998; 98US-00207359.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Bertin J;

XX



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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:11:47 ; Search time 22 Seconds  
(without alignments)  
544.419 Million cell updates/sec

Title: US-09-771-161a-93  
Perfect score: 232  
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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 20

Total number of hits satisfying chosen parameters: 25

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	284	4	US-09-069-023-5
2	227	97.8	478	4	US-09-069-023-4
3	227	97.8	530	4	US-09-069-023-3
4	227	97.8	531	4	US-09-069-023-1
5	227	97.8	540	4	US-09-069-023-27
6	227	97.8	540	4	US-09-345-473E-28
7	167	72.0	167	4	US-09-069-023-6
8	128	55.2	540	3	US-09-019-942-1
9	128	55.2	540	4	US-09-099-041A-2
10	128	55.2	540	4	US-09-245-281-2
11	128	55.2	540	4	US-09-470-271-1
12	128	55.2	540	4	US-09-207-359B-2
13	128	55.2	540	4	US-09-340-620A-2
14	128	55.2	540	4	US-09-865-364-2
15	128	55.2	540	4	US-09-748-537-1
16	110	47.4	110	4	US-09-207-359B-6
17	110	47.4	110	4	US-09-865-364-6
18	109	47.0	109	4	US-09-099-041A-6
19	109	47.0	109	4	US-09-245-281-6
20	109	47.0	109	4	US-09-340-620A-6
21	98	42.2	131	4	US-09-099-041A-5
22	98	42.2	131	4	US-09-245-281-5
23	98	42.2	131	4	US-09-207-359B-5
24	98	42.2	131	4	US-09-340-620A-5
25	98	42.2	131	4	US-09-865-364-5

ALIGNMENTS

RESULT 1  
US-09-069-023-5  
; Sequence 5, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-5

Query Match 97.8%; Score 227; DB 4; Length 284;  
Best Local Similarity 100.0%; Pred. No. 3.9e-220;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQNDLF 65  
DB 58 LQSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQNDLF 117  
QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISSGORAACDCHKTPCASSAIINPLSTAGNSERLQP 125  
DB 118 SRKAQDCYFMKLHHCPCGNHSDSTISSGORAACDCHKTPCASSAIINPLSTAGNSERLQP 177  
QY 126 GIAQWIOSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLDFT 185  
DB 178 GIAQWIOSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLDFT 237  
QY 186 TDIQGEFAKIVQKLKDKNKQGLQPYPEILVWSRPSLNLLQNKSM 232  
DB 238 TDIQGEFAKIVQKLKDKNKQGLQPYPEILVWSRPSLNLLQNKSM 284

RESULT 2  
US-09-069-023-4  
; Sequence 4, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 478  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-4

Query Match 97.8%; Score 227; DB 4; Length 478;  
Best Local Similarity 100.0%; Pred. No. 6.2e-220;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQNDLF 65  
DB 252 LQSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQNDLF 311



; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
; FILE REFERENCE: 35800/183781  
; CURRENT APPLICATION NUMBER: US/09/345,473E  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-345-473E-28

Query Match 97.8%; Score 227; DB 4; Length 540;  
Best Local Similarity 100.0%; Pred. No. 7e-220;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 LOSVSAIHLCKKXWELSLNIPVNHGPOEESGSQLHENGSPETSRLPAPQNDPL 65  
DB 314 LOSVSAIHLCKKXWELSLNIPVNHGPOEESGSQLHENGSPETSRLPAPQNDPL 373  
  
QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125  
DB 374 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433  
  
QY 126 GIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
DB 434 GIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 493  
  
QY 186 TDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSPLNLLQKSM 232  
DB 494 TDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSPLNLLQKSM 540

RESULT 7  
US-09-069-023-6  
; Sequence 6, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 167  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-6

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Best Local Similarity 100.0%; Pred. No. 4.8e-160;  
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125  
DB 1 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 60  
  
QY 126 GIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
DB 61 GIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 120  
  
QY 186 TDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSPLNLLQKSM 232  
DB 121 TDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSPLNLLQKSM 167

RESULT 8  
US-09-019-942-1

; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-019-942-1

Query Match 55.2%; Score 128; DB 3; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2.2e-120;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472  
  
QY 165 DYELVSTKPTRTSKVRQLLDTTDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSPL 224  
DB 473 DYELVSTKPTRTSKVRQLLDTTDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSPL 532  
  
QY 225 NLLQKSM 232  
DB 533 NLLQKSM 540  
  
RESULT 9  
US-09-099-041A-2  
; Sequence 2, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-2

Query Match      55.2%; Score 128; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.2e-120;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRPSL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRPSL 532

Qy 225 NLLQNKSM 232
Db 533 NLLQNKSM 540

RESULT 10
US-09-245-281-2
; Sequence 2, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES-OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-2

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Best Local Similarity 100.0%; Pred. No. 2.2e-120;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRPSL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRPSL 532

Qy 225 NLLQNKSM 232
Db 533 NLLQNKSM 540

RESULT 11
US-09-470-271-1
; Sequence 1, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; DOMAIN POLYPEPTIDES
```

```
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-470-271-1

Query Match      55.2%; Score 128; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.2e-120;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRPSL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRPSL 532

Qy 225 NLLQNKSM 232
Db 533 NLLQNKSM 540

RESULT 12
US-09-207-359B-2
; Sequence 2, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-207-359B-2

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 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
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 DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472  
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QY 165 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQMGLOPYPEILLVWSRPSL 224  
 |||||  
 DB 473 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQMGLOPYPEILLVWSRPSL 532  
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QY 225 NLLQNKSM 232  
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 DB 533 NLLQNKSM 540  
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RESULT 13  
 US-09-340-620A-2  
 ; Sequence 2, Application US/09340620A  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/340,620A  
 ; CURRENT FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US/09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US/09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US/09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US/09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-340-620A-2

Query Match 55.2%; Score 128; DB 4; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-120;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
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 DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472  
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QY 165 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQMGLOPYPEILLVWSRPSL 224  
 |||||  
 DB 473 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQMGLOPYPEILLVWSRPSL 532  
 |||||

QY 225 NLLQNKSM 232  
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 DB 533 NLLQNKSM 540  
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RESULT 14  
 US-09-865-364-2  
 ; Sequence 2, Application US/09865364  
 ; Patent No. 6613521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/865,364  
 ; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-865-364-2

Query Match 55.2%; Score 128; DB 4; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-120;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
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 DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472  
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QY 165 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQMGLOPYPEILLVWSRPSL 224  
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 DB 473 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQMGLOPYPEILLVWSRPSL 532  
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QY 225 NLLQNKSM 232  
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 DB 533 NLLQNKSM 540  
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RESULT 15  
 US-09-748-537-1  
 ; Sequence 1, Application US/09748537  
 ; Patent No. 6680167  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; APPLICANT: Chao, Moses V.  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-316001  
 ; CURRENT APPLICATION NUMBER: US/09/748,537  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US/09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US/09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-748-537-1

Query Match 55.2%; Score 128; DB 4; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-120;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
 |||||  
 DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472  
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QY 165 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQMGLOPYPEILLVWSRPSL 224  
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 DB 473 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQMGLOPYPEILLVWSRPSL 532  
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QY 225 NLLQNKSM 232  
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 DB 533 NLLQNKSM 540  
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Search completed: March 29, 2004, 14:15:28  
 Job time : 23 secs



Result No.	Score	Query		Length	DB	ID	Description
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1	232	100.0	232	9	US-09-771-161A-93		Sequence 93, Appl
2	227	97.8	540	9	US-09-771-161A-184		Sequence 184, App
3	227	97.8	540	9	US-09-862-037-28		Sequence 28, Appl
4	227	97.8	540	10	US-09-981-397A-14		Sequence 14, Appl
5	227	97.8	544	9	US-09-925-301-1015		Sequence 1015, Ap
6	128	55.2	540	9	US-09-748-537-1		Sequence 1, Appli
7	128	55.2	540	9	US-09-728-721-2		Sequence 2, Appli
8	128	55.2	540	13	US-10-133-780-1		Sequence 1, Appli
9	128	55.2	540	13	US-10-105-931-2		Sequence 2, Appli
10	128	55.2	540	13	US-10-118-984-2		Sequence 2, Appli
11	128	55.2	540	14	US-10-295-981-2		Sequence 2, Appli
12	109	47.0	109	9	US-09-728-721-6		Sequence 6, Appli
13	109	47.0	109	13	US-10-105-931-6		Sequence 6, Appli
14	109	47.0	109	13	US-10-118-984-6		Sequence 6, Appli
15	109	47.0	109	14	US-10-295-981-6		Sequence 6, Appli

US-09-771-161A-184

PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 184  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 97.8%; Score 227; DB 9; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.1e-212;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOESCGSSQLHENSGETSRLPAPQNDL 65  
DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOESCGSSQLHENSGETSRLPAPQNDL 373

QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
DB 374 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 433

QY 126 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 185  
DB 434 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 493

QY 186 TDIQGEFAKVIQKLDKQMGLOQYPPEILVVSRSPLNLLQKSM 232  
DB 494 TDIQGEFAKVIQKLDKQMGLOQYPPEILVVSRSPLNLLQKSM 540

RESULT 3

US-09-862-027-28  
Sequence 28, Application US/09862027  
Patent No. US20020142428A1

GENERAL INFORMATION:  
APPLICANT: Hodge, Martin R.  
TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof  
FILE REFERENCE: 35800/234862  
CURRENT APPLICATION NUMBER: US/09/862,027  
CURRENT FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: US 09/345,473  
PRIOR FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 82  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 97.8%; Score 227; DB 9; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.1e-212;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOESCGSSQLHENSGETSRLPAPQNDL 65  
DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOESCGSSQLHENSGETSRLPAPQNDL 373

QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
DB 374 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 433

QY 126 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 185  
DB 434 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 493

QY 186 TDIQGEFAKVIQKLDKQMGLOQYPPEILVVSRSPLNLLQKSM 232  
DB 494 TDIQGEFAKVIQKLDKQMGLOQYPPEILVVSRSPLNLLQKSM 540

RESULT 4

US-09-981-397A-14

Sequence 14, Application US/09981397A  
Publication No. US20030082519A1  
GENERAL INFORMATION:  
APPLICANT: Axixina Pharmaceuticals AG  
APPLICANT: Schubart, Daniel  
APPLICANT: Habenberger, Peter  
APPLICANT: Stein-Gerlach, Matthias  
APPLICANT: Bevec, Dorian  
TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
TITLE OF INVENTION: Inhibition  
FILE REFERENCE: AXM-004.1 US  
CURRENT APPLICATION NUMBER: US/09/981,397A  
CURRENT FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/240,750  
PRIOR FILING DATE: 2000-10-16  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 14  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 97.8%; Score 227; DB 10; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.1e-212;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOESCGSSQLHENSGETSRLPAPQNDL 65  
DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOESCGSSQLHENSGETSRLPAPQNDL 373

QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
DB 374 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 433

QY 126 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 185  
DB 434 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 493

QY 186 TDIQGEFAKVIQKLDKQMGLOQYPPEILVVSRSPLNLLQKSM 232  
DB 494 TDIQGEFAKVIQKLDKQMGLOQYPPEILVVSRSPLNLLQKSM 540

RESULT 5

US-09-925-301-1015

Sequence 1015, Application US/09925301  
Patent No. US20020052308A1

GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA106  
CURRENT APPLICATION NUMBER: US/09/925,301  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05882  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1694  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1015  
LENGTH: 544  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 97.8%; Score 227; DB 9; Length 544;  
Best Local Similarity 100.0%; Pred. No. 1.1e-212;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOESCGSSQLHENSGETSRLPAPQNDL 65

Db 318 LOSVSAIHLCDKKMELSLNIPVNHGQEBSCGSQLHENSQSGPETSRLPAPQDNDFL 377  
QY 66 SRKAQDCYFMKLHCPGNHWDSTTSGSQAFAFCDHKTTTPCSSAIINPLSTAGNSERLOP 125  
Db 378 SRKAQDCYFMKLHCPGNHWDSTTSGSQAFAFCDHKTTTPCSSAIINPLSTAGNSERLOP 437  
QY 126 GIAQOWIOSKREDIVNOMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDDT 185  
Db 438 GIAQOWIOSKREDIVNOMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDDT 497  
QY 186 TDIQGEERFAKVIQVOKLKNQKQMGLOPYPEILLVVSRSPLNLLQKSM 232  
Db 498 TDIQGEERFAKVIQVOKLKNQKQMGLOPYPEILLVVSRSPLNLLQKSM 544  
RESULT 6  
US-09-748-537-1  
; Sequence 1, Application US/09748537  
; Patent No. US20020061833A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Chao, Moses V.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-316001  
; CURRENT APPLICATION NUMBER: US/09/748,537  
; CURRENT FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US/09/999,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-748-537-1  
Query Match 55.2%; Score 128; DB 9; Length 540;  
Best Local Similarity 100.0%; Pred. No. 4e-116;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 105 PCSSAIINPLSTAGNSERLOPQIAQOWIOSKREDIVNOMTEACLNQSLDALLSRDLIMKE 164  
Db 413 PCSSAIINPLSTAGNSERLOPQIAQOWIOSKREDIVNOMTEACLNQSLDALLSRDLIMKE 472  
QY 165 DYELVSTKPTRTSKVRQLDDTTDIQGEERFAKVIQVOKLKNQKQMGLOPYPEILLVVSRSPL 224  
Db 473 DYELVSTKPTRTSKVRQLDDTTDIQGEERFAKVIQVOKLKNQKQMGLOPYPEILLVVSRSPL 532  
QY 225 NLLQKSM 232  
Db 533 NLLQKSM 540  
RESULT 7  
US-09-728-721-2  
; Sequence 2, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US/09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/999,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-728-721-2  
Query Match 55.2%; Score 128; DB 9; Length 540;  
Best Local Similarity 100.0%; Pred. No. 4e-116;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 105 PCSSAIINPLSTAGNSERLOPQIAQOWIOSKREDIVNOMTEACLNQSLDALLSRDLIMKE 164  
Db 413 PCSSAIINPLSTAGNSERLOPQIAQOWIOSKREDIVNOMTEACLNQSLDALLSRDLIMKE 472  
QY 165 DYELVSTKPTRTSKVRQLDDTTDIQGEERFAKVIQVOKLKNQKQMGLOPYPEILLVVSRSPL 224  
Db 473 DYELVSTKPTRTSKVRQLDDTTDIQGEERFAKVIQVOKLKNQKQMGLOPYPEILLVVSRSPL 532  
QY 225 NLLQKSM 232  
Db 533 NLLQKSM 540  
RESULT 8  
US-10-133-780-1  
; Sequence 1, Application US/10133780  
; Publication No. US20020123115A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/133,780  
; FILING DATE: 26-Apr-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-133-780-1  
Query Match 55.2%; Score 128; DB 13; Length 540;  
Best Local Similarity 100.0%; Pred. No. 4e-116;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 164
DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 472
QY 165 DYELVSTKPTRTSKVRQLDITDIOGEEFAKVIQVKLKNKQMGLOPYPEILVVSRSPL 224
DB 473 DYELVSTKPTRTSKVRQLDITDIOGEEFAKVIQVKLKNKQMGLOPYPEILVVSRSPL 532
QY 225 NLLQKSM 232
DB 533 NLLQKSM 540

RESULT 9
US-10-105-931-2
; Sequence 2, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-2

Query Match 55.2%; Score 128; DB 13; Length 540;
Best Local Similarity 100.0%; Pred. No. 4e-116;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 164
DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 472
QY 165 DYELVSTKPTRTSKVRQLDITDIOGEEFAKVIQVKLKNKQMGLOPYPEILVVSRSPL 224
DB 473 DYELVSTKPTRTSKVRQLDITDIOGEEFAKVIQVKLKNKQMGLOPYPEILVVSRSPL 532
QY 225 NLLQKSM 232
DB 533 NLLQKSM 540

RESULT 10
US-10-118-984-2
; Sequence 2, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-2

Query Match 55.2%; Score 128; DB 13; Length 540;
Best Local Similarity 100.0%; Pred. No. 4e-116;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 164
DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 472
QY 165 DYELVSTKPTRTSKVRQLDITDIOGEEFAKVIQVKLKNKQMGLOPYPEILVVSRSPL 224
DB 473 DYELVSTKPTRTSKVRQLDITDIOGEEFAKVIQVKLKNKQMGLOPYPEILVVSRSPL 532
QY 225 NLLQKSM 232
DB 533 NLLQKSM 540

RESULT 11
US-10-295-981-2
; Sequence 2, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-2

Query Match 55.2%; Score 128; DB 14; Length 540;
Best Local Similarity 100.0%; Pred. No. 4e-116;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 164
DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 472
QY 165 DYELVSTKPTRTSKVRQLDITDIOGEEFAKVIQVKLKNKQMGLOPYPEILVVSRSPL 224
DB 473 DYELVSTKPTRTSKVRQLDITDIOGEEFAKVIQVKLKNKQMGLOPYPEILVVSRSPL 532
QY 225 NLLQKSM 232
DB 533 NLLQKSM 540

RESULT 12
US-09-728-721-6
; Sequence 6, Application US/09728721
; Patent No. US20020061845A1
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; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-6

Query Match          47.0%; Score 109; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QPGIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 183
DB 1 QPGIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 60

QY 184 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 232
DB 61 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 109

RESULT 13
US-10-105-931-6
; Sequence 6, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-6

Query Match          47.0%; Score 109; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QPGIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 183
DB 1 QPGIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 60

QY 184 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 232
DB 61 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 109

RESULT 14
US-10-118-984-6
; Sequence 6, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-6

Query Match          47.0%; Score 109; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QPGIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 183
DB 1 QPGIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 60

QY 184 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 232
DB 61 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 109

RESULT 15
US-10-295-981-6
; Sequence 6, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-6

Query Match          47.0%; Score 109; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QPGIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 183
DB 1 QPGIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 60

```





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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:10:51 ; Search time 20 Seconds  
(without alignments)  
1115.822 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLQLQSVSSAIHLCDKKK.....PEILVVSRSPSLNLLQNKSM 232

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78:\*  
1: piri:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
-----						

No matches found

Search completed: March 29, 2004, 14:14:52  
Job time : 20 secs

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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:09:41 ; Search time 17 Seconds  
(without alignments)  
710.604 Million cell updates/sec

Title: US-09-771-161a-93

Perfect score: 232

Sequence: 1 MYSLQLQSVSAIHLCDKKK.....PEILVVSRSPLNLQNKSM 232

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 20

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	540	1 RIK2 HUMAN	O43353 h receptor-
2	27	11.6	539	1 RIK2_MOUSE	P58801 mus musculus

#### ALIGNMENTS

#### RESULT 1

RIK2 HUMAN  
ID RIK2 HUMAN STANDARD; PRT; 540 AA.  
AC O43353;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)  
DE (RIP-2) (CARD-containing IL-1 beta converting enzyme)  
DE (RIP-2) (CARD-containing IL-1 beta converting enzyme)  
DE associated kinase) (CARD-containing IL-1 beta converting enzyme).  
GN RIPK2 OR RICK OR RIP2 OR CARDIAK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.  
RX MEDLINE=98241596; PubMed=9575181;  
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;  
RT "RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis.";  
RL J. Biol. Chem. 273:12296-12300(1998).  
RN [2]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.  
RC TISSUE=Endothelial cells;

RX MEDLINE=98307936; PubMed=9642260;  
RA McCarthy J.V., Ni J., Dixit V.M.;  
RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing kinase.";  
RL J. Biol. Chem. 273:16968-16975(1998).  
RN [3]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.  
RX MEDLINE=98381580; PubMed=9705938;  
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,  
RA Matmann C., Tschoop J.;  
RT "Identification of CARDIAK, a RIP-like kinase that associates with caspase-1.";  
RL Curr. Biol. 8:885-888(1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Ozersky P., Holmes A., Broy M.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Platzner M., Varon R.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates CASP-8-mediated apoptosis. Activates NF-kappaB.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains. Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40 receptor complex.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -!- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung, peripheral blood leukocytes, spleen, kidney, testis, prostate, pancreas and lymph node.  
CC -!- PTM: Autophosphorylated.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
-----  
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-----  
DR EMBL; AF027706; AAC34970.1; -;  
DR EMBL; AF078530; AAC27722.1; -;  
DR EMBL; AF064824; AAC25668.1; -;  
DR EMBL; AC004003; AAC24561.1; -;  
DR EMBL; AF117829; AAD04634.1; -;

```
DR EMBL; BC004553; AAH04553.1; --
DR Genew; HGNC:10020; RPK2.
DR MIM; 603455; --
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00109; PROTEIN KINASE ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN KINASE.
FT NP_BIND 24 32 CARD.
FT BINDING 47 47 ATP.
FT ACT_SITE 146 146
FT MUTAGEN 47 47 K-A: ABOLISHES KINASE ACTIVITY.
FT MUTAGEN 47 47 K-S: REDUCES FAS-MEDIATED APOPTOSIS.
FT MUTAGEN 146 146 D-S: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 540 AA; 61194 MW; 575A692239505792 CRC64;

Query Match 97.8%; Score 227; DB 1; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.4e-233;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMSLNIPVNHGQPEESGSSQHSOLHNSGSPETSRSLPAPQNDL 65
DB 314 LQSVSSAIHLCDKKKMSLNIPVNHGQPEESGSSQHSOLHNSGSPETSRSLPAPQNDL 373

QY 66 SRQAQCYFVKLHPCPNHSDSTISGQRAAFCDHKTTPCSSAINPLSTAGNSERLQ 125
DB 374 SRQAQCYFVKLHPCPNHSDSTISGQRAAFCDHKTTPCSSAINPLSTAGNSERLQ 433

QY 126 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTSKVRLD 185
DB 434 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTSKVRLD 493

QY 186 TDIQGEFAKVIQKLDKDKQMGLOPYPEILVVSRSFSLNLLQKSM 232
DB 494 TDIQGEFAKVIQKLDKDKQMGLOPYPEILVVSRSFSLNLLQKSM 540

RESULT 2
RIK2 MOUSE
ID_RIK2_MOUSE STANDARD; PRT; 539 AA.
AC PS8801;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).
GN RPK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6;
RX MEDLINE=21891093; PubMed=11894097;
RA Chin A.I.; Dempsey P.W.; Bruhn K.; Miller J.F.; Xu Y.; Cheng G.;
RT "Involvement of receptor-interacting protein 2 in innate and adaptive
```

```
RT immune responses.";
RL Nature 416:190-194(2002).
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/C-IAP1 and BIRC2/C-IAP2, TRAF1, TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; AF461040; AAL96436.1; --
MGD; MGI:1891456; RPK2.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
FT DOMAIN 18 294 PROTEIN KINASE.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP (BY SIMILARITY).
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;

Query Match 11.6%; Score 27; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 QMTEACLNQSLDALLSRDLIMKEDYEL 168
DB 449 QMTEACLNQSLDALLSRDLIMKEDYEL 475

Search completed: March 29, 2004, 14:13:21
Job time : 17 secs
```

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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:10:16 ; Search time 45 Seconds  
(without alignments)  
1626.672 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLQLQSVSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
-----					

No matches found

Search completed: March 29, 2004, 14:14:19  
Job time : 45 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 11:22:08 ; Search time 4002 Seconds  
(without alignments)  
2512.640 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLQVSSAIHLCDKKK.....PEILVVSRSPLNLQNKSM 232

Scoring table:  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 20

Total number of hits satisfying chosen parameters: 39

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlh  
-O=/cn2 1/USPTO spool/US09771161/runat\_29032004.124851.19858/app.query.fasta\_1.391  
-DB=GenEmbl -QFMT=fastap -SUFFIX=oli20p2n.rge -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=20 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CN 1 1 2496 @runat\_29032004.124851.19858 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1:	gb.ba.*	GenEmbl.*
2:	gb.htg.*	
3:	gb.in.*	
4:	gb.om.*	
5:	gb.ov.*	
6:	gb.pat.*	
7:	gb.ph.*	
8:	gb.pl.*	
9:	gb.pr.*	
10:	gb.ro.*	
11:	gb.sts.*	
12:	gb.sy.*	
13:	gb.un.*	
14:	gb.vi.*	
15:	em.ba.*	
16:	em.fun.*	
17:	em.hum.*	
18:	em.in.*	
19:	em.mu.*	
20:	em.om.*	
21:	em.or.*	
22:	em.ov.*	
23:	em.pat.*	
24:	em.ph.*	
25:	em.pl.*	
26:	em.ro.*	
27:	em.sts.*	
28:	em.un.*	

RESULT 1  
AF078530  
LOCUS  
DEFINITION  
Homo sapiens receptor interacting protein 2 (RIP2) mRNA, complete cds.  
ACCESSION  
AF078530  
VERSION  
AF078530.1 GI:3342909

ALIGNMENTS

AF078530 1623 bp mRNA linear PRI 28-JUL-1998  
Homo sapiens receptor interacting protein 2 (RIP2) mRNA, complete

29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rod.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	227	97.8	1623	9	AF078530 Homo sapi
2	227	97.8	1623	12	AY335645 Synthetic
3	227	97.8	1886	9	AY358813 Homo sapi
4	227	97.8	1889	9	BC004553 Homo sapi
5	227	97.8	1902	9	AF064824 Homo sapi
6	227	97.8	2024	6	BD251808 Phosphory
7	227	97.8	2033	6	BD127583 Primer fo
8	227	97.8	2033	9	AK075213 Homo sapi
9	227	97.8	2098	6	A82777 Sequence 2
10	227	97.8	2098	6	BD106658 Modulator
11	227	97.8	2501	6	AR221453 Sequence
12	227	97.8	2501	6	AX429236 Sequence
13	227	97.8	2501	9	AF027706 Homo sapi
14	227	97.8	2502	6	AR194318 Sequence
15	227	97.8	2521	9	AY358814 Homo sapi
16	185	79.7	1060	6	AR380139 Sequence
17	128	55.2	1620	6	AR183235 Sequence
18	128	55.2	1620	6	AR205635 Sequence
19	128	55.2	1620	6	AR241237 Sequence
20	128	55.2	1620	6	AR256253 Sequence
21	128	55.2	1620	6	AR391600 Sequence
22	128	55.2	1620	6	AX082201 Sequence
23	128	55.2	1620	6	BD123999 Novel mol
24	128	55.2	1931	6	AR183234 Sequence
25	128	55.2	1931	6	AR205634 Sequence
26	128	55.2	1931	6	AR216112 Sequence
27	128	55.2	1931	6	AR241236 Sequence
28	128	55.2	1931	6	AR256252 Sequence
29	128	55.2	1931	6	AR391599 Sequence
30	128	55.2	1931	6	AX082199 Sequence
31	128	55.2	1931	6	BD123998 Novel mol
32	113	48.7	116650	9	AC004003 Homo sapi
33	113	48.7	320187	9	AF117829 Homo sapi
C 34	75	32.3	61099	2	AC139421 Homo sapi
C 35	40	17.2	575	6	BD126039 Primer fo
C 36	27	11.6	1620	10	AF461040 Mus muscu
C 37	27	11.6	1620	10	AF487539 Mus muscu
C 38	27	11.6	173259	2	AC117336 Rattus no
C 39	27	11.6	186519	10	AL807379 Mouse DNA

KEYWORDS	Homo sapiens (human)	Db	1180	TGGGACAGCACCATTCTCGATCTCAAGGGCTGCAATTCGTGATCACAAGACCACCTCCA	1239
SOURCE	Homo sapiens	Qy	106	CysSerSerAlaIleIleAsnProIleAsnSerThrAlaGlyAsnSerGluArgLeuGlnPro	125
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Db	1240	TGCTCTTCAGCAATAATAATTCACCTCTCACTGCGAGAACTCAGAAAGTCTGCGAGCCT	1299
REFERENCE	McCarthy, J.V., Ni, J. and Dixit, V.M.	Qy	126	GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu	145
AUTHORS	1 (bases 1 to 1623)	Db	1300	GGTATAGCCAGCAGTGGATCCAGACCAAAAGGAGACATTGTGAACCAATGACAGAA	1359
TITLE	TRP2 is a novel NF-kappaB-activating and cell death-inducing kinase	Qy	146	AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp	165
JOURNAL	J Biol Chem. 273 (27), 16968-16975 (1998)	Db	1360	GCTGCTCTTAACCCAGTCGCTAGATGCCCTCTGTCAGGAGCTGATCATGAAAGAGGAC	1419
MEDLINE	93307936	Qy	166	TyTGlulLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr	185
PUBMED	96422260	Db	1420	TATGAACCTTGTAGTACCAAGCTCAGAGACCTCAAAAGTCAGAAATTTACTAGACACT	1479
REFERENCE	2 (bases 1 to 1623)	Qy	186	ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys	205
AUTHORS	McCarthy, J.V., Ni, J. and Dixit, V.M.	Db	1480	ACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA	1539
TITLE	Direct Submission	Qy	206	GlnMetGlyLeuGlnProTyProGluIleLeuValValSerArgSerProSerLeuAsn	225
JOURNAL	Submitted (15-JUL-1998) Molecular Oncology, Genentech Inc, 1 DNA	Db	1540	CAATGGGTCTTCAGCCTTACCGGAAATACTTGTGTTTCTAGATCACCATCTTTAAAT	1599
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AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1886)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
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AUTHORS   Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalley, D.E.,
Schnerich, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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AUTHORS   Strausberg, R.
TITLE     Submitted (14-MAR-2001) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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Email: cgabbs-r@mail.nih.gov
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Sequencing by: National Institutes of Health Intramural
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Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nigri.nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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LOCUS      AF064824                1902 bp      mRNA      linear      PRI 07-JUL-1998
DEFINITION Homo sapiens CARD-containing ICE associated kinase mRNA, complete cds.
ACCESSION  AF064824
VERSION    AF064824.1  GI:3290171
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1902)
            Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
            Mattmann C. and Tschopp J.
            Identification of CARDIAK, a RIP-like kinase that associates with
            caspase-1
            Curr. Biol. 8 (1998) In press
REFERENCE  2 (bases 1 to 1902)
            Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
            Mattmann C. and Tschopp J.
            Direct Submission
            Submitted (12-MAY-1998) Institute of Biochemistry, University of
            Lausanne, Chemin des Boveresses, 155, Epalinges, CH 1066,
            Switzerland
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Query Match:      97.84%       Indels:      0
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QY      26 AenIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45
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RESULT 6  
BD251808  
LOCUS  
DEFINITION Phosphorylation effectors.  
ACCESSION BD251808  
VERSION BD251808.1 GI:33061578  
KEYWORDS JP 2002526035-A/6.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2024)  
Hillman,J.L., Lal,P., Tang,T.Y., Corley,N.C., Guegler,K.J.,  
Baughn,M.R., Patterson,C., Bandman,O., Young,J.A., Gorgone,G.A.,  
Yue,H., Azimzai,Y., Reddy,R., Lu,D.A.M. and Shih,L.I.  
Phosphorylation effectors  
Patent: JP 2002526035-A 6 20-AUG-2002;  
INCYTE PHARMACEUTICALS INC  
OS Homo sapiens (human)  
PN JP 2002526035-A/6  
PD 20-AUG-2002  
PF 28-JUL-1999 JP 2000362510  
PR 28-JUL-1998 US 60/155213,14-SEP-1998 US 60/155196 PR  
14-OCT-1998 US 60/155239,03-NOV-1998 US 60/106889 PR  
19-NOV-1998 US 60/109093,22-DEC-1998 US 60/113796 PR  
12-JAN-1999 US 60/155233  
PI JENNIFER L HILLMAN, PREETI LAL, TOM Y TANG, NEIL C CORLEY, KARL J  
PI GUEGLER,  
PI MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDMAN, JANICE AU  
YOUNG,  
PI GINA A GORGONE, HENRY YUE, YALDA AZIMZAI, ROOPA REDDY, DYUNG AINA  
PI M LU,  
PI LEO L SHIH

PC C12N15/09,A61K38/00,A61K45/00,A61P1/04,A61P1/16,A61P3/10 PC  
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A61P21/04,  
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Db 1262 AATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCCCTCAAGACAATGATTTTAA 1321  
Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
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DEFINITION
ACCESSION      BD127583
VERSION      BD127583.1 GI:23222528
KEYWORDS      JP 2002017375-A/3014.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE      Primer for synthesizing full-length cDNA and use thereof
JOURNAL      Patent: JP 2002017375-A 3014 22-JAN-2002;
COMMENT      HELIX RESEARCH INSTITUTE
OS      Homo sapiens (human)
PN      JP 2002017375-A/3014
PD      22-JAN-2002
PF      07-JUL-2000 JP 2000253172
PI      TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI      YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI      TETSUJI OTSUKI, HISASHI KOGA
PC      C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
PC      10,
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Primer for synthesizing full-length cDNA and use thereof FH Key
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Alignment Scores:
Pred. No.:      6,75e-218      Length:      2033
Score:      227.00      Matches:      227
Percent Similarity:      100.00%      Conservative:      0
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Qy      46  AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
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DEFINITION      to Homo sapiens serine/threonine kinase RICK (RICK) mRNA.
ACCESSION      AK075213
VERSION      AK075213.1 GI:22761157
KEYWORDS      oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuma,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE      NEDO human cDNA sequencing project
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 2033)
AUTHORS      Isogai,T. and Otsuki,T.
JOURNAL      Direct Submission
TITLE      Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT      NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5' & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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ORIGIN

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Pred. No.: 6,75e-218 Length: 2033
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.84% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x AK075213 (1-2033)

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RESULT 9
LOCUS A82777 2098 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 2 from Patent WO9855507.
ACCESSION A82777
VERSION A82777.1 GI:6732464
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2098)
BOLDIN,M. and WALLACH,D.
MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL
SURVIVAL PATHWAYS
JOURNAL Patent: WO 9855507-A 2 10-DEC-1998;
BOLDIN MARK (IL); WALLACH DAVID (IL)
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ORIGIN

Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0
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US-09-771-161A-93 (1-232) x A82777 (1-2098)

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DB 1679 TATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGCTCAGACAAATTTACTAGACACT 1738
QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
DB 1739 ACTGACATCCAGAGAGAAATTTGCAAGTTATAGTACAAAAATGAAAGATACAAA 1798
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225
DB 1799 CAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTAAAT 1858
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DB 1859 TTACTTCAAAATAAAGCATG 1879

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LOCUS BD106658 2098 bp DNA linear PAT 18-SEP-2002  
DEFINITION Modulators of intracellular inflammation, cell death and cell survival pathways.  
ACCESSION BD106658  
VERSION BD106658.1 GI:23201476  
KEYWORDS JP 2002502258-A/1.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 2098)  
AUTHORS Wallach,D., Boldin,M. and Malinin,N.  
TITLE Modulators of intracellular inflammation, cell death and cell survival pathways  
JOURNAL Patent: JP 2002502258-A 1 22-JAN-2002;  
COMMENT YEDA RESEARCH AND DEVELOPMENT CO LTD  
PN JP 2002502258-A/1  
PD 22-JAN-2002  
PR 01-JUN-1998 JP 1999501993  
PR 05-JUN-1997 IL 121011,30-JUN-1997 IL 121199 PR  
11-SEP-1997 IL 121746  
PI DAVID WALLACH,MARK BOLDIN,NIKOLAI MALININ  
PC C12N15/12,C07K14/47,C07K16/18,C12Q1/68,A61K38/17,G01N33/68 CC  
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CC Topology: Linear;  
FH Key Location/Qualifiers.  
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Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
DB: 6 Gaps: 0  
US-09-771-161A-93 (1-232) x BD106658 (1-2098)  
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QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1259 AACATACCTGTAAATCATGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1318  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1319 AATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1378  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
DB 1379 TCTAGAAAAGCTCAAGACTGTTATTTATGAAAGCTGCATCAGTCTCTGGAATCAGACT 1438  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105  
DB 1439 TGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCGTGATCACAAGACCCTCCA 1498  
QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
DB 1499 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGAGCCT 1558  
QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
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QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspIleMetLysGluAsp 165  
DB 1619 GCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGTATCATGAAGAGGAC 1678

QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
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QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
DB 1739 ACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1798  
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
DB 1799 CAAATGGGTCTTCAGCCTTACCCGGAATACITGTGGTTTCTAGATCACCATCTTTAAAT 1858  
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DB 1859 TTACTTCAAAATAAAAGCATG 1879  
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LOCUS AR221453 2501 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 3 from patent US 6426221.  
ACCESSION AR221453  
VERSION AR221453.1 GI:23328503  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2501)  
AUTHORS Ward,D.T. and Cowser,L.M.  
TITLE Antisense modulation of RIP2 expression  
JOURNAL Patent: US 6426221-A 3 30-JUL-2002;  
FEATURES Location/Qualifiers  
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Pred. No.: 8e-218 Length: 2501  
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Best Local Similarity: 100.00% Mismatches: 0  
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QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1224 AACATACCTGTAAATCATGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1283  
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QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
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Db      1584 GCGTGCTTAAACAGTCGCTAGATGCGCTTCTGTCCAGGACTTGTATCATGAAGAAGAGGAC 1643
QY      166  TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
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QY      186  ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsnLys 205
Db      1704 ACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1763
QY      206  GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225
Db      1764 CAAATGGGCTTCAGCCTTACCCGGAAATACCTTGTGGTTTCTAGATCACCATCTTTAAT 1823
QY      226  LeuLeuGlnAsnLysSerMet 232
Db      1824 TTACTTCAAAATAAAGCATG 1844

RESULT 12
AX429236
LOCUS      AX429236
DEFINITION Sequence 13 from Patent EP1201765.
ACCESSION AX429236
VERSION   AX429236.1 GI:21540548
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.

REFERENCE 1
AUTHORS  Schubart,D., Habenberger,P., Stein-Gerlach,M. and Bevec,D.
TITLE    Cellular kinases involved in cytomagalovirus infection and their
          inhibition
JOURNAL  Patent: EP 1201765-A 13 02-MAY-2002;
          Axxima Pharmaceuticals Aktiengesellschaft (DE)
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Score:          227.00      Matches:      227
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    97.84%      Indels:      0
DB:             6          Gaps:         0

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Db      1224 AACATACCTGAAATCATGTGTCCACAGAGAGAAATCATGTGGATCCTCTCAGCTCCATGAA 1283
QY      46  AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db      1284 AATAGTGGTCTCTCGAAACTTCAAGTCCCTCGCAGCTCCTCAAGACAATGATTTTAA 1343
QY      66  SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db      1344 TCTAGAAAGACTCAAGACTGTTATTTATGAAGCTGCATCAGTCTCTCGAAATCAGAGT 1403
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Db      1524 GGTATAGCCAGCAGTGGATCCAGACCAAGGGAAGACATTGTGAACCAAAATGACAGAA 1583
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QY      166  TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
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QY      186  ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsnLys 205
Db      1704 ACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1763
QY      206  GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225
Db      1764 CAAATGGGCTTTCAGCCTTACCCGGAAATACCTTGTGGTTTCTAGATCACCATCTTTAAT 1823
QY      226  LeuLeuGlnAsnLysSerMet 232
Db      1824 TTACTTCAAAATAAAGCATG 1844

RESULT 13
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LOCUS      AF027706
DEFINITION Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
ACCESSION AF027706
VERSION   AF027706.1 GI:3123886
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE 1 (bases 1 to 2501)
AUTHORS  Inohara,N., Koseki,T., Chen,S., Chen,S. and Nunez,G.
TITLE    RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis
JOURNAL  J. Biol. Chem. 273 (20), 12296-12300 (1998)
MEDLINE  98241596
PUBMED   9575181
REFERENCE 2 (bases 1 to 2501)
AUTHORS  Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.
TITLE    Direct Submission
JOURNAL  Submitted (01-OCT-1997) Dept. Pathology, Comprehensive Cancer & Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr, Ann Arbor, MI 48109, USA

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DB      1704 ACTGACATCCAGGAGAAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAACAAA 1763
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DB      1764 CAAATGGGTCTTCAGCCTTACC CGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT 1823
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LOCUS      Sequence 2 from patent US 6348573.
DEFINITION
ACCESSION      AR194318
VERSION      AR194318.1      GI:20240910
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 2502)
AUTHORS      Nunez,G., Inohara,N. and Koseki,T.
TITLE      Compositions and methods for identifying apoptosis signaling
           pathway inhibitors and activators
JOURNAL      Patent: US 6348573-A 2 19-FEB-2002;
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Best Local Similarity: 100.00%      Mismatches:  0
Query Match:     97.84%      Indels:      0
DB:              6          Gaps:         0

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QY      46 AnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB      1285 AATAGTGGTTCCTCGAAACTTCAGAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1344
QY      66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
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DB      1405 TGGGATAGCACCATTTCTGGTTCCTCAAGGGCTGCATTCCTGTGATCACAGACCCTCCA 1464
QY      106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
DB      1465 TGCCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCGAGCCT 1524
QY      126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
DB      1525 GGTATAGCCAGCAGCTGGATCCAGACCAAAAGGAAGACATTGTGAACCAATGACAGAA 1584
QY      146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
DB      1585 GCCTGCTTTAAACCAAGTCGTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC 1644
QY      166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
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RESULT 15  
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 LOCUS Homo sapiens clone DNA43305 RIPK2 (UNQ277) mRNA, complete cds.  
 DEFINITION  
 ACCESSION AY358814  
 VERSION AY358814.1 GI:37182745  
 KEYWORDS FLI CDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2521)  
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wleand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.  
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
 PUBMED 12975309  
 REFERENCE 2 (bases 1 to 2521)  
 AUTHORS Clark,H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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 Best Local Similarity: 100.00% Mismatches: 0  
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 Db 1491 TGTCTTTACAGCAATAAATCACCCTCTCACTGCGAGGAAACTCAGAACCTCTGCGACCT 1550  
 Qy 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 Db 1551 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAA 1610  
 Qy 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 Db 1611 GCCTGCTCTTAACCAAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGGAC 1670  
 Qy 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 Db 1671 TATGAATCTGTAGTACCAAGCTCAGAGCACTCAAGAGTCAACAATTTACTAGACACT 1730  
 Qy 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsnLys 205  
 Db 1731 ACTGACATCCAGAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAA 1790  
 Qy 206 GlnMetGlyLeuGlnProTyrProGluLysValSerArgSerProSerLeuAsn 225  
 Db 1791 CAAATGGGCTTTCAGCGCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTAAAT 1850  
 Qy 226 LeuLeuGlnAsnLysSerMet 232  
 Db 1851 TTACTTCAAAATAAAGCATG 1871

Search completed: April 1, 2004, 14:05:47  
 Job time : 4018 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 13:59:15 ; Search time 61 Seconds  
(without alignments)  
1074.607 Million-cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLOQSVSSAIHLCDKKK.....PEILVVSRSPLNLLQKSM 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182	98.0	284	3 AAY59406	Aay59406 Human RIC
2	1182	98.0	478	3 AAY59405	Aay59405 Human RIC
3	1182	98.0	531	3 AAY59404	Aay59404 Human RIC
4	1182	98.0	540	2 AA92795	AA92795 Human B1
5	1182	98.0	540	3 AAY68774	Aay68774 Amino aci
6	1182	98.0	540	4 AA93621	AA93621 Human pol
7	1182	98.0	540	5 AAU80369	AAU80369 Human cel
8	1182	98.0	540	5 AAU827882	AAU827882 Human rec
9	1182	98.0	544	3 AAB43570	Aab43570 Human can
10	1176	97.5	540	2 AAY31140	Aay31140 Human CAR
11	1176	97.5	540	4 AAB20079	Aab20079 Human CAR
12	1176	97.5	540	5 AAB31075	Abg31075 Human cas
13	1176	97.5	540	5 AAO22107	Aao22107 Protein o
14	1176	97.5	540	6 ABU56269	Abu56269 Human cas
15	1176	97.5	540	7 ADB81362	Adb81362 Human cas
16	1027	85.2	510	7 ADC99079	Adc99079 Human KXP
17	867	71.9	167	3 AAY59407	Aay59407 Human RIC
18	632	52.4	131	5 AAO22109	Aao22109 Protein o
19	632	52.4	131	6 ABU56271	Abu56271 Human CAR
20	548	45.4	110	6 ABU56272	Abu56272 Human CAR
21	544	45.1	109	5 AAO22110	Aao22110 Protein o
22	461	38.2	92	5 ABJ04754	Abj04754 RICK prot
23	125	10.2	959	4 AAM79473	Aam79473 Human pro
24	122.5	10.2	164	2 AAY31144	Aay31144 Human CAR
25	122.5	10.2	164	4 AAB20083	Aab20083 Human CAR

26	122.5	10.2	164	5 ABG31079	Abg31079 Human cas
27	122.5	10.2	164	5 AAO22135	Aao22135 Protein o
28	122.5	10.2	164	6 ABU56297	Abu56297 Human Cas
29	122.5	10.2	249	2 AAY31143	Aay31143 Human CAR
30	122.5	10.2	249	4 AAB20082	Aab20082 Human CAR
31	122.5	10.2	249	5 ABG31078	Abg31078 Human cas
32	122.5	10.2	249	5 AAO22134	Aao22134 Protein o
33	122.5	10.2	249	6 ABU56296	Abu56296 Human Cas
34	122.5	10.2	409	6 ABU56299	Abu56299 Human Cas
35	122.5	10.2	779	4 AAB95610	Aab95610 Human pro
36	122.5	10.2	953	2 AAY31141	Aay31141 Human CAR
37	122.5	10.2	953	3 AAB15552	Aab15552 Apoptosis
38	122.5	10.2	953	4 AAB20080	Aab20080 Human CAR
39	122.5	10.2	953	4 AAM78489	Aam78489 Human pro
40	122.5	10.2	953	5 AAO22111	Aao22111 Protein o
41	122.5	10.2	953	6 ABU56273	Abu56273 Human Cas
42	122.5	10.2	953	7 ABJ72227	Abj72227 Human nuc
43	121.5	10.1	953	5 ABG31076	Abg31076 Human cas
44	119	9.9	100	5 AAO22112	Aao22112 Human CAR
45	119	9.9	100	6 ABU56274	Abu56274 Human CAR

## ALIGNMENTS

## RESULT 1

AA59406  
ID AAY59406 standard; protein; 284 AA.  
XX  
AC AAY59406;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Human RICK protein sequence residues 248-531.  
XX

KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
CIDE-A; CIDE-B; DRP-1; diagnosis; cell growth; apoptosis dysregulation;  
gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
PN WO9955134-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 27-APR-1999; 99WO-US009183.  
XX  
PR 27-APR-1998; 98US-00069023.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Nunez G, Inohara N, Koseki T;  
XX  
DR WPI; 2000-072163/06.  
XX  
PT Compositions for identifying apoptosis signaling pathway inhibitors  
useful for treating diseases.  
XX  
PS Claim 6; Page; 93pp; English.  
XX

CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP  
kinase) protein of the invention. RICK acts as a positive regulator of  
apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
during CD95 signalling. The invention provides methods for identifying  
apoptosis signalling pathway inhibitors and activators, and methods and  
compositions for screening compounds which will modulate the interactions  
of the various compositions identified: ARC, RICK, and the CIDE family of  
activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening  
assays for agents, useful in the diagnosis, prognosis or treatment of  
disease associated with excess cell growth and dysregulation of  
apoptosis. Complexes containing RICK and CLARP can be used in drug

CC screening assays to identify inhibitor molecules blocking CD95-mediated  
CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
CC to identify inhibitors of the enzymatic activity of caspase-8.  
CC Identification of ARC-like inhibitory compounds may be useful for gene  
CC therapy treatment of disease with increased cell death in muscle tissue  
CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
CC can be used as reagents for the preparation or affinity chromatography  
CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
CC of an essential step in the biochemistry of apoptosis is needed. RICK  
CC interaction with intracellular factors such as CtARP and FADD appears to  
CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
CC apoptosis factors are potential drug candidates. Note: This sequence was  
CC created using information given in the specification  
XX  
XX Sequence 284 AA:  
SQ

Query Match	98.0%;	Score 1182;	DB 3;	Length 284;
Best Local Similarity	99.6%;	Pred. No. 2.1e-115;		
Matches 227;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	5	QLQSVSAIHLCDKKKMWLSLNI	PVNHGPQESCGSSQLHNSGSP	PETSRSLPAPQDNDF 64
Db		:		
Db	57	KLQSVSAIHLCDKKKMWLSLNI	PVNHGPQESCGSSQLHNSGSP	PETSRSLPAPQDNDF 116
Qy	65	LSRKAQDCYFMKLHHCPCGNHSDST	ITSGSQRAAFCDHKTTPCSSAI	INPLTAGNSERLQ 124
Db	117	LSRKAQDCYFMKLHHCPCGNHSDST	ITSGSQRAAFCDHKTTPCSSAI	INPLTAGNSERLQ 176
Qy	125	PGIAQOMIQSKREDIVNQMTQACINQSL	DALLSRDLIMKEDYELVSTKPTTSKV	QRLD 184
Db	177	PGIAQOMIQSKREDIVNQMTQACINQSL	DALLSRDLIMKEDYELVSTKPTTSKV	QRLD 236
Qy	185	TTDIQGEEFAKVIQKLDKDNQMGLOPY	PEILVVSRSPLNLLQNSM	232
Db	237	TTDIQGEFAKVIQKLDKDNQMGLOPY	PEILVVSRSPLNLLQNSM	284

RESULT 2	
AAV59405	
ID	AAV59405 standard; protein; 478 AA.
XX	
XX	
AC	AAV59405;
XX	
XX	
DT	21-MAR-2000 (first entry)
XX	
DE	Human RICK protein sequence residues 54-531.
XX	
RICK;	human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;
KW	caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;
KW	CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;
KW	gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;
KW	aplastic anaemia; ischaemic injury; toxin-induced liver disease.
XX	
OS	Homo sapiens.
XX	
PN	WO9955134-A2.
XX	
PD	04-NOV-1999.
XX	
PF	27-APR-1999; 99WO-US009183.
XX	
PR	27-APR-1998; 98US-00069023.
XX	
PA	(UNMI ) UNIV MICHIGAN.
XX	
PI	Nunez G, Inohara N, Koseki T;
XX	
DR	WPI; 2000-072163/06.
XX	
PT	Compositions for identifying apoptosis signaling pathway inhibitors
PT	useful for treating diseases.

Claim 6; Page; 93pp; English.

This sequence is a fragment of the human RICK (RIP-like interactor of caspase-8 and caspase-10) protein of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CP95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDF family of activators (CIDF-A, CIDF-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CP95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.

Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDF can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation of affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates. Note: This sequence was created using information given in the specification

Query Match	98.0%;	Score 1182;	DB 3;	Length 478;
Best Local Similarity	99.6%;	Pred. No. 4.6e-115;		
Matches 227;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	5	QLQSVSSAIHLCDKKWELSLINPVNHGPOEESCGSSQLHENS	GSPETSRSLP	QNDNF 64
Db	251	KLQSVSSAIHLCDKKWELSLINPVNHGPOEESCGSSQLHENS	GSPETSRSLP	QNDNF 310
Qy	65	LSRKAQDCYFMKLHHCPCGNHISWSTISGSORAAFCDHKTT	PCSSAIINPL	STAGNSERLQ 124
Db	311	LSRKAQDCYFMKLHHCPCGNHISWSTISGSORAAFCDHKTT	PCSSAIINPL	STAGNSERLQ 370
Qy	125	PGTAQQWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKED	YELVSKPTST	KVRQLLD 184
Db	371	PGTAQQWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKED	YELVSKPTST	KVRQLLD 430
Qy	185	TTDIQGEFEAKVIQVKLKDNKQMGLOPYPEILVVSRSPSMLLNQ	KSM	232
Db	431	TTDIQGEFEAKVIQVKLKDNKQMGLOPYPEILVVSRSPSMLLNQ	KSM	478

RESULT 3	
AAAY59404	
ID	AAAY59404 standard; protein; 531 AA.
XX	
XX	
XX	AAAY59404;
XX	
DT	21-MAR-2000 (first entry)
XX	
DE	Human RICK protein sequence.
XX	
KW	RICK; human; RIP-like interacting C
KW	casepase-8; caspase-10; CD95 signal
KW	CIDE-A; CIDE-B; DREP-1; diagnosis;
KW	gene therapy; cardiac disorder; can
KW	aplastic anaemia; ischaemic injury;
XX	
OS	Homo sapiens.
XX	
PN	WO955134-A2.
FN	

PD 04-NOV-1999.  
 XX  
 PF 27-APR-1999; 99WO-US009183.  
 XX  
 PR 27-APR-1998; 98US-00069023.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Nunez G, Inohara N, Koseki T;  
 XX  
 DR WPI: 2000-072163/06.  
 DR N-PSDB; AA248762.  
 XX  
 PT Compositions for identifying apoptosis signaling pathway inhibitors  
 PT useful for treating diseases.  
 PS  
 PS Claim 1; Fig 7a; 93pp; English.  
 XX  
 CC This sequence is the human RICK (RIP-like interacting CLARP kinase)  
 CC protein of the invention. The RICK protein acts as a positive regulator  
 CC of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
 CC during CD95 signalling. The invention provides methods for identifying  
 CC apoptosis signalling pathway inhibitors and activators, and methods and  
 CC compositions for screening compounds which will modulate the interactions  
 CC of the various compositions identified: ARC, RICK, and the CIDE family of  
 CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening  
 CC assays for agents, useful in the diagnosis, prognosis or treatment of  
 CC disease associated with excess cell growth and dysregulation of  
 CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
 CC screening assays to identify inhibitor molecules blocking CD95-mediated  
 CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
 CC to identify inhibitors of the enzymatic activity of caspase-8.  
 CC Identification of ARC-like inhibitory compounds may be useful for gene  
 CC therapy treatment of disease with increased cell death in muscle tissue  
 CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
 CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
 CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
 CC can be used as reagents for the preparation or affinity chromatography  
 CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
 CC of an essential step in the biochemistry of apoptosis is needed. RICK  
 CC interaction with intracellular factors such as CLARP and FADD appears to  
 CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
 CC apoptosis factors are potential drug candidates  
 XX  
 SQ Sequence 531 AA;  
 Query Match 98.0%; Score 1182; DB 3; Length 531;  
 Best Local Similarity 99.6%; Pred. No. 5.5e-115;  
 Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QLQSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSGLSPETSRSLPAPQDNDF 64  
 DB 304 KLQSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSGLSPETSRSLPAPQDNDF 363  
 QY 65 LSRKAQDCYFMKLHCHPGNHSWDSTISGSORAAFCDHKTPCSSLINPLSTAGNSERLQ 124  
 DB 364 LSRKAQDCYFMKLHCHPGNHSWDSTISGSORAAFCDHKTPCSSLINPLSTAGNSERLQ 423  
 QY 125 PGIAQOWIOSKREDIVNQMTACLNSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
 DB 424 PGIAQOWIOSKREDIVNQMTACLNSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 483  
 QY 185 TTDIQGEFAKIVQKLDKQKMGLOPYEILLVSRSPSLNLLQKSM 232  
 DB 484 TTDIQGEFAKIVQKLDKQKMGLOPYEILLVSRSPSLNLLQKSM 531  
 RESULT 4  
 ID AA92795  
 XX AA92795 standard; protein; 540 AA.  
 AC  
 XX AA92795;  
 XX

DT 07-MAY-1999 (first entry)  
 XX Human B1 protein.  
 DE  
 XX  
 KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
 KW cell survival pathway; intracellular signalling; AIDS; cancer; human.  
 OS Homo sapiens.  
 XX  
 PN WO9855507-A2.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 01-JUN-1998; 98WO-IL000255.  
 XX  
 PR 05-JUN-1997; 97IL-00121011.  
 PR 30-JUN-1997; 97IL-00121199.  
 PR 11-SEP-1997; 97IL-00121746.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Wallach D, Boldin M, Malinin N;  
 XX  
 DR WPI: 1999-070258/06.  
 DR N-PSDB; AAX02558.  
 XX  
 CC New B1 protein regulates cell death and cell survival pathways -  
 CC derivatives, DNA and antibodies, also regulate intracellular inflammation  
 CC ; for treating AIDS, cancer.  
 PT  
 PT Claim 4; Fig 3A; 90pp; English.  
 PS  
 CC This invention describes the isolation of a novel human B1 protein which  
 CC can interact with, intracellular mediators or modulators of inflammation,  
 CC cell death and/or cell survival pathways, directly or indirectly. Cells  
 CC can be modulated or mediated in inflammation, cell death or cell survival  
 CC pathways or another intracellular signalling activity using B1.  
 CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
 CC oligonucleotides and ribozymes can also be used to regulate the above  
 CC pathways  
 XX  
 SQ Sequence 540 AA;  
 Query Match 98.0%; Score 1182; DB 2; Length 540;  
 Best Local Similarity 99.6%; Pred. No. 5.6e-115;  
 Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QLQSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSGLSPETSRSLPAPQDNDF 64  
 DB 313 KLQSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSGLSPETSRSLPAPQDNDF 372  
 QY 65 LSRKAQDCYFMKLHCHPGNHSWDSTISGSORAAFCDHKTPCSSLINPLSTAGNSERLQ 124  
 DB 373 LSRKAQDCYFMKLHCHPGNHSWDSTISGSORAAFCDHKTPCSSLINPLSTAGNSERLQ 432  
 QY 125 PGIAQOWIOSKREDIVNQMTACLNSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
 DB 433 PGIAQOWIOSKREDIVNQMTACLNSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
 QY 185 TTDIQGEFAKIVQKLDKQKMGLOPYEILLVSRSPSLNLLQKSM 232  
 DB 493 TTDIQGEFAKIVQKLDKQKMGLOPYEILLVSRSPSLNLLQKSM 540  
 RESULT 5  
 ID AA92774  
 XX AA92774 standard; protein; 540 AA.  
 AC  
 XX AA92774;  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human phosphorylation effector PHSP-6.

XX Human; phosphorylation effector; PHSP; proliferative disorder;  
 KW immune disorder; neuronal disorder.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 18..287  
 FT /note= "protein kinase family signature sequence"  
 FT Modified-site 23  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 34  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 58  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 100  
 FT /note= "potential glycosylation site"  
 FT Modified-site 102  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 180  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 183  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 207  
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 FT /note= "potential phosphorylation site"  
 FT Modified-site 301  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 360  
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 FT /note= "potential phosphorylation site"  
 FT Modified-site 391  
 FT /note= "potential glycosylation site"  
 FT Modified-site 401  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 428  
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 FT Modified-site 442  
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 FT Modified-site 478  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 484  
 FT /note= "potential phosphorylation site"  
 FT Modified-site 537  
 FT /note= "potential glycosylation site"  
 XX WO200006728-A2.  
 XX 10-FEB-2000.  
 XX 28-JUL-1999; 99WO-US017132.  
 XX 28-JUL-1998; 98US-0155213P.  
 XX 14-SEP-1998; 98US-0155196P.  
 XX 14-OCT-1998; 98US-0155239P.  
 XX 03-NOV-1998; 98US-0106889P.  
 XX 19-NOV-1998; 98US-0109093P.  
 XX 22-DEC-1998; 98US-0113796P.  
 XX 12-JAN-1999; 99US-0155233P.  
 XX (INCY-) INCYTE PHARM INC.  
 PA Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
 PI

PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
 PI Reddy R, Lu DAM, Shih LL;  
 XX WPI; 2000-183125/16.  
 DR N-PSDB; AAZ46143.  
 XX New human phosphorylation effectors useful for the diagnosis, treatment  
 PT and prevention of proliferative, immune and neuronal disorders.  
 XX Claim 1; Page 84-85; 142pp; English.  
 XX AA68769-95 and AA68797-99 represent human phosphorylation effectors  
 CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
 CC given in the specification). The sequences were isolated from CDNA  
 CC libraries prepared from various human tissues. The PHSP proteins are  
 CC useful for the diagnosis, treatment and prevention of proliferative  
 CC disorders, immune disorders and neuronal disorders. The PHSP proteins  
 CC form pharmaceutical compositions which useful for treating or preventing  
 CC disorders associated with decreased PHSP expression/activity. PHSP  
 CC antagonists are useful for treating or preventing disorders associated  
 CC with increased PHSP expression/activity  
 XX Sequence 540 AA;  
 SQ  
 Query Match 98.0%; Score 1182; DB 3; Length 540;  
 Best Local Similarity 99.6%; Pred. No. 5.6e-115;  
 Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QLOSVAIHLCDKKMELSLNIPVNHGPOEESGSSQLHENSGETSRLPAPQDNDF 64  
 DB :|||||  
 313 KQSVSAIHLCDKKMELSLNIPVNHGPOEESGSSQLHENSGETSRLPAPQDNDF 372  
 QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 124  
 DB :|||||  
 373 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 432  
 QY 125 PGIAQWIOKREDIVNQMTAEACINQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLLD 184  
 DB :|||||  
 433 PGIAQWIOKREDIVNQMTAEACINQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLLD 492  
 QY 185 TTDIQGEFAKIVQKLKONKMGLOPYPEILVVSRLNLLQNSM 232  
 DB :|||||  
 493 TTDIQGEFAKIVQKLKONKMGLOPYPEILVVSRLNLLQNSM 540  
 RESULT 6  
 AA93621  
 ID AA93621 standard; protein; 540 AA.  
 XX AC AA93621;  
 XX AC  
 DT 06-NOV-2001 (first entry)  
 XX Human polypeptide, SEQ ID NO: 3454.  
 DE Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX EF1130094-A2.  
 PN EF1130094-A2.  
 XX 05-SEP-2001.  
 PD 07-JUL-2000; 2000EP-00114089.  
 XX 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX (HELI-) HELIX RES INST.  
 PA Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 PI

XX WPI; 2001-524255/58.  
DR N-PSDB; AAK94554.  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX  
XX Claim 8; SEQ ID NO 3454; 1380pp + Sequence Listing; English.  
PS  
XX The invention relates to primers for synthesising full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have  
CC been determined. Primers for synthesising the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a polypeptide encoded by a full length  
CC human cDNA of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in CD-ROM  
CC format directly from EPO  
XX  
XX Sequence 540 AA;  
SQ

Query Match 98.0%; Score 1182; DB 4; Length 540;  
Best Local Similarity 99.6%; Pred. No. 5.6e-115;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHENSGETSRSPLAPQDNDF 64  
DB 313 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHENSGETSRSPLAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIQGEFAKVIQKLDKQKQGLQPYPEILVVSRSPLNLLQNKSM 232  
DB 493 TTDIQGEFAKVIQKLDKQKQGLQPYPEILVVSRSPLNLLQNKSM 540

RESULT 7  
AAU80369  
ID AAU80369 standard; protein; 540 AA.  
XX  
XX AAU80369;  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX Human cellular kinase RICK protein.  
XX  
XX Human; viricide; cytomegalovirus infection; CMV; cellular kinase; RICK;  
XX RIP; Nck-Interacting kinase; MKK3; SRPK-2.  
XX  
XX Homo sapiens.  
XX  
XX EP1201765-A2.  
XX  
XX 02-MAY-2002.  
XX  
XX 15-OCT-2001; 2001EP-00124604.  
XX  
XX 16-OCT-2000; 2000US-0240750P.  
XX  
XX (AXXI-) AXIXIMA PHARM AG.  
XX  
XX Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;  
XX WPI; 2002-373930/41.  
XX  
XX

DR N-PSDB; ABK51169.  
XX  
XX Identifying agents for treatment or prevention of cytomegalovirus  
PT infection, comprises contacting test compound with cellular kinase and  
PT detecting change in cellular kinase activity.  
XX  
XX Disclosure; Page 23-24; 49pp; English.  
XX  
XX The present invention relates to a new method for identifying compounds  
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
CC related diseases. The method of the invention comprises contacting a test  
CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
CC Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
CC activity. The method of the invention can be used to treat and/or prevent  
CC CMV infections and related diseases. Oligonucleotides that can detect the  
CC specified kinases can also be used for diagnosis of infection. The  
CC present amino acid sequence represents the human cellular kinase RICK  
CC protein of the invention, as described above  
XX  
XX Sequence 540 AA;  
SQ

Query Match 98.0%; Score 1182; DB 5; Length 540;  
Best Local Similarity 99.6%; Pred. No. 5.6e-115;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHENSGETSRSPLAPQDNDF 64  
DB 313 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHENSGETSRSPLAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIQGEFAKVIQKLDKQKQGLQPYPEILVVSRSPLNLLQNKSM 232  
DB 493 TTDIQGEFAKVIQKLDKQKQGLQPYPEILVVSRSPLNLLQNKSM 540

RESULT 8  
AAE27882  
ID AAE27882 standard; protein; 540 AA.  
XX  
XX AAE27882;  
XX  
XX 27-DEC-2002 (first entry)  
XX  
XX Human receptor interacting protein (RIP) 2.  
XX  
XX Human; receptor interacting protein; RIP2; antisense; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX US6426221-B1.  
XX  
XX 30-JUL-2002.  
XX  
XX 01-AUG-2001; 2001US-00920663.  
XX  
XX 01-AUG-2001; 2001US-00920663.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Ward DT, Cowser LM;  
XX WPI; 2002-673017/72.  
XX N-PSDB; AAD45172.  
XX  
XX New antisense oligonucleotide that targets regions of a nucleic acid  
PT encoding human receptor interacting protein (RIP) 2, for treating diseases

PT		associated with RIP2 expression.
XX		
PS		
XX	Example 15;	Col 49-54; 35pp; English.
CC	The invention relates to antisense compounds targetted to a nucleic acid encoding human receptor interacting protein (RIP)2 to inhibit its expression. Antisense compounds are used for treating diseases associated with RIP2 expression. They are also useful in antisense gene therapy. The present sequence is human RIP2 protein	
CC		
XX		
SQ	Sequence 540 AA;	
	Query Match	98.0%; Score 1182; DB 5; Length 540;
	Best Local Similarity	99.6%; Pred. No. 5.7e-115;
	Matches 227; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
Qy	5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPQEESCSSLHNSGSPETSRSLPAPQDNDF	64
Dd	:	
Dd	313 KLOSVAIAIHLCDKKKMWLSLNPVNHGPQEESCSSLHNSGSPETSRSLPAPQDNDF	372
Qy	65 LSRKAODCYFMKLHCPCGNHSWDSTISGSORAAFCDHKTTPCSSAIIINPLTAGNRSRLQ	124
Dd	:	
Dd	373 LSRKAODCYFMKLHCPCGNHSWDSTISGSORAAFCDHKTTPCSSAIIINPLTAGNRSRLQ	432
Qy	125 PGIAQQWIOSKREDIVNQTEACLNSLDALLSRDLIMKEDYELVSTRTSKVRQLLD	184
Dd	:	
Dd	433 PGIAQQWIOSKREDIVNQTEACLNSLDALLSRDLIMKEDYELVSTRTSKVRQLLD	492
Qy	185 TTDIOGEFAKVIVQKLKDKNKGLOPYPEILVWSRPSLNLLQNKS	232
Dd	:	
Dd	493 TTDIOGEFAKVIVQKLKDKNKGLOPYPEILVWSRPSLNLLQNKS	540
RESULT 9		
AAB43570		
ID	AAB43570 standard; protein; 544 AA.	
AC	AAB43570;	
DT	08-FEB-2001 (first entry)	
DE	Human cancer associated protein sequence SEQ ID NO:1015.	
KW	Human; cancer associated gene; cancer antigen; detection; cancer;	
KW	diagnosis; cytostatic; proliferative; vulnery; immunomodulator;	
KW	antidiabetic; antisthmatic; antiarthritis; antiviral;	
KW	antiinflammatory; antihypertensive; antibacterial; cardiant;	
KW	dermatological; neuroprotective; thrombolytic; coagulant; neutropenic;	
KW	vasotropic; antipsoriasis; angiogenesis; gene therapy; inflammation;	
KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;	
KW	allergic reaction; graft versus host disease; organ rejection;	
KW	haemostatic; thrombolytic; cardiovascular disorder; infection;	
KW	neurological disease; drug screening.	
OS	Homo sapiens.	
PB	WO2000055350-A1.	
PD	21-SEP-2000.	
PF	08-MAR-2000; 2000WO-US005882.	
PR	12-MAR-1999; 99US-0124270P.	
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Ruben SW;	
DR	WPI: 2000-587533/55.	
N-PSDB:	AAC77779.	
Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.		

Claim 11;	Page 1595-1597;	2352pp; English.
AAC77607	to AAC78448	encode the human cancer associated proteins given in ABA43398 to ABA44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytosstatic; proliferative; vulnerary; immunomodulator; antidiabetic; antisthmatic; antiarthritis; antiviral; antiinflammatory; antihypertensive; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; neutropenic; vasotropic; antipsoriasis; angiogenesis; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
Query Match	98.0%;	Score 1182; DB 3; Length 544;
Best Local Similarity	99.6%;	Pred. No. 5.7e-115;
Matches 227;	Conservative	1; Mismatches 0; Indels 0; Gaps 0;
Qy	5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPQEESCSSLHNSGSPETSRSLPAPQDNDF	64
Dd	:	
Dd	317 KLOSVAIAIHLCDKKKMWLSLNPVNHGPQEESCSSLHNSGSPETSRSLPAPQDNDF	376
Qy	65 LSRKAODCYFMKLHCPCGNHSWDSTISGSORAAFCDHKTTPCSSAIIINPLTAGNRSRLQ	124
Dd	:	
Dd	377 LSRKAODCYFMKLHCPCGNHSWDSTISGSORAAFCDHKTTPCSSAIIINPLTAGNRSRLQ	436
Qy	125 PGIAQQWIOSKREDIVNQTEACLNSLDALLSRDLIMKEDYELVSTRTSKVRQLLD	184
Dd	:	
Dd	437 PGIAQQWIOSKREDIVNQTEACLNSLDALLSRDLIMKEDYELVSTRTSKVRQLLD	496
Qy	185 TTDIOGEFAKVIVQKLKDKNKGLOPYPEILVWSRPSLNLLQNKS	232
Dd	:	
Dd	497 TTDIOGEFAKVIVQKLKDKNKGLOPYPEILVWSRPSLNLLQNKS	544
RESULT 10		
AAY31140		
ID	AAY31140 standard; protein; 540 AA.	
AC	AAY31140;	
DT	25-OCT-1999 (first entry)	
DE	Human CARD-3 protein.	
KW	CARD-3; caspase recruitment domain; CARD-4; regulation; detection;	
KW	caspase activation; detection; screening; therapy; diagnosis; disease;	
KW	apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;	
KW	cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;	
KW	hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;	
KW	systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;	
KW	Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;	
KW	spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;	
KW	myelodysplastic syndrome; myocardial infarction; cell proliferation;	
KW	cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;	
KW	human.	
OS	Homo sapiens.	
Key	Location/Qualifiers	





Query Match 97.5%; Score 1176; DB 4; Length 540;  
Best Local Similarity 99.1%; Pred. No. 2.4e-114;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNIPVNHGPOESCGSSQLHENSGLSPETSRSLPAPQDNDF 64  
:|||||  
DB 313 QLOSVSSAIHLCDKKKMWLSLNIPVNHGPOESCGSSQLHENSGLSPETSRSLPAPQDNDF 372  
:|||||

QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTTSGSQAACFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
:|||||  
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTTSGSQAACFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
:|||||

QY 125 PGTAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
:|||||  
DB 433 PGTAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
:|||||

QY 185 TTDIOGEEFAKIVQKLNKQKMGLOPYPEILVVSRSPLNLQNKSM 232  
:|||||  
DB 493 TTDIOGEEFAKIVQKLNKQKMGLOPYPEILVVSRSPLNLQNKSM 540  
:|||||

RESULT 12  
ABG31075  
ID ABG31075 standard; protein; 540 AA.

AC ABG31075;  
XX  
DT 21-OCT-2002 (first entry)  
XX

Human caspase recruitment domain protein CARD-3.  
XX  
DE Human; caspase recruitment domain; CARD-3; CARD-4; LRR;  
XX  
KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;  
KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;  
KW systemic lupus erythematosus; immune-mediated glomerulonephritis;  
KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;  
KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;  
KW gastrointestinal allergy; insulin-dependent diabetes;  
KW bacterial infection; tuberculosis; lepromatous leprosy;  
KW cell signalling disorder; tissue disorder.  
XX

Homo sapiens.  
OS  
XX  
XX WO200253765-A1.  
XX  
XX 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-US049798.  
XX  
XX 29-DEC-2000; 2000US-0258724P.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Bertin J, Philpott D, Sansonetti P, Girardin S;  
XX  
XX WPI; 2002-583627/62.  
XX  
XX N-PSDB; ABK89280.  
XX

Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.  
PT  
PT  
XX  
XX Example 2; Fig 2; 139pp; English.  
XX  
XX The invention relates to identifying (MI) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of

CC identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (MI) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, such as immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence represents human CARD-3 protein  
XX  
XX  
SQ Sequence 540 AA;

Query Match 97.5%; Score 1176; DB 5; Length 540;  
Best Local Similarity 99.1%; Pred. No. 2.4e-114;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNIPVNHGPOESCGSSQLHENSGLSPETSRSLPAPQDNDF 64  
:|||||  
DB 313 QLOSVSSAIHLCDKKKMWLSLNIPVNHGPOESCGSSQLHENSGLSPETSRSLPAPQDNDF 372  
:|||||

QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTTSGSQAACFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
:|||||  
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTTSGSQAACFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
:|||||

QY 125 PGTAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
:|||||  
DB 433 PGTAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
:|||||

QY 185 TTDIOGEEFAKIVQKLNKQKMGLOPYPEILVVSRSPLNLQNKSM 232  
:|||||  
DB 493 TTDIOGEEFAKIVQKLNKQKMGLOPYPEILVVSRSPLNLQNKSM 540  
:|||||

RESULT 13  
AAO22107  
ID AAO22107 standard; protein; 540 AA.

AC AAO22107;  
XX  
DT 27-SEP-2002 (first entry)  
XX  
DE Protein of human CARD-3 SEQ ID No 2.  
XX

Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers; cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological; nontropic; antiataxic; caspase Recruitment Domain; CARD; CARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human.  
XX  
XX Homo sapiens.  
XX  
XX US6369196-B1.  
XX  
XX 09-APR-2002.  
XX  
XX 05-FEB-1999; 99US-00245281.  
XX  
XX 06-FEB-1998; 98US-00019942.  
XX  
XX 17-JUN-1998; 98US-0009041.  
XX  
XX 08-DEC-1998; 98US-00207359.  
XX

PA (MILL-) MILLENNIUM PHARM INC.  
 XX Bertin J;  
 PI WPI; 2002-391988/42.  
 XX N-PSDB; AAL40752, AAL40753.  
 DR Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD  
 XX -4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's  
 PT disease, cancers and viral infections.  
 PT Example 2; Fig 2; 116pp; English.  
 XX  
 PS The invention relates to novel isolated Caspase Recruitment Domain (CARD)  
 XX polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may  
 CC be used to treat disorders associated with decreased CARD expression by  
 CC supplementing the patient's own production of CARD. Disorders associated  
 CC with the expression and activity of CARD include cancers (particularly  
 CC follicular lymphomas, carcinomas associated with mutations in p53, and  
 CC hormone-dependent tumours such as breast cancer, prostate cancer, and  
 CC ovarian cancer), autoimmune disorders (such as systemic lupus  
 CC erythematosus, immune-mediated glomerulonephritis), viral infections  
 CC (such as those caused by herpes viruses, poxviruses, and adenoviruses),  
 CC neurological diseases (such as Alzheimer's disease, Parkinson's disease,  
 CC amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal  
 CC muscular atrophy, and various forms of cerebellar degeneration), anaemia  
 CC associated with chronic disease, aplastic anaemia, chronic neutropenia,  
 CC and the myelodysplastic syndromes. This sequence represents a human CARD  
 CC protein relating to the invention  
 XX  
 XX Sequence 540 AA;  
 SQ  
 Query Match 97.5%; Score 1176; DB 5; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 2.4e-114;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 QLOSVSSAIHLCDKKKMKELSLNIPVNHGQPEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
 DB 313 KLOSVSSAIHLCDKKKMKELSLNIPVNHGQPEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
 QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLTAGNSERLQ 124  
 DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLTAGNSERLQ 432  
 QY 125 PGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
 DB 433 PGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
 QY 185 TTDIOGEFAKIVQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 232  
 DB 493 TTDIOGEFAKIVQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 540  
 RESULT 14  
 ABUS56269  
 ID ABUS56269 standard; protein; 540 AA.  
 XX  
 AC ABUS56269;  
 XX  
 DT 30-APR-2003 (first entry)  
 XX  
 DE Human Caspase recruitment domain protein, CARD-3.  
 KW Human; caspase recruitment domain; CARD; CARD-3; CARD-4; CARD-4L;  
 KW CARD-4S; CARD-4Y; apoptosis; cancer; AIDS; autoimmune disorder;  
 KW systemic lupus erythematosus; viral infection;  
 KW immune related glomerulonephritis; acquired immunodeficiency syndrome;  
 KW neurological disease; Alzheimer's disease; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular atrophy; cerebellar degeneration; haematological disease;  
 KW anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;  
 KW stroke; chromosome 7.  
 XX

OS Homo sapiens.  
 XX US6469140-B1.  
 PN 22-OCT-2002.  
 PD  
 XX 08-DEC-1998; 98US-00207359.  
 PF 06-FEB-1998; 98US-00019942.  
 PR 17-JUN-1998; 98US-00099041.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Bertin J;  
 XX WPI; 2003-147109/14.  
 DR N-PSDB; ABX75869, ABX74870.  
 DR Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z  
 PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,  
 PT detection assays, predictive medicine, and in therapeutic applications.  
 XX Example 2; Fig 2; 99pp; English.  
 PS The invention relates to an isolated polypeptide, comprising at least 25  
 CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,  
 CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)  
 CC polypeptide. Also included is an isolated fusion protein, comprising the  
 CC CARD polypeptide covalently linked by a peptide bond to a heterologous  
 CC polypeptide. The CARD polypeptide is useful in screening assays,  
 CC detection assays (e.g. chromosomal mapping, tissue typing and forensic  
 CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,  
 CC monitoring clinical trials and pharmacogenomics), and in therapeutic and  
 CC prophylactic treatments (in diseases associated with apoptotic cell death  
 CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and  
 CC immune related glomerulonephritis), viral infections, AIDS (acquired  
 CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
 CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),  
 CC haematological diseases (e.g. anaemia, neutropaenia and myelodysplastic  
 CC syndromes), myocardial infarction and stroke). The CARD polypeptide is  
 CC useful as bait protein in a two-hybrid assay or three hybrid assay to  
 CC identify other proteins, which bind to or interact with other CARD  
 CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
 CC human CARD-4 is located on chromosome 7. The present sequence is a human  
 CC CARD protein  
 XX  
 SQ Sequence 540 AA;  
 Query Match 97.5%; Score 1176; DB 6; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 2.4e-114;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 QLOSVSSAIHLCDKKKMKELSLNIPVNHGQPEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
 DB 313 KLOSVSSAIHLCDKKKMKELSLNIPVNHGQPEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
 QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLTAGNSERLQ 124  
 DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLTAGNSERLQ 432  
 QY 125 PGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
 DB 433 PGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
 QY 185 TTDIOGEFAKIVQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 232  
 DB 493 TTDIOGEFAKIVQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 540  
 RESULT 15  
 ADB81362  
 ID ADB81362 standard; protein; 540 AA.

[illegible]

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:07:10 ; Search time 22 Seconds  
(without alignments)  
544.419 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLQSVSSAIHLCDKKK.....PEILVSRSPSLNLLQKSM 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/2/1aa/5A-COMB.pep.\*  
2: /cgn2\_6/prodata/2/1aa/5B-COMB.pep.\*  
3: /cgn2\_6/prodata/2/1aa/6A-COMB.pep.\*  
4: /cgn2\_6/prodata/2/1aa/6B-COMB.pep.\*  
5: /cgn2\_6/prodata/2/1aa/6C-COMB.pep.\*  
6: /cgn2\_6/prodata/2/1aa/6D-COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182	98.0	284	US-09-069-023-5	Sequence 5, Appli
2	1182	98.0	478	US-09-069-023-4	Sequence 4, Appli
3	1182	98.0	530	US-09-069-023-3	Sequence 3, Appli
4	1182	98.0	531	US-09-069-023-1	Sequence 1, Appli
5	1182	98.0	540	US-09-069-023-27	Sequence 27, Appli
6	1182	98.0	540	US-09-345-473B-28	Sequence 28, Appli
7	1176	97.5	540	US-09-019-942-1	Sequence 1, Appli
8	1176	97.5	540	US-09-099-041A-2	Sequence 2, Appli
9	1176	97.5	540	US-09-245-281-2	Sequence 2, Appli
10	1176	97.5	540	US-09-470-271-1	Sequence 1, Appli
11	1176	97.5	540	US-09-207-359B-2	Sequence 2, Appli
12	1176	97.5	540	US-09-340-620A-2	Sequence 2, Appli
13	1176	97.5	540	US-09-865-364-2	Sequence 2, Appli
14	1176	97.5	540	US-09-748-537-1	Sequence 1, Appli
15	867	71.9	167	US-09-069-023-6	Sequence 6, Appli
16	632	52.4	131	US-09-099-041A-5	Sequence 5, Appli
17	632	52.4	131	US-09-245-281-5	Sequence 5, Appli
18	632	52.4	131	US-09-207-359B-5	Sequence 5, Appli
19	632	52.4	131	US-09-340-620A-5	Sequence 5, Appli
20	632	52.4	131	US-09-865-364-5	Sequence 5, Appli
21	548	45.4	110	US-09-207-359B-6	Sequence 6, Appli
22	548	45.4	110	US-09-865-364-6	Sequence 6, Appli
23	544	45.1	109	US-09-099-041A-6	Sequence 6, Appli
24	544	45.1	109	US-09-245-281-6	Sequence 6, Appli
25	544	45.1	109	US-09-340-620A-6	Sequence 6, Appli
26	149.5	12.4	109	US-09-340-620A-71	Sequence 71, Appli
27	122.5	10.2	164	US-09-245-281-41	Sequence 41, Appli

28	122.5	10.2	164	US-09-207-359B-41	Sequence 41, Appli
29	122.5	10.2	164	US-09-340-620A-41	Sequence 41, Appli
30	122.5	10.2	164	US-09-865-364-41	Sequence 41, Appli
31	122.5	10.2	249	US-09-245-281-39	Sequence 39, Appli
32	122.5	10.2	249	US-09-207-359B-39	Sequence 39, Appli
33	122.5	10.2	249	US-09-340-620A-39	Sequence 39, Appli
34	122.5	10.2	249	US-09-865-364-39	Sequence 39, Appli
35	122.5	10.2	409	US-09-207-359B-46	Sequence 46, Appli
36	122.5	10.2	409	US-09-865-364-46	Sequence 46, Appli
37	122.5	10.2	953	US-09-099-041A-8	Sequence 8, Appli
38	122.5	10.2	953	US-09-245-281-8	Sequence 8, Appli
39	122.5	10.2	953	US-09-207-359B-8	Sequence 8, Appli
40	122.5	10.2	953	US-09-340-620A-8	Sequence 8, Appli
41	122.5	10.2	953	US-09-865-364-8	Sequence 10, Appli
42	119	9.9	100	US-09-099-041A-10	Sequence 10, Appli
43	119	9.9	100	US-09-245-281-10	Sequence 10, Appli
44	119	9.9	100	US-09-207-359B-10	Sequence 10, Appli
45	119	9.9	100	US-09-340-620A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1  
US-09-069-023-5  
; Sequence 5, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-5

Query Match	98.0%	Score 1182;	DB 4;	Length 284;
Best Local Similarity	99.6%	Pred. No. 1.9e-125;		
Matches 227;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	5	QLQSVSSAIHLCDKKKMEISLNPVNHGPOEESCGSSQLHENSGLSPETSRSLPAPQDNDF	64	
Db	57	QLQSVSSAIHLCDKKKMEISLNPVNHGPOEESCGSSQLHENSGLSPETSRSLPAPQDNDF	116	
QY	65	LSRKAQDCYFVKMLHCHPCGNHSDWSTISGSORAAFCDHKTTPCSSALINPLSTAGNSERLQ	124	
Db	117	LSRKAQDCYFVKMLHCHPCGNHSDWSTISGSORAAFCDHKTTPCSSALINPLSTAGNSERLQ	176	
QY	125	PGIAQWQISQKREEDIVNQWTEACLNQSLDALLSRDLINKEDYELVSTKTRTSKVRQLLD	184	
Db	177	PGIAQWQISQKREEDIVNQWTEACLNQSLDALLSRDLINKEDYELVSTKTRTSKVRQLLD	236	
QY	185	TTDIGEEFAKVIQKLDKDKKMGLOPYPEILVSRSPSLNLLQKSM	232	
Db	237	TTDIGEEFAKVIQKLDKDKKMGLOPYPEILVSRSPSLNLLQKSM	284	
RESULT 2				
US-09-069-023-4				
; Sequence 4, Application US/09069023A				
; Patent No. 6348573				
; GENERAL INFORMATION:				
; APPLICANT: Nunez, Gabriel				
; APPLICANT: Inohara, Naohiro				
; APPLICANT: Koseki, Takeyoshi				

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 478  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-4

Query Match 98.0%; Score 1182; DB 4; Length 478;  
Best Local Similarity 99.6%; Pred. No. 4.2e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db 251 KLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 310  
Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 124  
Db 311 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 370  
Qy 125 PGIAQWIOQKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
Db 371 PGIAQWIOQKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 430  
Qy 185 TTDIQGEFAKVIQVOKLKDKNKQMGLOPYPEILVVSRSPLNLLQNKSM 232  
Db 431 TTDIQGEFAKVIQVOKLKDKNKQMGLOPYPEILVVSRSPLNLLQNKSM 478

RESULT 3  
US-09-069-023-3  
; Sequence 3, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-3

Query Match 98.0%; Score 1182; DB 4; Length 530;  
Best Local Similarity 99.6%; Pred. No. 5e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db 303 KLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 362  
Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 124  
Db 363 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 422  
Qy 125 PGIAQWIOQKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
Db 423 PGIAQWIOQKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 482  
Qy 185 TTDIQGEFAKVIQVOKLKDKNKQMGLOPYPEILVVSRSPLNLLQNKSM 232  
Db 482 TTDIQGEFAKVIQVOKLKDKNKQMGLOPYPEILVVSRSPLNLLQNKSM 530

Db 483 TTDIQGEFAKVIQVOKLKDKNKQMGLOPYPEILVVSRSPLNLLQNKSM 530

RESULT 4  
US-09-069-023-1  
; Sequence 1, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-1

Query Match 98.0%; Score 1182; DB 4; Length 531;  
Best Local Similarity 99.6%; Pred. No. 5e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db 304 KLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 363  
Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 124  
Db 364 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 423  
Qy 125 PGIAQWIOQKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
Db 424 PGIAQWIOQKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 483  
Qy 185 TTDIQGEFAKVIQVOKLKDKNKQMGLOPYPEILVVSRSPLNLLQNKSM 232  
Db 484 TTDIQGEFAKVIQVOKLKDKNKQMGLOPYPEILVVSRSPLNLLQNKSM 531

RESULT 5  
US-09-069-023-27  
; Sequence 27, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-27

Query Match 98.0%; Score 1182; DB 4; Length 540;  
Best Local Similarity 99.6%; Pred. No. 5.1e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db 313 KLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIQGEFAKVIQKLDKQKMGLOPYPEILLVSRSPSLNLLQKSM 232  
DB 493 TTDIQGEFAKVIQKLDKQKMGLOPYPEILLVSRSPSLNLLQKSM 540

RESULT 6

US-09-345-473E-28  
; Sequence 28, Application US/09345473E  
; Patent No. 6558903  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin  
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
; FILE REFERENCE: 35800/183781  
; CURRENT APPLICATION NUMBER: US/09/345,473E  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-345-473E-28

Query Match 98.0%; Score 1182; DB 4; Length 540;  
Best Local Similarity 99.6%; Pred. No. 5.1e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPGQESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
DB 313 QLOSVSSAIHLCDKKKMWLSLNPVNHGPGQESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIQGEFAKVIQKLDKQKMGLOPYPEILLVSRSPSLNLLQKSM 232  
DB 493 TTDIQGEFAKVIQKLDKQKMGLOPYPEILLVSRSPSLNLLQKSM 540

RESULT 7

US-09-019-942-1  
; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95

3/7/00

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,942

FILING DATE: 06-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 540 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-019-942-1

Query Match 97.5%; Score 1176; DB 3; Length 540;

Best Local Similarity 99.1%; Pred. No. 2.5e-124;

Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPGQESCGSSQLHNSGSPETSRSLPAPQDNDF 64

DB 313 QLOSVSSAIHLCDKKKMWLSLNPVNHGPGQESCGSSQLHNSGSPETSRSLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124

DB 373 LSRKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432

QY 125 PGIAQOQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184

DB 433 PGIAQOQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

QY 185 TTDIQGEFAKVIQKLDKQKMGLOPYPEILLVSRSPSLNLLQKSM 232

DB 493 TTDIQGEFAKVIQKLDKQKMGLOPYPEILLVSRSPSLNLLQKSM 540

RESULT 8

US-09-099-041A-2  
; Sequence 2, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-099-041A-2

Query Match 97.5%; Score 1176; DB 4; Length 540;

Best Local Similarity 99.1%; Pred. No. 2.5e-124;

Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPGQESCGSSQLHNSGSPETSRSLPAPQDNDF 64

DB 313 QLOSVSSAIHLCDKKKMWLSLNPVNHGPGQESCGSSQLHNSGSPETSRSLPAPQDNDF 372

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Qy 65 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 184
Db 433 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 492

Qy 185 TTDIQGEFAKVIIVQKLKDNKQMGLOPYPEILVVSRSPSLNLLQKSM 232
Db 493 TTDIQGEFAKVIIVQKLKDNKQMGLOPYPEILVVSRSPSLNLLQKSM 540

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RESULT 9
US-09-245-281-2
; Sequence 2, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-2

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Query Match 97.5%; Score 1176; DB 4; Length 540;
Best Local Similarity 99.1%; Pred. No. 2.5e-124;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 OLOSVSAIHLCDKKKMWLSLNIPVNHGPOEESCGSQLHENSGETSRLPAPQDNDF 64
Db 313 KLOSVSAIHLCDKKKMWLSLNIPVNHGPOEESCGSQLHENSGETSRLPAPQDNDF 372

Qy 65 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 184
Db 433 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 492

Qy 185 TTDIQGEFAKVIIVQKLKDNKQMGLOPYPEILVVSRSPSLNLLQKSM 232
Db 493 TTDIQGEFAKVIIVQKLKDNKQMGLOPYPEILVVSRSPSLNLLQKSM 540

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RESULT 10
US-09-470-271-1
; Sequence 1, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA

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; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-470-271-1

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Query Match 97.5%; Score 1176; DB 4; Length 540;
Best Local Similarity 99.1%; Pred. No. 2.5e-124;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 OLOSVSAIHLCDKKKMWLSLNIPVNHGPOEESCGSQLHENSGETSRLPAPQDNDF 64
Db 313 KLOSVSAIHLCDKKKMWLSLNIPVNHGPOEESCGSQLHENSGETSRLPAPQDNDF 372

Qy 65 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 184
Db 433 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 492

Qy 185 TTDIQGEFAKVIIVQKLKDNKQMGLOPYPEILVVSRSPSLNLLQKSM 232
Db 493 TTDIQGEFAKVIIVQKLKDNKQMGLOPYPEILVVSRSPSLNLLQKSM 540

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RESULT 11
US-09-207-359B-2
; Sequence 2, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-2

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Query Match 97.5%; Score 1176; DB 4; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 64  
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 Db 313 KLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 372  
 :|||||

QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124  
 :|||||  
 Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432  
 :|||||

QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
 :|||||  
 Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
 :|||||

QY 185 TTDIQGEFAKIVQKLDKDKQKGLQPYPEILLVSRSPSLNLLQKSM 232  
 :|||||  
 Db 493 TTDIQGEFAKIVQKLDKDKQKGLQPYPEILLVSRSPSLNLLQKSM 540  
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RESULT 12  
 US-09-340-620A-2  
 ; Sequence 2, Application US/09340620A  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/340,620A  
 ; CURRENT FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US/09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US/09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US/09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US/09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-340-620A-2

Query Match 97.5%; Score 1176; DB 4; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 64  
 :|||||  
 Db 313 KLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 372  
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QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124  
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 Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432  
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QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
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 Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
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QY 185 TTDIQGEFAKIVQKLDKDKQKGLQPYPEILLVSRSPSLNLLQKSM 232  
 :|||||  
 Db 493 TTDIQGEFAKIVQKLDKDKQKGLQPYPEILLVSRSPSLNLLQKSM 540  
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RESULT 13  
 US-09-865-364-2  
 ; Sequence 2, Application US/09865364  
 ; Patent No. 6613521  
 ; GENERAL INFORMATION:

APPLICANT: Bertin, John  
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 FILE REFERENCE: 07334-112001  
 CURRENT APPLICATION NUMBER: US/09/865,364  
 CURRENT FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: US/09/207,359  
 PRIOR FILING DATE: 1998-12-08  
 PRIOR APPLICATION NUMBER: US/09/099,041  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: US/09/019,942  
 PRIOR FILING DATE: 1998-02-06  
 NUMBER OF SEQ ID NOS: 47  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 2  
 LENGTH: 540  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-865-364-2

Query Match 97.5%; Score 1176; DB 4; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 64  
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 Db 313 KLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 372  
 :|||||

QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124  
 :|||||  
 Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432  
 :|||||

QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
 :|||||  
 Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
 :|||||

QY 185 TTDIQGEFAKIVQKLDKDKQKGLQPYPEILLVSRSPSLNLLQKSM 232  
 :|||||  
 Db 493 TTDIQGEFAKIVQKLDKDKQKGLQPYPEILLVSRSPSLNLLQKSM 540  
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RESULT 14  
 US-09-748-537-1  
 ; Sequence 1, Application US/09748537  
 ; Patent No. 6680167  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; APPLICANT: Chao, Moses V.  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THERE  
 ; FILE REFERENCE: 07334-316001  
 ; CURRENT APPLICATION NUMBER: US/09/748,537  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US/09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US/09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-748-537-1

Query Match 97.5%; Score 1176; DB 4; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 64  
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 Db 313 KLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 372  
 :|||||

QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124  
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Db 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTPCSSAIINPLSTAGNSERLQ 432
Qy 125 PGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
Qy 185 TTDIQGEFAKVIQVKLDKNKQMGLOPYPEILVVSRSPSLNLQNKSM 232
Db 493 TTDIQGEFAKVIQVKLDKNKQMGLOPYPEILVVSRSPSLNLQNKSM 540
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RESULT 15
US-09-069-023-6
; Sequence 6, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-6
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Query Match 71.9%; Score 867; DB 4; Length 167;
Best Local Similarity 100.0%; Prad. No. 4e-90;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTPCSSAIINPLSTAGNSERLQ 125
Db 1 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTPCSSAIINPLSTAGNSERLQ 60

Qy 126 GIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 185
Db 61 GIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 120

Qy 186 TTDIQGEFAKVIQVKLDKNKQMGLOPYPEILVVSRSPSLNLQNKSM 232
Db 121 TTDIQGEFAKVIQVKLDKNKQMGLOPYPEILVVSRSPSLNLQNKSM 167
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Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:08:11 ; Search time 43 Seconds  
(without alignments)  
1411.757 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLOQSVSSAIHLCDKKK.....PEILVVSRSPLNLQNKSM 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues  
Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/ECTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1206	100.0	232	9	US-09-771-161A-93
2	1182	98.0	540	9	US-09-771-161A-184
3	1182	98.0	540	9	US-09-862-027-28
4	1182	98.0	540	10	US-09-981-397A-14
5	1182	98.0	540	9	US-09-925-301-1015
6	1176	97.5	540	9	US-09-748-537-1
7	1176	97.5	540	9	US-09-728-721-2
8	1176	97.5	540	13	US-10-133-780-1
9	1176	97.5	540	13	US-10-105-931-2
10	1176	97.5	540	13	US-10-118-984-2
11	1176	97.5	540	14	US-10-295-981-2
12	632	52.4	131	9	US-09-728-721-5
13	632	52.4	131	13	US-10-105-931-5
14	632	52.4	131	13	US-10-118-984-5
15	632	52.4	131	14	US-10-295-981-5

16	544	45.1	109	9	US-09-728-721-6	Sequence 6, Appli
17	544	45.1	109	13	US-10-105-931-6	Sequence 6, Appli
18	544	45.1	109	13	US-10-118-984-6	Sequence 6, Appli
19	544	45.1	109	14	US-10-295-981-6	Sequence 6, Appli
20	461	38.2	92	13	US-10-014-269-21	Sequence 21, Appli
21	461	38.2	92	13	US-10-002-974-21	Sequence 21, Appli
22	461	38.2	92	14	US-10-314-506-21	Sequence 21, Appli
23	451	37.4	90	9	US-09-841-879B-10	Sequence 10, Appli
24	447	37.1	89	9	US-09-931-071-11	Sequence 11, Appli
25	149.5	12.4	109	9	US-09-728-721-71	Sequence 71, Appli
26	149.5	12.4	109	14	US-10-295-981-71	Sequence 71, Appli
27	143.5	11.9	95	9	US-09-841-879B-12	Sequence 12, Appli
28	122.5	10.2	164	9	US-09-728-721-41	Sequence 41, Appli
29	122.5	10.2	164	13	US-10-118-984-41	Sequence 41, Appli
30	122.5	10.2	164	14	US-10-295-981-41	Sequence 41, Appli
31	122.5	10.2	249	9	US-09-728-721-39	Sequence 39, Appli
32	122.5	10.2	249	13	US-10-118-984-39	Sequence 39, Appli
33	122.5	10.2	249	14	US-10-295-981-39	Sequence 39, Appli
34	122.5	10.2	507	15	US-10-401-194-3	Sequence 3, Appli
35	122.5	10.2	953	9	US-09-728-721-8	Sequence 8, Appli
36	122.5	10.2	953	13	US-10-105-931-8	Sequence 8, Appli
37	122.5	10.2	953	13	US-10-118-984-8	Sequence 8, Appli
38	122.5	10.2	953	14	US-10-013-477-12	Sequence 12, Appli
39	122.5	10.2	953	14	US-10-295-981-8	Sequence 8, Appli
40	122.5	10.2	953	14	US-10-028-374-4	Sequence 4, Appli
41	122.5	10.2	953	14	US-10-183-770-4	Sequence 4, Appli
42	119	9.9	100	9	US-09-728-721-10	Sequence 10, Appli
43	119	9.9	100	13	US-10-105-931-10	Sequence 10, Appli
44	119	9.9	100	13	US-10-118-984-10	Sequence 10, Appli
45	119	9.9	100	14	US-10-295-981-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1  
US-09-771-161A-93  
; Sequence 93, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 93  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-93

Query Match	100.0%	Score 1206;	DB 9;	Length 232;
Best Local Similarity	100.0%	Pred. No. 3.4e-111;		
Matches 232;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MYSLOQSVSSAIHLCDKKKMSLNI	PVNHGQPQESCGSSQHLHNSGSPETSRSLPAPQ	60
Db	1	MYSLOQSVSSAIHLCDKKKMSLNI	PVNHGQPQESCGSSQHLHNSGSPETSRSLPAPQ	60
QY	61	DNDFLSRQAQDCYFMKLHHCPCGNHNSWDSTISGSQRAAFCDHKTTPC	SSAIINPLSTAGNS	120
Db	61	DNDFLSRQAQDCYFMKLHHCPCGNHNSWDSTISGSQRAAFCDHKTTPC	SSAIINPLSTAGNS	120
QY	121	ERLQPGIAQWQTSKREDIVNOMTACLNQSLDALLSRDLINKEDYELVSTKPTRTSKVR		180

Db 121 ERLQPGIAQOIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVR 180

Qy 181 QLLDTTDDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 232

Db 181 QLLDTTDDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 232

RESULT 2

US-09-771-161A-184

; Sequence 184, Application US/09771161A

; Patent No. US2002011081A1

; GENERAL INFORMATION:

; APPLICANT: LEVINE, et al.

; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES

; FILE REFERENCE: 802620-2005.1

; CURRENT APPLICATION NUMBER: US/09/771,161A

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 09/724,676

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 136776

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 135619

; PRIOR FILING DATE: 2000-04-12

; NUMBER OF SEQ ID NOS: 273

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 184

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-771-161A-184

Query Match 98.0%; Score 1182; DB 9; Length 540;

Best Local Similarity 99.6%; Pred. No. 2.7e-108;

Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSSAIHLCDKXKMWLSLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 64

Db 313 KLOSVSSAIHLCDKXKMWLSLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 372

Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 124

Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQOIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184

Db 433 PGIAQOIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

Qy 185 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 232

Db 493 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 540

RESULT 3

US-09-862-027-28

; Sequence 28, Application US/09862027

; Patent No. US20020142428A1

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin R.

; TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof

; FILE REFERENCE: 35800/234862

; CURRENT APPLICATION NUMBER: US/09/862,027

; CURRENT FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: US 09/345,473

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-862-027-28

Query Match 98.0%; Score 1182; DB 9; Length 540;

Best Local Similarity 99.6%; Pred. No. 2.7e-108;

Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSSAIHLCDKXKMWLSLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 64

Db 313 KLOSVSSAIHLCDKXKMWLSLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 372

Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 124

Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQOIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184

Db 433 PGIAQOIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

Qy 185 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 232

Db 493 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 540

RESULT 4

US-09-981-397A-14

; Sequence 14, Application US/09981397A

; Publication No. US20030082519A1

; GENERAL INFORMATION:

; APPLICANT: Axxima Pharmaceuticals AG

; APPLICANT: Schubart, Daniel

; APPLICANT: Habenberger, Peter

; APPLICANT: Stein-Gerlach, Matthias

; APPLICANT: Bevec, Dorian

; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their

; FILE REFERENCE: AXM-004.1 US

; CURRENT APPLICATION NUMBER: US/09/981,397A

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: 60/240,750

; PRIOR FILING DATE: 2000-10-16

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-981-397A-14

Query Match 98.0%; Score 1182; DB 10; Length 540;

Best Local Similarity 99.6%; Pred. No. 2.7e-108;

Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSSAIHLCDKXKMWLSLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 64

Db 313 KLOSVSSAIHLCDKXKMWLSLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 372

Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 124

Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQOIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184

Db 433 PGIAQOIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

Qy 185 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 232

Db 493 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 540

RESULT 5

US-09-925-301-1015

; Sequence 1015, Application US/09925301

; Patent No. US20020052308A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106  
CURRENT APPLICATION NUMBER: US/09/925,301  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05882  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1694  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1015  
LENGTH: 544  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-301-1015

Query Match  
Best Local Similarity 98.0%; Score 1182; DB 9; Length 544;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 317 KLQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 376  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTPCSSLINPLSTAGNSERLQ 124  
DB 377 LSRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTPCSSLINPLSTAGNSERLQ 436  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 437 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 496  
QY 185 TTDIOGEFAKVIQKLDKDKMGLQPYPEILVWSRSPSLNLLQKSM 232  
DB 497 TTDIOGEFAKVIQKLDKDKMGLQPYPEILVWSRSPSLNLLQKSM 544

RESULT 6  
US-09-748-537-1  
Sequence 1, Application US/09748537  
Patent No. US20020061833A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
APPLICANT: Chao, Moses V.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
FILE REFERENCE: 07334-316001  
CURRENT APPLICATION NUMBER: US/09/748,537  
CURRENT FILING DATE: 2000-12-26  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-748-537-1

Query Match  
Best Local Similarity 97.5%; Score 1176; DB 9; Length 540;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 313 KLQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTPCSSLINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTPCSSLINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIOGEFAKVIQKLDKDKMGLQPYPEILVWSRSPSLNLLQKSM 232  
DB 493 TTDIOGEFAKVIQKLDKDKMGLQPYPEILVWSRSPSLNLLQKSM 540

RESULT 8  
US-10-133-780-1  
Sequence 1, Application US/10133780  
Publication No. US20020123115A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
DOMAIN POLYPEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIOGEFAKVIQKLDKDKMGLQPYPEILVWSRSPSLNLLQKSM 232  
Db 493 TTDIOGEFAKVIQKLDKDKMGLQPYPEILVWSRSPSLNLLQKSM 540

RESULT 7  
US-09-728-721-2  
Sequence 2, Application US/09728721  
Patent No. US20020061845A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
FILE REFERENCE: 07334-124001  
CURRENT APPLICATION NUMBER: US/09/728,721  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/340,620  
PRIOR FILING DATE: 1999-06-28  
PRIOR APPLICATION NUMBER: US 09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-728-721-2

Query Match  
Best Local Similarity 97.5%; Score 1176; DB 9; Length 540;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 313 KLQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTPCSSLINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTPCSSLINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIOGEFAKVIQKLDKDKMGLQPYPEILVWSRSPSLNLLQKSM 232  
DB 493 TTDIOGEFAKVIQKLDKDKMGLQPYPEILVWSRSPSLNLLQKSM 540

RESULT 8  
US-10-133-780-1  
Sequence 1, Application US/10133780  
Publication No. US20020123115A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
DOMAIN POLYPEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/133,780  
FILING DATE: 26-Apr-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/019,942  
FILING DATE: 06-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/068001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-133-780-1

Query Match 97.5%; Score 1176; DB 13; Length 540;  
Best Local Similarity 99.1%; Pred. No. 1.1e-107;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 5 QLOSVSIAHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db :|||||  
313 KLOSVSIAHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
  
Qy 65 LSRKAQDCYFMKLHPCGNHSDSTISGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 124  
Db :|||||  
373 LSRKAQDCYFMKLHPCGNHSDSTISGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 432  
  
Qy 125 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 184  
Db :|||||  
433 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 492  
  
Qy 185 TTIOGEEFAKVIQKLDKQKMGLOPYPEILVVSRSPLNLLQNKSM 232  
Db :|||||  
493 TTIOGEEFAKVIQKLDKQKMGLOPYPEILVVSRSPLNLLQNKSM 540

## RESULT 9

US-10-105-931-2  
; Sequence 2, Application US/10105931  
; Publication No. US20020150987A1  
; GENERAL INFORMATION:

; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/10/105,931  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-931-2

Query Match 97.5%; Score 1176; DB 13; Length 540;  
Best Local Similarity 99.1%; Pred. No. 1.1e-107;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QLOSVSIAHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db :|||||  
313 KLOSVSIAHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
  
Qy 65 LSRKAQDCYFMKLHPCGNHSDSTISGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 124  
Db :|||||  
373 LSRKAQDCYFMKLHPCGNHSDSTISGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 432  
  
Qy 125 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 184  
Db :|||||  
433 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 492  
  
Qy 185 TTIOGEEFAKVIQKLDKQKMGLOPYPEILVVSRSPLNLLQNKSM 232  
Db :|||||  
493 TTIOGEEFAKVIQKLDKQKMGLOPYPEILVVSRSPLNLLQNKSM 540

## RESULT 10

US-10-118-984-2  
; Sequence 2, Application US/10118984  
; Publication No. US20020197693A1  
; GENERAL INFORMATION:

; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/10/118,984  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-118-984-2

Query Match 97.5%; Score 1176; DB 13; Length 540;  
Best Local Similarity 99.1%; Pred. No. 1.1e-107;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QLOSVSIAHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db :|||||  
313 KLOSVSIAHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
  
Qy 65 LSRKAQDCYFMKLHPCGNHSDSTISGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 124  
Db :|||||  
373 LSRKAQDCYFMKLHPCGNHSDSTISGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 432  
  
Qy 125 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 184  
Db :|||||  
433 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 492  
  
Qy 185 TTIOGEEFAKVIQKLDKQKMGLOPYPEILVVSRSPLNLLQNKSM 232  
Db :|||||  
493 TTIOGEEFAKVIQKLDKQKMGLOPYPEILVVSRSPLNLLQNKSM 540

## RESULT 11

US-10-295-981-2  
; Sequence 2, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:

; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001

```

; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-2

Query Match      97.5%; Score 1176; DB 14; Length 540;
Best Local Similarity 99.1%; Pred. No. 1.1e-107;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64
DB 313 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 372
QY 65 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQ 124
DB 373 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQ 432
QY 125 PGIAQWQISQKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
DB 433 PGIAQWQISQKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTDIQGEPAKVIQKLDKQKMGLOPYEILVWSRSPSLNLQKSM 232
DB 493 TTDIQGEPAKVIQKLDKQKMGLOPYEILVWSRSPSLNLQKSM 540

RESULT 12
US-09-728-721-5
; Sequence 5, Application US/09/728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-5

Query Match      52.4%; Score 632; DB 9; Length 131;
Best Local Similarity 98.3%; Pred. No. 1.3e-54;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64
; :|||||

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DB 13 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 72
QY 65 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERL 123
; :|||||
DB 73 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERL 131

RESULT 13
US-10-105-931-5
; Sequence 5, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-5

Query Match      52.4%; Score 632; DB 13; Length 131;
Best Local Similarity 98.3%; Pred. No. 1.3e-54;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64
; :|||||
DB 13 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 72
QY 65 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERL 123
; :|||||
DB 73 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERL 131

RESULT 14
US-10-118-984-5
; Sequence 5, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-5

Query Match      52.4%; Score 632; DB 13; Length 131;
Best Local Similarity 98.3%; Pred. No. 1.3e-54;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 5 QLOSVSSAIHLCDKKKMWLSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQDNDF 64  
:|||||  
Db 13 KLOSVSSAIHLCDKKKMWLSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQDNDF 72  
:|||||  
Qy 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERL 123  
:|||||  
Db 73 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERL 131  
:|||||

## RESULT 15

US-10-295-981-5  
; Sequence 5, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/10/295,981  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-981-5

Query Match 52.4%; Score 632; DB 14; Length 131;  
Best Local Similarity 98.3%; Pred. No. 1.3e-54;  
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QLOSVSSAIHLCDKKKMWLSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQDNDF 64  
:|||||  
Db 13 KLOSVSSAIHLCDKKKMWLSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQDNDF 72  
:|||||  
Qy 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERL 123  
:|||||  
Db 73 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERL 131  
:|||||

Search completed: March 29, 2004, 14:11:39  
Job time : 43 secs



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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:06:05 ; Search time 20 Seconds  
(without alignments)  
1115.822 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLQVSSSAIHLCDKKK.....PEILVSRSPSLNLLQNSM 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	8.3	943	2 S44636	f22b7.5 protein -
2	98	8.1	830	2 T00029	Miranda protein -
3	93	7.7	692	2 T32980	hypothetical prote
4	92.5	7.7	618	2 S68450	apoptosis inhibito
5	90	7.5	2288	2 T29999	hypothetical prote
6	89	7.4	242	2 S71757	MADS box protein D
7	89	7.4	1360	2 T33922	hypothetical prote
8	89	7.4	1944	2 A55117	tsg24 protein - mo
9	88	7.3	283	2 B81996	RNA polymerase sig
10	88	7.3	524	2 S35551	transcription fact
11	88	7.3	1135	2 T30561	Scythe protein - A
12	88	7.3	2368	2 S46005	ESR1 protein - yea
13	87.5	7.3	340	2 T27389	hypothetical prote
14	87	7.2	147	2 F84869	hypothetical prote
15	87	7.2	1205	2 T41987	hypothetical prote
16	86.5	7.2	407	2 S27774	transforming prote
17	86.5	7.2	528	2 T52092	DNA-binding protei
18	86.5	7.2	1203	2 T17415	mycelial surface a
19	85.5	7.1	212	2 G75458	conserved hypothet
20	85.5	7.1	455	1 JC4338	tryptophan dimethy
21	85.5	7.1	1758	2 T30560	resistance protein
22	85	7.0	690	2 A24545	triacylglycerol li
23	85	7.0	3898	1 GNMVHC	genome polyprotein
24	84.5	7.0	224	2 S23728	MADS box protein T
25	84.5	7.0	810	2 S69652	hypothetical prote
26	84	7.0	691	2 B89797	glycerol ester hyd
27	83.5	6.9	201	2 S66712	hypothetical prote
28	83.5	6.9	486	2 I55449	gene P22A protein
29	83.5	6.9	956	2 T40953	hypothetical prote

30	83	6.9	576	2 S59829	hypothetical prote
31	83	6.9	853	2 S58375	aryl hydrocarbon r
32	83	6.9	1544	2 T29482	hypothetical prote
33	82.5	6.8	591	2 T25636	hypothetical prote
34	82.5	6.8	1129	2 T25635	hypothetical prote
35	82.5	6.8	1175	2 T25634	hypothetical prote
36	82	6.8	383	2 A56084	interleukin-lbeta
37	82	6.8	427	2 S53021	G-box-binding prot
38	82	6.8	622	2 S45129	VPS27 protein - ye
39	82	6.8	721	2 S31824	gene Mx protein -
40	82	6.8	884	2 T40690	hypothetical prote
41	81.5	6.8	243	2 S71756	MADS box protein D
42	81.5	6.8	489	2 S50548	hypothetical prote
43	81.5	6.8	651	2 D72042	conserved hypothet
44	81.5	6.8	651	2 E86581	CHLPN 76 kDa homol
45	81.5	6.8	715	2 I40729	hypothetical 76k p

ALIGNMENTS

RESULT 1  
S44636  
f22b7.5 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Dec-1997  
C:Accession: S44636  
R:Anderson, K.  
submitted to the EMBL Data Library, March 1993  
A:Description: Sequence of the C. elegans cosmid F22B7.  
A:Reference number: S44628  
A:Accession: S44636  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-943 <AND>  
A:Cross-references: EMBL:U12018; NID:G156298; PID:G156307  
C:Genetics:  
A:Introns: 83/2; 250/2; 453/1; 484/2; 519/1; 553/3; 580/3; 632/3; 729/3; 830/2; 905/1  
A:Superfamily: dnaJ amino-terminal homology  
F:531-595/Domain: dnaJ amino-terminal homology <DNJ>

Query Match	8.3%;	Score 100.5;	DB 2;	Length 943;
Best Local Similarity	19.4%;	Pred. No. 2;		
Matches	45;	Conservative 44;	Mismatches 84;	Indels 59; Gaps 10;
QY	25	LNIPVNHGPOESCGSSQLHENSIGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHCPGNH	84	
Db	349	IDVANNQERSETATQDVCLATDSSPDPTSS-----NDMINK-----FWVELEHATNVE	397	
QY	85	SWDSTISG-----SQRAAFCDHKTPCSSLII--NPLS	115	
Db	398	TWEMIVNGIIDDQKKPVAIEKKENEPEVDMMDLIFSMSSRMDQRTFLPAARFIPRPVS	457	
QY	116	TAG-----NSERLQPGIAQMIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVST	171	
Db	458	SASKTKTSHRILPGLRANWTQVMKVLGMFV---LNRS-SGLIHRSPVLLAQ---VST	510	
QY	172	KPTRTSKVRQLLDTDDIOGEFEPAKVI-VOKLKDNK-----QMGLOPYEPI	215	
Db	511	PTSTTKLAQLHTHALSKEDYKTLGVDDKSDAKAKAYQLAKKYPHDV	562	

RESULT 2  
T00029  
Miranda protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 17-Nov-2000  
C:Accession: T00029  
R:Ikeshima-Kataoka, H.; Skeath, J.B.; Nabeshima, Y.; Doe, C.Q.; Matsuzaki, F.  
Nature 390, 625-629, 1997  
A:Title: Miranda directs Prospero to a daughter cell during Drosophila asymmetric division  
A:Reference number: Z14067; MUID:98065952; PMID:9403694  
A:Accession: T00029

A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A;Residues: 1-830 <IKE>  
A;Cross-references: EMBL:AB005661; NID:g2749776; PIDN:BAA24111.1; PID:g2749777  
A;Experimental source: strain Canton-S  
C;Genetics:  
A;Cross-references: FlyBase:FBgn0021776  
A;Map position: 92B-C

Query Match 8.1%; Score 98; DB 2; Length 830;  
Best Local Similarity 21.3%; Pred. No. 2.7;  
Matches 44; Conservative 39; Mismatches 78; Indels 46; Gaps 8;

Qy 12 AIHLCDKKKMSLNIPVNHGPOEESGSSQLHENSGETSRLPAPQDNDFLSRAQD 71  
Db 64 AVRFASSSKEAKFAIP-----KEDKSKGLRFTPLPQLRFRPPPSHTDTATSG-- 117  
Qy 72 CYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSAIIINPLSTAGNSERLQFGIAQW 131  
Db 118 -----SGASTAA-----STPLHSAATTPVKEAKSASRLKGEALQY 153  
Qy 132 -IQSKREDIVNQWTEA-CLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQ 189  
Db 154 EIRKHNELIESQLSDVLRHVDQLKEAKLREHELATSK---TDRLIEALTSENLS 210  
Qy 190 GEEPAKVIQKLNKDKMKGLOPYEIL 216  
Db 211 HKAL-----NEQMG-QEHADLL 226

RESULT 3  
T32980  
hypothetical protein T21D12.7 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
A;Accession: T32980  
R;Du, Z.; Maggi, L.  
A;Description: The sequence of C. elegans cosmid K02D7.  
A;Reference number: 221259  
A;Accession: T32980  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A;Residues: 1-692 <DUZ>  
A;Cross-references: EMBL:AF045645; PIDN:AAC02606.1; GSPDB:GN00022; CESP:T21D12.7  
A;Experimental source: strain Bristol N2; clone K02D7  
C;Genetics:  
A;Gene: CESP:T21D12.7  
A;Map position: 4  
A;Introns: 29/1; 89/1; 127/1; 186/1; 233/1; 291/1; 379/3; 586/3; 611/3; 643/3

Query Match 7.7%; Score 93; DB 2; Length 692;  
Best Local Similarity 18.6%; Pred. No. 5.8;  
Matches 48; Conservative 35; Mismatches 67; Indels 108; Gaps 11;

Qy 8 SVSSAHLHC-----DKKKMELSLNIPVNHGPOEESGSSQLHENSGETS 53  
Db 427 SFGAARHLCKPKKCKVYVDPDKR-----PIRCFPGDQSC-----PIST 468  
Qy 54 RSLPAPQDNDFLSR--KAQDCYFMKLH-----HC 80  
Db 469 DCLPALENSESFLNTAIDVFFCCHTVTSIFSCPDGASPLDPNSGQPATCLASNPFS 528  
Qy 81 PGNHSDSTISGSQRAAFCDHKTTPCSAII-----NPLSTAGNSERLQPG 126  
Db 529 PAEHCCTALMDGS--TACCPQTPLCVLVEALVSDGSPKTCGLWDNNTCPQKCKQKAMDG 586  
Qy 127 IAQWIOQSKREDIVNQWTEA-CLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTT 186  
Db 587 ILQK-----MHHSISVILA--LVISISHALLTSDPSNFA-IRQFPRPM 626  
Qy 187 DIQGE-----EFAKVI 197

Db 627 SMSSECNTPDEAHFCKTI 644

RESULT 4  
S68450  
apoptosis inhibitor hiap-2 - human  
C;Species: Homo sapiens (man)  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000  
A;Accession: S68450  
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996  
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP A;Reference number: A58182; MUID:96149249; PMID:8552191  
A;Accession: S68450  
A;Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A;Residues: 1-618 <LIS>  
A;Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318  
C;Function:  
A;Description: apoptotic suppressor  
C;Superfamily: RING finger homology  
C;Keywords: apoptosis; zinc finger  
F;567-611/Domain: RING finger homology <RNG>

Query Match 7.7%; Score 92.5; DB 2; Length 618;  
Best Local Similarity 24.5%; Pred. No. 5.5;  
Matches 27; Conservative 24; Mismatches 46; Indels 13; Gaps 2;

Qy 132 IQSKREDIVNQWTEACLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIOGE 191  
Db 461 IRKRMALFQOLT--CVLPILDNLLKANVINQEHDIIKQTKIPLQARELIDTIWVKN 518  
Qy 192 EFAKVIQKLNK-----NKQMGLOPYEILVSVSRSPSLNLLQNK 230  
Db 519 AAANIFKNCLEKEDSTLYKNLFDVKMKVPTEDVSGLSLEQLRRLQEE 568

RESULT 5  
T29999  
hypothetical protein ZC8.4 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
A;Accession: T29999  
R;Latreille, P.; Bradshaw, H.  
submitted to the EMBL Data Library, July 1996  
A;Description: The sequence of C. elegans cosmid ZC8.  
A;Reference number: Z20719  
A;Accession: T29999  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A;Residues: 1-2288 <LAT>  
A;Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CESP:ZC8.4  
A;Experimental source: strain Bristol N2; clone ZC8  
C;Genetics:  
A;Gene: CESP:ZC8.4  
A;Map position: X  
A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/1

Query Match 7.5%; Score 90; DB 2; Length 2288;  
Best Local Similarity 20.8%; Pred. No. 53;  
Matches 47; Conservative 40; Mismatches 85; Indels 54; Gaps 10;

Qy 5 QLOSVSSAHLCDKKKMSLN-----IPVNHGPOEESGSSQLHENSGETS 49  
Db 712 ELEHAQKAAHLAEQQLKEIKIQRDDYQKQDEHARHLFDIRHKLKLEIKRQDLEKNGA- 770  
Qy 50 PETERSLPAPQDNDFLSRAQ-----DCVFMKLHHCPCGNHSDSTISGSQRAAFCDHK 102  
Db 771 -----RNDELKRLQTTSDYESQINLRRH-----NDELDTTIKGHQ-----GK 810  
Qy 103 TTPCSSAIINPLSTAGNSERLQFGIAQWIOQSKREDIVNQWTEACLNOSLDALLSRDLIM 162  
Db 811 ITHLENEL---HSRSGBIEKIND--LNQRLQKQKQDILNQKLNK--LDGDVQAL--KETIR 861

QY 163 KEDYELVSTKPTRTSKVRLQDLTDIOGEFF-AKVIVQKLKDKNQ 206  
 Db 862 KLENELEKLRNENKELVGKEARDAANQQLSRANLNKLELEDITQ 907

RESULT 6  
 S71757  
 MADS box protein DBFH200 - garden snapdragon  
 C:Species: Antirrhinum majus (garden snapdragon)  
 C>Date: 11-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 20-Jun-2000  
 C:Accession: S71757  
 R:Davies, B.; Egea-Cortines, M.; de Andrade Silva, E.; Saedler, H.; Sommer, H.  
 EMO J. 15, 4330-4343, 1996  
 A:Title: Multiple interactions amongst floral homeotic MADS box proteins.  
 A:Reference number: S71756; MUID:97015133; PMID:8861961  
 A:Accession: S71757  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-242 <DAV>  
 A:Cross-references: EMBL:X95469; NID:g1239958; PIDN:CAA64743.1; PID:g1239959  
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homolog  
 C:Keywords: DNA binding; transcription regulation  
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>  
 F:94-159/Domain: domain K <KOO>

Query Match 7.4%; Score 89; DB 2; Length 242;  
 Best Local Similarity 21.1%; Pred. No. 3.1;  
 Matches 48; Conservative 30; Mismatches 65; Indels 84; Gaps 7;

QY 15 LCDKKKMLSLNIPVNHGQESCGSSQLHE-----NSGSPETSRSLPAPQDNDFLS 66  
 Db 38 LCD---AEVALIIFSNGKLYEFCSTSMNLTRYQKCYGPPETNVS----- 83

QY 67 RKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAINPLSTAGNSERLQPG 126  
 Db 84 -----TRALELS 91

QY 127 IAQOWIQSK-REDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLQDLTD 185  
 Db 92 SQOYLKUKARYEALQORSQNLGDLGPLNSKELESLESLQKLSRTRTQAMLDIT 151

QY 186 -TDIOGEFFA-----KVIVQKLKDKNQGLQYPY---EILVVSRS 223  
 Db 152 LTDLQKHEALNEARSLKRLMDGQISLQWNPNAEDHVGYGROPS 198

RESULT 7  
 T33922  
 Hypothetical protein Y8A9A.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T33922  
 R:Courtney, L.; Langston, Y.; Drone, K.; Mead, K.  
 submitted to the EMBL Data Library, February 1999  
 A:Description: The sequence of C. elegans cosmid Y8A9A.  
 A:Reference number: Z21439  
 A:Accession: T33922  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1360 <COU>  
 A:Cross-references: EMBL:AF125461; PIDN:AAD12852.1; GSPDB:GN00020; CESP:Y8A9A.2  
 A:Experimental source: strain Bristol N2; clone Y8A9A  
 C:Genetics:  
 A:Gene: CESP:Y8A9A.2  
 A:Map position: 2  
 A:Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3; 848/2; 944/2; 1044/2; 1

Query Match 7.4%; Score 89; DB 2; Length 1360;  
 Best Local Similarity 20.5%; Pred. No. 32;  
 Matches 39; Conservative 25; Mismatches 68; Indels 58; Gaps 7;

QY 8 SVSSAIHLCDKKKMLSLNIPVNHGQESCGSSQLHEN-----SGSPETSRSLPAPQD 61

Db 972 TVSGTQHICGPOP-----NYTTPYAPYDPTDNCPCPETGIWSWDSTPNQCRDYCGSGG 1026  
 QY 62 NDFLSRKAQD-----CYFMKLHCPGNHSDSTISGSQRAAFCD 100  
 Db 1027 NQTRTRCTSDADGCPGCGPTTITEPCGTGVCYFRLSCPG---YTATVEGNQ----- 1077

QY 101 HKTTPCSSAIINP--LSTAGNSERLQPGIAQOWIQ-----SKREDIVNQ 143  
 Db 1078 HICGLTAVADPKLNTCGVSCCPSAGIENGWVSVCNDCGSCGQGTETRRKRLSLQY 1137

QY 144 TEACLNQSLD 153  
 Db 1138 GCACGTGNATD 1147

RESULT 8  
 A55117  
 tsq24 protein - mouse  
 N:Alternate names: bime protein homolog  
 C:Species: Mus musculus (house mouse)  
 C>Date: 28-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 17-Mar-2000  
 C:Accession: A55117  
 R:Starborg, M.; Brundell, E.; Gell, K.; Hoeoeg, C.  
 J. Biol. Chem. 269, 24133-24137, 1994  
 A:Title: A novel murine gene encoding a 216-kDa protein is related to a mitotic checkpoint  
 A:Reference number: A55117; MUID:95014147; PMID:7929068  
 A:Accession: A55117  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1944 <STA>  
 A:Cross-references: GB:X80169; NID:g562764; PIDN:CAA56450.1; PID:g642252  
 C:Genetics:  
 A:Gene: tsq24  
 C:Superfamily: bime protein

Query Match 7.4%; Score 89; DB 2; Length 1944;  
 Best Local Similarity 25.4%; Pred. No. 52;  
 Matches 52; Conservative 25; Mismatches 72; Indels 56; Gaps 10;

QY 3 SILOQSVSSAI--HLCDKKKMLSLNIPVNH---GPOEESCGSSQLHNSGSPETSRSL 56  
 Db 291 TLQWATSSSLTAHLRLSLKESPVASFPQNVSSHTSQRSTSSPSLHRS----- 341

QY 57 PAPQDNDFLSRKAQDCYFMKLHCP--GNHSDSTISGSQRAAFCDHKTTPCSSAINPL 114  
 Db 342 PSISNMGVLSRA-----HSPALGVHSP---SGAQRFNLSHSSQPKRHSHSP 387

QY 115 STAGNSERLQPGIAQOWIQSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPT 174  
 Db 388 SGSFNDSFLAP-----ETEPV---PELCI-----DHLMTETLPNIREKNS 425

QY 175 RTSKVRLQDLTDIOGEFFAKVIVQ 199  
 Db 426 QASKV---FITDLCGQKFLCLVE 447

RESULT 9  
 B81996  
 RNA polymerase sigma factor NMA0049 [imported] - Neisseria meningitidis (strain Z2491 ser  
 C:Species: Neisseria meningitidis  
 C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C:Accession: B81996  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A:Reference number: B81995; MUID:20222556; PMID:10761919  
 A:Accession: B81996  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-283 <PAR>  
 A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83366.1; PID:g7378824

A;Experimental source: serogroup A, strain Z2491  
 C;Genetics:  
 A;Gene: NMA0049

Query Match 7.3%; Score 88; DB 2; Length 283;  
 Best Local Similarity 23.2%; Pred. No. 4.6;  
 Matches 52; Conservative 27; Mismatches 85; Indels 60; Gaps 9;

QY 61 DNDPLSRKAD-----CYFMKLHCPGNHSD--STISGSQ-----RAAFCDHKT 104  
 DB 42 DNPLLERKOTDESDAEFSHTYTPAQIIGDGEDMLSNITAGSQDFKQYLHAQVCEHPLS 101  
 QY 105 PCSAIIINPLSTAGNSERLOFGIAQWIOQSKREDIVN-----QMTACINQSLDAL--- 155  
 DB 102 DQESACVHILIDFLDE-----QGYLTDSIEDLHTPLEWMLDEAMLKQALTALKKF 153  
 QY 156 -----LSRDLIMK-EYELVSTKPTRTSKVRQLLDTTDIOGEEFAKIVVQKLKDNK 205  
 DB 154 DPAGVAADLNESLILQIERSGECAKPSALHIVRNALDSIDGNRSQTLARIKKRLPQTD 213  
 QY 206 Q-----MGLQPYPEILVVSRS-----LNLLQKSM 232  
 DB 214 SGTLEAALDLIASLNPFPVAFASSTPYSDALANLAFRGM 257

RESULT 10  
 S35551  
 transcriptions factor IIF chain RAP74 - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 09-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jul-2000  
 C;Accession: S35551  
 R;Gong, D.W.; Hasegawa, S.; Wada, K.; Roeder, R.G.; Nakatani, Y.; Horikoshi, M.  
 Nucleic Acids Res. 20, 6736, 1992  
 A;Title: Elucidation of three putative structural subdomains by comparison of primary structure  
 A;Reference number: S35551; MUID: 93126122; PMID:1480494  
 A;Accession: S35551  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 1-524 <GON>  
 A;Cross-references: EMBL:Z17426; NID:G65029; PIDN:CAA78999.1; PID:G65030  
 C;Genetics:  
 A;Gene: RAP74  
 C;Keywords: DNA binding; transcription regulation

Query Match 7.3%; Score 88; DB 2; Length 524;  
 Best Local Similarity 23.9%; Pred. No. 11;  
 Matches 54; Conservative 22; Mismatches 90; Indels 60; Gaps 9;

QY 27 IPVNHGQESCGSSQLHNSGSPETS-----RSLPAPQDNDFLSRKAQDCY 73  
 DB 290 LPGKIRPAKEEGPKGLDEQSSERSEERKAEKEEKEKAPTPQDNK--KKKKGD-- 345  
 QY 74 FMKLHCPGNHSDSTISGQRAAFCDHKTTP-----CSAIIIN-----PLSTAGN 119  
 DB 346 -----SDSESTSDSDIDGASSLFLMOKKTPPKKKKGGNSSSRSGNSRPGTPSDTGN 401  
 QY 120 SERLOFGIAQWIOQSKREDIVNQTACLNQSLDA-----LLSRDL 160  
 DB 402 TSSTLRAAASKLQSKRGKTSVN--TPAAKLKWEAGPQNTSGKSTPQPSGKSTPSSGDI 459  
 QY 161 IMKED--YELVSTKPTRTSKVRQLLDT--TDIOGEEFAKIVVQKLK 202  
 DB 460 QLTEEAARRYLTRKPMPTKDLLKKFQPKTKGLSSEQTVNVLQILK 505

RESULT 11  
 T30561  
 Scythe protein - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 11-May-2000  
 C;Accession: T30561  
 R;Thress, K.; Henzel, W.; Shillinglaw, W.; Kornbluth, S.  
 EMBO J. 17, 6135-6143, 1998

A;Title: Scythe: a novel reaper-binding apoptotic regulator.  
 A;Reference number: Z20860; MUID:99016035; PMID:9799223  
 A;Accession: T30561  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-1135 <THR>  
 A;Cross-references: EMBL:AF098511; NID:G3983138; PID:G3983139; PIDN:AAAC83822.1  
 C;Function:  
 A;Description: is a apoptotic regulator that is an essential component in the pathway of  
 C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match 7.3%; Score 88; DB 2; Length 1135;  
 Best Local Similarity 23.1%; Pred. No. 31;  
 Matches 30; Conservative 26; Mismatches 40; Indels 34; Gaps 5;

QY 112 NPLSTAGNSERLOFGIAQWIOQSKREDIVN-----MTEACL----- 148  
 DB 1002 HPTQEDGSGEQAASVPPEVPVIRQDMQNKIKQOPPLSDAYLSGMPAKRRTWQGE 1061  
 QY 149 -NOSLDALLSRDLIMKEDYELVSTKPTRTSK-VRLQLLDTTDIOG---EEFAKIVVQKLK 203  
 DB 1062 PHLSLSEAVSRAM-----KATCAKPSSAECVRELDNSEAGRYREQLCQDIQKTLQD 1115  
 QY 204 NKQMLQPYP 213  
 DB 1116 NESYSQRP 1125

RESULT 12  
 S46005  
 ESr1 protein - yeast (Saccharomyces cerevisiae)  
 N;Alternate names: MEC1 protein; protein YBR1012; protein YBR136W  
 C;Species: Saccharomyces cerevisiae  
 C;Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 29-Oct-1999  
 C;Accession: S46005; S46578; S46663; S47954; S64650  
 R;Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.  
 submitted to the Protein Sequence Database, August 1994  
 A;Reference number: S45995  
 A;Accession: S46005  
 A;Molecule type: DNA  
 A;Residues: 1-2368 <BE2>  
 A;Cross-references: EMBL:Z36005; NID:G536429; PIDN:CAA85094.1; PID:G536430; MIPS:YBR136W  
 A;Experimental source: strain S288C  
 R;Becam, A.M.; Cullin, C.; Grzybowski, E.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos,  
 Yeast 10(Suppl.A), S1-S11, 1994  
 A;Title: The sequence of 29.7kb from the right arm of chromosome II reveals 13 complete  
 A;Reference number: S46569; MUID:94378717; PMID:8091856  
 A;Accession: S46578  
 A;Molecule type: DNA  
 A;Residues: 1-2368 <BE2>  
 A;Cross-references: EMBL:X75891; NID:G496856; PIDN:CAA53494.1; PID:G496866  
 A;Experimental source: strain S288C  
 R;Kato, R.; Ogawa, H.  
 submitted to the EMBL Data Library, May 1992  
 A;Description: An essential gene, ESr1, is required for mitotic cell growth, DNA repair  
 A;Reference number: S46662  
 A;Accession: S46663  
 A;Molecule type: DNA  
 A;Residues: 1-196, 'D', 198-2368 <KAT>  
 A;Cross-references: EMBL:D11088; NID:G506874; PIDN:BAA01860.1; PID:dl002337; PID:G506876  
 R;Kato, R.; Ogawa, H.  
 Nucleic Acids Res. 22, 3104-3112, 1994  
 A;Title: An essential gene, ESr1, is required for mitotic cell growth, DNA repair and meiosis  
 A;Reference number: S47953; MUID:94344772; PMID:8065923  
 A;Accession: S47954  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 195-196, 'D', 198-322; 671-744; 848-1796; 1803-2003; 2004-2368 <KAT>  
 A;Cross-references: EMBL:D11088  
 R;Weinert, T.A.; Harlow, D.  
 submitted to the EMBL Data Library, July 1995  
 A;Reference number: S64650  
 A;Accession: S64650

A:Molecule type: DNA  
A:Residues: 1-715, P, 717-1254, Q, 1256-1275, G, 1277-2368 <WEI>  
A:Cross-references: EMBL:U31109; NID:9950172; PIDN:AAA74482.1; PID:G950173  
C:Genetics:  
A:Gene: SGD:BSR1; MEC1  
A:Cross-references: SGD:S0000340; MIPS:YBR136W  
A:Map position: 2R  
C:Function:  
A:Description: required for mitotic cell growth, DNA repair, and meiotic recombination  
A:Keywords: ATP; P-loop; purine nucleotide binding; transmembrane protein  
F:74-90/Domain: transmembrane #status predicted <TM1>  
F:218-234/Domain: transmembrane #status predicted <TM2>  
F:771-787/Domain: transmembrane #status predicted <TM3>  
F:922-938/Domain: transmembrane #status predicted <TM4>  
F:1152-1169/Domain: transmembrane #status predicted <TM5>  
F:1288-1304/Domain: transmembrane #status predicted <TM6>  
F:1315-1331/Domain: transmembrane #status predicted <TM7>  
F:1682-1689/Region: nucleotide-binding motif A (P-loop)  
F:1918-1934/Domain: nucleotide-binding motif A (P-loop)  
F:2126-2142/Domain: transmembrane #status predicted <TM8>  
F:2126-2142/Domain: transmembrane #status predicted <TM9>  
F:1688/Binding site: ATP/GTP (Lys) #status predicted

Query Match 7.3%; Score 88; DB 2; Length 2368;  
Best Local Similarity 22.3%; Pred. No. 83;  
Matches 56; Conservative 38; Mismatches 105; Indels 52; Gaps 11;

QY 14 HLCDDKKK-----MELSLNIPVNHGPOEESGSGSQ-----LHNSGSPETSRSLPAPQDNDF 64  
DB 491 HLCDEIKTGNPFVRINPNRP-----EAAGKSEIFRILHSN-----FLSHPNIDEF 535  
QY 65 LSKKAQDCYFMKLHH-----CPGNHSDSTISGQRAAFCDHKTTPCSSALINPL 114  
DB 536 -SESLSGLFSLHRIFFSHFQPKLTGNGQINKSPKLVQKCPMNSRYRLRLSTRILPL 594  
QY 115 ---STAGNERLQPGIAQOWIOSKRDIV-----NOMTEACLNOSLDALLSR--DLI 161  
DB 595 FNISDSHNSDEHTALIFELQSQKLPVVKENLVIAWTQTLTSDNDVFTLLKLIDIF 654  
QY 162 MKEDYELVSTKPTRTSKVRQLDITDIQ-GEFPAKIVIVQKLKDN---KOMGLQPYPEILAV 217  
DB 655 NSDDYSLRIMMTLQIKNAKILKTPYQLLSPLPVLRLQGLKLVVERKVGQNLIELAG 714  
QY 218 VSRSPSLNLLQ 228  
DB 715 YSSKTILDIFQ 725

RESULT 13  
T27389  
hypothetical protein Y75B8A.29 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T27389  
R.Barlow, K.  
submitted to the EMBL Data Library, November 1998  
A:Reference number: Z20361  
A:Accession: T27389  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-340 <WIL>  
A:Cross-references: EMBL:AL033514; NID:61343251; PIDN:CAA22089.1; CESP:Y75B8A.29  
A:Experimental source: clone Y75B8A  
C:Genetics:  
A:Gene: CESP:Y75B8A.29  
A:Introns: 116/3; 216/3; 267/3

Query Match 7.3%; Score 87.5; DB 2; Length 340;  
Best Local Similarity 23.3%; Pred. No. 6.6;  
Matches 37; Conservative 34; Mismatches 63; Indels 25; Gaps 6;

QY 75 MKLHCPGNHSDSTISGQRAAFCDHKTTPCSSALINPLSTAGNSERLQPGIAQOWIOS 134  
DB 26 VKLEH---ESSDNNESSGSGNFVF-----NFLMSQLQNMG-----PVEIKQVEA 67

A:Molecule type: DNA  
A:Residues: 135 KR-EDIVNOMTEACLNQSLDAL-LSRDLIMKEDYELVSTKPTRTSKVRQLDITDIQGESE 192  
DB 68 KWLDDIEDYTDNNYNEGYSKMDTDGDLWEFEFKLANPKSPKMDKREQERHRQMAKNRE 127  
QY 193 FAKVIVQKLKDNKOMGLQPYPEILVSRSPSLNLLQNK 231  
DB 128 YARKCVQKKDQRK-----HAIIRNQIKRKRIQLLNKKT 161

RESULT 14  
F84869  
hypothetical protein At2g43720 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: F84869  
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: F84869  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-147 <STO>  
A:Cross-references: GB:AE002093; NID:G2281098; PIDN:AAB64034.1; GSPDB:GNO0139  
C:Genetics:  
A:Gene: At2g43720  
A:Map position: 2

Query Match 7.2%; Score 87; DB 2; Length 147;  
Best Local Similarity 24.2%; Pred. No. 2.3;  
Matches 37; Conservative 25; Mismatches 43; Indels 48; Gaps 8;

QY 53 SRSLPAPQDNFLSRKAQDCYFMKLHCPGNHSDSTISGQRAAFCDHKTTPCSSALIN 112  
DB 25 SOSLSLSPV-QDHINFITLOKAYFKAYEC-----FQRTTHAE-----ISRCAESCSV 70  
QY 113 PLSTAGN-----SERLOPG-----IAQOWIOSKREDIVNOMTEACLNQSLDA 154  
DB 71 PITNAQNVFDNEMSVFQERLNLVVCQDKFEVAQK-QKTRSEAVNDL-EHCVNQTVD- 126  
QY 155 LLSRDLIMKEDYELVSTKPTRTSKVRQLDITTD 187  
DB 127 -----EAVKTLPLNLVSRMKKALSITD 147

RESULT 15  
T41987  
hypothetical protein U86 - human herpesvirus 7 (strain JI)  
C:Species: human herpesvirus 7  
A:Variety: Strain JI  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T41987  
R.Nicholas, J.  
submitted to the EMBL Data Library, December 1995  
A:Description: Determination and analysis of the complete nucleotide sequence of human he  
A:Reference number: Z22022  
A:Accession: T41987  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1205 <NIC>  
A:Cross-references: EMBL:U43400; PIDN:AAC54747.1  
A:Experimental source: strain JI  
C:Genetics:  
A:Note: U86

Query Match 7.2%; Score 87; DB 2; Length 1205;  
Best Local Similarity 22.6%; Pred. No. 41;  
Matches 52; Conservative 34; Mismatches 98; Indels 46; Gaps 10;

QY 8 SVSSAIHLCDKKKMELSLN-----IPVNHGPOEESGSGS--QLHNSGSPETSRSLPAP 59

Db	833	SKSRTCKVCNNKQDSQSETQCKHLISIRSNSEHSISESTYQSCKNKNS-ETLRSRRS	891
Qy	60	QDNDFLSRKAQDCYFMKLLHPCGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGN	119
Db	892	SESDCKKRSRSC-----SNHSWS--GSTQSKRVDDIDFTGAKSIPN-----	933
Qy	120	SERLQPGIAQOWIQSKREDIVNQWTE-----ACLNQSLDALLSRDLIMKED	165
Db	934	-EYEQKSTNKPFFKNERNARKRFSDDSDSSMQLFYKKRISGTQKSDSELSDNDLSYREY	992
Qy	166	YELVSTKPTTSKV-ROLLDTDIQGEERPAKVIQKLNKQMGLOPYPE	214
Db	993	VKLQEQKQSAKFKVQGRVPTKDFE-KLFRKTI--RAFYKQIPKPFPE	1039

Search completed: March 29, 2004, 14:10:09  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:02:15 ; Search time 18 Seconds  
(without alignments)  
671.126 Million cell updates/sec

Title: US-09-771-161a-93

Perfect score: 1206

Sequence: 1 MYSLQLQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNSKM 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1182	98.0	540	1 RIK2 HUMAN	O43353 h receptor-
2	839.5	69.6	539	1 RIK2_MOUSE	P58801 mus musculus
3	122.5	10.2	953	1 CAR4_HUMAN	Q9Y239 homo sapien
4	100.5	8.3	943	1 YLM5_CAEEL	P34408 caenorhabdi
5	96.5	8.0	953	1 CAR4_MOUSE	Q8bbh0 mus musculus
6	92.5	7.7	618	1 BIR2_HUMAN	Q13490 homo sapien
7	90	7.5	357	1 REPI_ZYGBA	P13776 zygosacchar
8	89	7.4	1944	1 ANCI_MOUSE	P53995 mus musculus
9	88	7.3	524	1 T2FA_XENLA	Q04870 xenopus lae
10	88	7.3	2368	1 ESRI_YEAST	P38111 saccharomyc
11	86.5	7.2	365	1 SYAP_MOUSE	Q9d5v6 mus musculus
12	86.5	7.2	407	1 MYC_ASTVU	Q17103 asterias vu
13	86.5	7.2	612	1 BIR2_MOUSE	Q62210 mus musculus
14	86.5	7.2	1088	1 MRTE_HUMAN	Q9uhh7 homo sapien
15	85	7.0	627	1 ABPX_YEAST	Q08641 saccharomyc
16	85	7.0	690	1 LIP_STAAR	P10335 staphylococ
17	85	7.0	3898	1 POLG_HCVA	P19712 hog cholera
18	84.5	7.0	224	1 AGL9_LYCES	Q42464 lycopersico
19	84.5	7.0	733	1 ACE1_TIRE	Q9p8w3 trichoderma
20	84	7.0	690	1 LIP_STAAR	Q8nyc2 staphylococ
21	83.5	6.9	486	1 ZASA_HUMAN	Q15172 h serine/th
22	83.5	6.9	805	1 HIFA_XENLA	Q9i8a9 xenopus lae
23	83.5	6.9	2567	1 M18B_HUMAN	Q8iug5 homo sapien
24	83	6.9	853	1 AHR_RAT	P41738 rattus norv
25	83	6.9	1499	1 PGFI_HUMAN	Q9Y4g8 homo sapien
26	81.5	6.8	489	1 YEN5_YEAST	P39970 saccharomyc
27	81	6.7	721	1 MX_ANAPL	P33238 anas platyr
28	81	6.7	1203	1 SMC2_XENLA	P50533 xenopus lae
29	80.5	6.7	1878	1 BR11_CANFA	Q95153 canis fami
30	80	6.6	647	1 LK1_RAT	P53669 rattus norv
31	80	6.6	918	1 YNEC_CAEEL	P30845 caenorhabdi
32	79.5	6.6	943	1 YMI1_YEAST	P39523 saccharomyc
33	79.5	6.6	1324	1 IRS2_HUMAN	Q9Y4h2 homo sapien

#### ALIGNMENTS

##### RESULT 1

ID	RIK2_HUMAN	STANDARD;	PRT;	540 AA.
AC	O43353;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)			
DE	(RIP-like interacting CLARP kinase) (Receptor-interacting protein 2)			
DE	(RIP-2) (CARD-containing interleukin-1 beta converting enzyme			
DE	associated kinase) (CARD-containing IL-1 beta ICE-kinase).			
GN	RIPK2 OR RICK OR RIP2 OR CARDIAK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.			
RX	MEDLINE=98241596; PubMed=9575181;			
RA	Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;			
RT	"RICK, a novel protein kinase containing a caspase recruitment domain,			
RT	interacts with CLARP and regulates CD95-mediated apoptosis.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.			
RC	TISSUE=Endothelial cells;			
RX	MEDLINE=98307936; PubMed=9642260;			
RA	McCarthy J.V., Ni J., Dixit V.M.;			
RT	"RIP2 is a novel NF-kappaB-activating and cell death-inducing			
RT	kinase.";			
RL	J. Biol. Chem. 273:16968-16975(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.			
RX	MEDLINE=98381580; PubMed=9705938;			
RA	Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,			
RA	Mattmann C., Tschopp J.;			
RT	"Identification of CARDIAK, a RIP-like kinase that associates with			
RT	caspase-1.";			
RL	Curr. Biol. 8:885-888(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Ozereky P., Holmes A., Brody M.;			
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBDJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Platzter M., Varon R.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBDJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore H., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			

O62640 sus scrofa  
Q9M367 arabidopsis  
Q03569 caenorhabdi  
P53667 homo sapien  
Q35800 rattus norv  
O61221 mus musculus  
O74522 schizosacch  
P07866 saccharomyc  
Q03489 petunia hyb  
Q91a06 lactococcus  
Q9V7e5 drosophila  
P70478 rattus norv

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
CC CASP-8-mediated apoptosis. Activates NF-kappaB.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.  
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and  
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
CC receptor complex.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -1- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,  
CC peripheral blood leukocytes, spleen, kidney, testis, prostate,  
CC pancreas and lymph node.  
CC -1- PM: Autophosphorylated.  
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -1- SIMILARITY: Contains 1 CARD domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AF027706; AAC34970.1; -  
CC EMBL: AF078530; AAC27722.1; -  
CC EMBL: AF064824; AAC25668.1; -  
CC EMBL: AC004003; AAC24561.1; -  
CC EMBL: AF117829; AAD04634.1; -  
CC EMBL: BC004553; AAH04553.1; -  
CC Genew: HGNC:10020; RIPK2.  
CC MIM: 603455; -  
CC GO: GO:0004674; F:protein serine/threonine kinase activity; TAS.  
CC GO: GO:0004871; F:signal transducer activity; TAS.  
CC GO: GO:0006915; P:apoptosis; TAS.  
CC GO: GO:0006954; P:inflammatory response; TAS.  
CC GO: GO:0007165; P:signal transduction; TAS.  
CC InterPro: IPR001315; CARD.  
CC InterPro: IPR000719; Prot\_kinase.  
CC InterPro: IPR008271; Ser\_Thr\_pkin\_AS.  
CC InterPro: IPR001245; Tyr\_pkinase.  
CC Pfam: PF00619; CARD; 1.  
CC Pfam: PF00069; pkinase; 1.  
CC PRINTS: PR00109; TYRKINASE.  
CC ProDom: PD000001; Prot\_kinase; 1.  
CC SMART: SM00114; CARD; 1.  
CC PROSITE: PS02029; CARD; 1.  
CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
CC PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
CC Transferase: Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation; Apoptosis.  
FT DOMAIN 18 294 PROTEIN KINASE.  
FT DOMAIN 432 524 CARD.  
FT NP\_BIND 24 32 ATP (BY SIMILARITY).  
FT BINDING 47 47 ATP.  
FT ACT\_SITE 146 146  
FT MUTAGEN 47 47 K->A: ABOLISHES KINASE ACTIVITY.  
FT MUTAGEN 47 47 K->M: REDUCES FAS-MEDIATED APOPTOSIS.

FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.  
SQ SEQUENCE 540 AA; 61194 MW; 575A692239505792 CRC64;  
Query Match 98.0%; Score 1182; DB 1; Length 540;  
Best Local Similarity 99.6%; Pred. No. 1.5e-91;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QLQSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 313 KLQSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
QY 65 LSRKAODCYFMKLHCPGNHSDSTISGQRAAFCDHKHTPCSSALINPLSTAGNSERLQ 124  
DB 373 LSRKAODCYFMKLHCPGNHSDSTISGQRAAFCDHKHTPCSSALINPLSTAGNSERLQ 432  
QY 125 PGIAQQWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLLD 184  
DB 433 PGIAQQWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLLD 492  
QY 185 TTDIOGEEFAKIVQKLKDKNQKMGLOPYPEILLVVSRLNLLQNKSM 232  
DB 493 TTDIOGEEFAKIVQKLKDKNQKMGLOPYPEILLVVSRLNLLQNKSM 540  
RESULT 2  
RIK2 MOUSE STANDARD; PRT; 539 AA.  
ID RIK2 MOUSE STANDARD; PRT; 539 AA.  
AC P58801;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).  
GN RIPK2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=21891093; PubMed=11894097;  
RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;  
RT "Involvement of receptor-interacting protein 2 in innate and adaptive  
RT immune responses";  
RL Nature 416:190-194(2002).  
CC -1- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.  
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and  
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
CC receptor complex (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -1- PTM: Autophosphorylated (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -1- SIMILARITY: Contains 1 CARD domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AF461040; AAL96436.1; -  
CC MGI:1891456; Ripk2.  
CC InterPro: IPR001315; CARD.  
CC InterPro: IPR000719; Prot\_kinase.  
CC InterPro: IPR008271; Ser\_Thr\_pkin\_AS.  
CC InterPro: IPR001245; Tyr\_pkinase.  
CC Pfam: PF00619; CARD; 1.  
CC Pfam: PF00069; pkinase; 1.





```
FT REPEAT 839 862 LRR 6.
FT REPEAT 867 891 LRR 7.
FT REPEAT 895 918 LRR 8.
FT REPEAT 923 946 LRR 9.
FT MUTAGEN 41 41 V->Q: ABOLISHES CASPASE-9 ACTIVATION AND
FT MUTAGEN 208 208 INTERACTION WITH RICK.
FT MUTAGEN 447 447 K->R: REDUCES CASPASE-9 ACTIVATION.
FT CONFLICT 447 447 R -> H (IN REF. 3).
SQ SEQUENCE 953 AA; 107690 MW; 0A9DF5FC6487E21A CRC64;

Query Match 10.2%; Score 122.5; DB 1; Length 953;
Best Local Similarity 37.1%; Pred. No. 0.021;
Matches 39; Conservative 19; Mismatches 36; Indels 11; Gaps 6;

QY 130 QWTQSKREDIVNQMTEA-CLNQSLDALLSRDLIMKEDYELVSTKPTKSVKQLLDTDI 188
DB 21 QLLKSNRELIVTHRTQCL---VDNLLKNDYFSAEDAIVCACTPQDKVKRILDLVQS 77

QY 189 QGE---EFKAVIVQKLDKDKQMGLOPYPELLVVSRSPLNLLQNK 230
DB 78 KGEVSEFFYLILQQLAD-AYVDLRPW--LLEIGFSPSL-LTQSK 118

RESULT 4
YLW5 CABEL STANDARD; PRT; 943 AA.
AC P34408;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein F22B7.5 in chromosome III.
GN F22B7.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laissner N.,
RA Lathelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonnhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -!- SIMILARITY: Contains 1 GoLoco domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L12018; AAA65459.1; -
CC PIR; S44636;
CC HSSP; P08622; 1XBL.
CC WormPep; F22B7.5; CE00158.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGK.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR003109; GoLoco.
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DR InterPro; IPR008971; HSP40 DnaJ_pep.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGK; 1.
DR Pfam; PF02188; GoLoco; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR SMART; SM00390; GoLoco; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS0877; GoLoco; 1.
KW Hypothetical protein.
FT DOMAIN 424 445 GOLOCO.
FT DOMAIN 531 595 J-DOMAIN.
SQ SEQUENCE 943 AA; 105926 MW; 9847F95977E0418E CRC64;

Query Match 8.3%; Score 100.5; DB 1; Length 943;
Best Local Similarity 19.4%; Pred. No. 1.4;
Matches 45; Conservative 44; Mismatches 84; Indels 59; Gaps 10;

QY 25 LNIPVNHGQERSCGSSQLHENSGETSRSLPAPQDNDFLSKQAQDCYFMKLHHCNGH 84
DB 349 IDVAMNQERSETATQDQVCLADSSPDPTSS-----NDMNK-----FVVELEHATNVE 397

QY 85 SWDSTISG-----SQRAAFCDHKTTPCSSAI--NPLS 115
DB 398 TWEMIVNGIIDDOKKPAIEKKEKEEPVMDMLFSSSRMDDORTELPAAREIPRPVS 457

QY 116 TAG---NSERLQPGIAQWIOSKREDIVNQMTEACINOSLDALLSRDLIMKEDYELVST 171
DB 458 SASKTKTKSHRILPGLRANWTKVQSMKVLGMFV---LNRS-SGLIHSVPLLAQ---VST 510

QY 172 KPRTSKVQLLDTTIDQGEFAKVI-VOKLKNK-----QMGLOPYPEI 215
DB 511 PTTSTTKLAQLHTHALSKEDYIKTLGVDKKSDAKAIKKAYFQIAKKYHPDV 562

RESULT 5
CAR4 MOUSE STANDARD; PRT; 953 AA.
ID CAR4_MOUSE
AC Q8BHB0; Q8BUT6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 4.
GN CARD4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=NOD; TISSUE=Cerebellum, and Spleen;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirani L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Ciothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
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RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzley D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP STRUCTURE BY NMR OF 266-363.  
RX MEDLINE=93332054; PubMed=10404221;  
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)  
RT repeat.";  
RL Nat. Struct. Biol. 6:648-651(1999).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions  
CC inhibit apoptotic suppressor activity.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.  
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,  
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD  
CC LEUKOCYTES.  
CC -1- SIMILARITY: Belongs to the IAP family.  
CC -1- SIMILARITY: Contains 3 BIR repeats.  
CC -1- SIMILARITY: Contains 1 CARD domain.  
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.  
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CC  
CC EMBL; L49431; AAC41942.1; -  
CC EMBL; U45879; AAC50372.1; -  
CC EMBL; U37547; AAC50508.1; -  
CC EMBL; BC016174; AAH16174.1; -  
CC EMBL; BC028578; AAH28578.1; -  
CC PIR; S68450; S68450.  
CC PDB; 1QBH; 20-OCT-99.  
CC Genew; HGNC:590; BIRC2.  
CC MIM; 601712; -  
CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.  
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
CC InterPro; IPR001370; BIR.  
CC InterPro; IPR001315; BIR.  
CC InterPro; IPR001841; Znf\_ring.  
CC Pfam; PF00653; BIR; 3.  
CC Pfam; PF00619; CARD; 1.  
CC Pfam; PF00097; zf-C3HC4; 1.  
CC SMART; SM00238; BIR; 3.  
CC SMART; SM00114; CARD; 1.  
CC SMART; SM00184; RING; 1.  
CC PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
CC PROSITE; PS01043; BIR\_REPEAT\_2; 3.  
CC PROSITE; PS50209; CARD; 1.  
CC PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
CC PROSITE; PS50089; ZF\_RING\_2; 1.  
KW Apoptosis; zinc-finger; Repeat; 3D-structure.  
FT REPEAT 46 113 BIR 1.  
FT REPEAT 184 250 BIR 2.

FT REPEAT 269 336 BIR 3.  
FT DOMAIN 453 543 CARD.  
FT ZN\_FING 571 606 RING-TYPE.  
FT CONFLICT 157 157 S -> P (IN REF. 2).  
FT CONFLICT 308 308 C -> G (IN REF. 2).  
FT CONFLICT 414 414 Q -> L (IN REF. 2).  
FT CONFLICT 514 514 L -> W (IN REF. 2).  
FT TURN 269 270  
FT HELIX 271 274  
FT HELIX 287 293  
FT TURN 294 294  
FT TURN 296 297  
FT TURN 301 304  
FT STRAND 309 309  
FT HELIX 322 325  
FT TURN 326 328  
FT STRAND 333 333  
FT TURN 334 343  
FT HELIX 344 351  
FT TURN 353 354  
SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;  
Query Match 7.7%; Score 92.5; DB 1; Length 618;  
Best Local Similarity 24.5%; Pred. No. 3.9;  
Matches 27; Conservative 24; Mismatches 46; Indels 13; Gaps 2;  
QY 132 IQSKREDIVNQMTPEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLDITDQGE 191  
DB 461 IRKNRVALFQOLT--CVLPILDNLKXNVINKQEHDIKQKTIPLQARELIDTILVKGN 518  
QY 192 EFAKVTIVQKLKD-----NKQMGLQPYPEILVWSRSPSLNLRK 230  
DB 519 AAANIFKNCLEKIDSTLYKNLFVDKKNKYIPTEDVSGLSLEQRRLQEE 568  
RESULT 7  
REPL\_ZYGBA STANDARD; PRT; 357 AA.  
ID REPL\_ZYGBA AC P13776;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-AUG-1990 (Rel. 15, Last annotation update)  
DE Trans-acting factor B (REPL).  
GN B.  
OS Zygosaccharomyces bailii.  
OG Plasmid pSB2.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.  
OX NCBI\_TaxID=4954;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IFO 1047;  
RX MEDLINE=88058763; PubMed=3680169;  
RA Uchatsu I., Sakamoto S., Imura I., Toh-E A.;  
RT "yeast plasmids resembling 2 micron DNA: regional similarities and  
RT diversities at the molecular level.";  
RL J. Bacteriol. 169:5537-5545(1987).  
CC -1- FUNCTION: PLASMID PARTITION REQUIRE REPL1, REP2, AND A CIS-ACTING  
CC DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN  
CC THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA  
CC REP2.  
CC -1- SIMILARITY: TO THE P GENE PRODUCT OF PSR1.  
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CC  
CC EMBL; M18274; AAA35283.1; -  
CC InterPro; IPR008897; Yeast\_TAF.





Query Match		7.3%; Score 88; DB 1; Length 2368;
Best Local Similarity		22.3%; Pred. No. 54;
Matches		56; Conservative 38; Mismatches 105; Indels 52; Gaps 11;
QY	14 HLCDDKKK-----MELSLNIPVNHGPOEESGSGS-----LHNSGSPETSRLPAPQDNDF	64
DB	491 HLCDEKTKGNPVRINP-----EAAGSEIFRILHSN-----FLSHPNIDF	535
QY	65 LSKAQCOCYFMKLHH-----CPGNHSDSTIGSQRAAFCDHKTPPCSSAIINPL	114
DB	536 -SESLLSGILFSLHRIFFSHFQPPKPLTGDNGQINKSPKLVQKFMNSRYRLRLLSRIEPL	594
QY	115 ----STAGNERLOPAGTAQWIOQSKREDIV-----NMTAECLNQSLDALLSR--DLI	161
DB	595 FNISDSHNSDEHTAFILFQSQKLPVVKENLVIAWTQTLTTSNDVFTLLKLIDIF	654
QY	162 MKEDYELVSTKPRTSKVQLDITDIO-GEFAKVIIVKLDN---KMGLOQPYPEILV	217
DB	655 NDDVSLRIMTLOIKMAKILKTPYQLLSPLPVLKQLKNLVERKVGQNLIELLG	714
QY	218 VSRSPSLNLLQ 228	
DB	715 YSSKTILDFQ 725	
RESULT 11		
SYAP MOUSE		
ID	SYAP MOUSE	STANDARD; PRT; 365 AA.
AC	Q9D5V6; Q9D870;	
DT	10-OCT-2003 (Rel. 42, Created)	
DT	10-OCT-2003 (Rel. 42, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Synapse associated protein 1.	
GN	SYAP1.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J;	
RC	TISSUE=Dorsal root ganglion, Small intestine, and Testis;	
RX	MEDLINE=22354683; PubMed=12466851;	
RA	Okazaki Y., Furuno M., Kasukawa T.,	
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,	
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,	
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,	
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,	
RA	Blake J.A., Bratt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,	
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,	
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,	
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,	
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,	
RA	Kongaya A., Kurochkin I.V., Lee Y., Lenhard R., Lyons P.A.,	
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,	
RA	Nagashima T., Numata K., Okitido T., Pavan W.J., Pertea G., Pesole G.,	
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,	
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,	
RA	Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,	
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,	
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,	
RA	Wilm L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,	
RA	Yuan Z., Zvolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,	
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,	
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,	
RA	Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,	
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,	
RA	Birney E., Hayashizaki Y.;	
RT	"Analysis of the mouse transcriptome based on functional annotation of	
RT	60,770 full-length cDNAs."	
RL	Nature 420:563-573 (2002).	
RN	[2]	
SEQUENCE FROM N.A.		
RX	MEDLINE=22388257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Hellon E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
CC	1- SIMILARITY: Contains 1 BSD domain.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; AK008390; BAB25643.1; -	
DR	EMBL; AK014893; BAB29608.1; -	
DR	EMBL; AK051251; BAC34575.1; -	
DR	EMBL; BC021373; AAH21373.1; -	
DR	MGD; MGI:1914293; Syapi.	
DR	GO; GO:0005634; C:nucleus; IDA.	
DR	InterPro; IPR005607; BSD.	
DR	Pfam; PF03909; BSD; 1.	
DR	PROSITE; PS50858; BSD; 1.	
FT	DOMAIN 172 224	
FT	CONFLICT 243 243	
SQ	SEQUENCE 365 AA; 41350 MW; 7553E79C050B96B CRC64;	
Query Match		
Best Local Similarity 7.2%; Score 86.5; DB 1; Length 365;		
Matches 28; Conservative 15; Mismatches 50; Indels 5; Gaps 1;		
QY	114 LSTAGNSERLOPAGIAQWIOQSKREDIVNQ-----MTEACLNQSLDALLSRDLIMKEDYEL	168
DB	220 ISLIQSAQLTALAAQQASGKESNRDNDLPLTEAVRPTPPVVIKSLKQSDDEE	279
QY	169 VSTKTRTSKVQLDITDIOGEERFAKVIVOKLKNQKQ 206	
DB	280 ISTSPGVSEFVSADFATCSLNQEDLRKEMEQLVLDKKQ 317	
RESULT 12		
MYC ASTVU		
ID	MYC ASTVU	STANDARD; PRT; 407 AA.
AC	Q17103;	
DT	15-DEC-1998 (Rel. 37, Created)	
DT	15-DEC-1998 (Rel. 37, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Myo protein (c-myc) (fragment).	
GN	MYC.	
OS	Asterias vulgaris (Northern sea star).	
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;	
OC	Asteroidea; Forcipulatacea; Forcipulata; Asteriidae; Asterias.	
OX	NCBI_TaxID=7605;	
RN	[1]	
RP	SEQUENCE FROM N.A.	



```

RX MEDLINE=93026376; PubMed=1408141;
RA Walker C.W., Boom J.D., Marsh A.G.;
RT "First non-vertebrate member of the myc gene family is seasonally
RL expressed in an invertebrate testis.";
RL Oncogene 7:2007-2012(1992).
CC -1- FUNCTION: Participates in the regulation of gene transcription.
CC Binds DNA both in a non-specific manner and also specifically to
CC recognizes the core sequence CAC[GA]TG. Seems to activate the
CC transcription of growth-related genes (By similarity).
CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another
CC BHLH protein (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; M80364; AAA27788.1; -.
CC PIR; S27774; S27774.
CC HSP; P25912; IHLO.
CC TRANSFAC; T03463; -.
CC InterPro; IPR001092; HLH basic.
CC InterPro; IPR002418; TF_Myc.
CC Pfam; PF00010; HLH; 1.
CC Pfam; PF01056; Myc_N_term; 1.
CC SMART; SM0044; LEUZIPPRMYC.
CC PRINTS; SM00353; HLH; 1.
CC PROSITE; PS00888; HLH; 1.
CC Nuclear protein; DNA-binding; Transcription regulation; Activator.
CC
CC NON_TER 1
CC DNA_BIND 321 334 BASIC DOMAIN.
CC DOMAIN 335 374 HELIX-LOOP-HELIX MOTIF.
CC DOMAIN 380 401 LEUCINE-ZIPPER (POTENTIAL).
CC SEQUENCE 407 AA; 45673 MW; F4E52DD01182113A CRC64;
SQ
Query Match 7.2%; Score 86.5; DB 1; Length 407;
Best Local Similarity 21.9%; Pred. No. 7.1;
Matches 59; Conservative 40; Mismatches 91; Indels 79; Gaps 14;
QY 19 KMELSLNIPV--NHGPOE--ESCGSSQLHNSGSPETSRLPAPQDNDEL----- 65
DB 43 KKELYTPTPLSPSHNPDDESHPRHQDGDGSPSRSYQHLMDDDLPLVNPQVPLL 102
QY 66 -----SRKAQDCYPMKLHCPGNHSDSTISGSQRAAFCDHK-----TTP 105
DB 103 DLSSAPPAALIQD-----WSSIIAERRKLFMKSEKKHAERATKKASTP 150
QY 106 CSSAINPL---STAGNSERLOP-GIAQQWIOSKREDIVNQMTACLNQSLDALLSDLI 161
DB 151 SSGVMLPPLVPASVYSGDCVDSAVCPYPLSETRLDLFSST-----NTPSDSEEEIDVV 206
QY 162 MKED-----YELSTKP--TRTSKVRQLLD-----TTDIOGEPAKVI---VOKLK 202
DB 207 TVEKKHSHVHKINTRYHQSTKVRQHLHRPISVALVGLRGPSTATILSPICKLK 266
QY 203 DNKQMGLOPYEILVSRSPSLNLLQNK 231
DB 267 --TEGNLEEVKQILQKS-----NLRSSS 288

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## RESULT 13

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BIR2_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; Q08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis

```

```

DE protein 2) (MIAP2) (MIAP-2).
GN BIRC2 OR BIRC3 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RL to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes.";
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
CC liver, skeletal muscle, kidney and testis.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC
CC ENBL; L49433; AAC42078.1; -.
CC EMBL; U88909; AAC53532.1; -.
CC HSP; Q13490; IQBH.
CC MGD; MGI:1197009; Birc3.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001315; CARD.
CC Pfam; PF00653; BIR; 3.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS01143; BIR_REPEAT_2; 3.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC Apoptosis; Zinc-finger; Repeat.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C10D CRC64;

```

## Query Match

7.2%; Score 86.5; DB 1; Length 612;

Best Local Similarity 23.6%; Pred. No. 12;

Matches 26; Conservative 21; Mismatches 50; Indels 13; Gaps 2;





```
Db 610 PGHSVSKDQKHGSLGSIKDEASLPDCSSRQPIPVASHAVGPVSTGG-----OTLVAK 664
Qy 130 QWI-----OSKREDIVNMQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVR 180
Db 665 KAVIKQEVPGAEQOQSVVSQFVSSQGGPPPAVNAQ-----PQALLTIQTA 712
Qy 181 QLLDITDIQEEFAKVIQV----KLKDNKQMGQLPYPEILVWRSRPSLNL 226
Db 713 QLLLPVSIQSSVTSVQLPVGSLKQTSPOAGMTQPOIATAAQIPTAAL 762

RESULT 15
ABPX YEAST
ID ABPX YEAST STANDARD; PRT; 627 AA.
AC Q08641; Q08644;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Actin-binding protein ABP140.
GN ABP140 OR YOR239W/YOR240W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=97127829; PubMed=8972580;
RA Boyer J., Michaux G., Fairhead C., Gaillon L., Dujon B.;
RT "Sequence and analysis of a 26.9 kb fragment from chromosome XV of
RL the yeast Saccharomyces cerevisiae.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97313270; PubMed=9169874;
RA Dujon B., Albermann K., Aldea M., Alexandraki D., Ansoorge W.,
RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,
RA Boyer J., Camasses A., Casamayor A., Casas C., Cheret G.,
RA Criepluch C., Daigman-Fornier B., Dang D.V., de Haan M., Delius H.,
RA Durand P., Fairhead C., Goffeau A., Gaillon L., Galisson F.,
RA Gamo F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,
RA Habbig B., Hand N.J., Hani J., Hattenhorst U., Hebling U.,
RA Hernandez Y., Herrero E., Heumann K., Hiesel R., Hilger F., Hofmann B.,
RA Hollenberg C.P., Hughes B., Jauniaux J.-C., Kaloogeropoulos A.,
RA Katsoulou C., Kordes E., Lafuente M.J., Landt O., Louis E.J.,
RA Maarse C., Madania A., Mannhaupt G., Marck C., Martin R.P.,
RA Mewes H.-W., Michaux G., Paces V., Farie-McDermott A.G., Pearson B.M.,
RA Perrin A., Pettersson B., Poch O., Pohl T.M., Poirey R.,
RA Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Rechmann S.,
RA Schwager C., Schweizer M., Sor F., Sterky F., Tarassov I.A.,
RA Teodoru C., Tettelin H., Thierry A., Tobiasch E., Tzermia M.,
RA Uhlen M., Unsel M., Valens M., Vandenbol M., Vetter I., Vleck C.,
RA Voet M., Voickaert G., Voss H., Wambutt R., Wedler H., Wiemann S.,
RA Winsor B., Wolfe K.H., Zollner A., Zumstein E., Kleine K.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.";
RL Nature 387:98-102(1997).
RN [3]
RP PARTIAL SEQUENCE FROM N.A., SEQUENCE OF 1-12; 38-72; 102-115; 244-286;
RP 560-574 AND 598-608, FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=BU5457;
RX MEDLINE=98127445; PubMed=9467951;
RA Asakura T., Sasaki T., Nagano F., Satoh A., Obaishi H., Nishioka H.,
RA Inamura H., Hotta K., Tanaka K., Nakanishi H., Takai Y.;
RT "Isolation and characterization of a novel actin filament-binding
RL protein from Saccharomyces cerevisiae.";
CC CC -1- FUNCTION: Potential methyltransferase (By similarity). Binds F-
CC actin and shows weak F-actin crosslinking activity.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic and cortical cytoskeleton.
CC CC -1- MISCELLANEOUS: A ribosomal frameshift occurs between the codons
CC for Leu-276 and Gly-277.
CC CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. METL
```

```
CC family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z75147; CAA99460.1; ALT_SEQ.
CC EMBL; Z75147; CAA99461.1; ALT_SEQ.
CC GermOnline; I43827; -.
CC SGD; S0005765; ABP140.
CC GO; GO:0005884; C:actin filament; IDA.
CC GO; GO:0003780; F:actin cross-linking activity; IDA.
CC GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; IDA.
CC GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; IDA.
CC InterPro; IPR001601; Methyltransf.
CC InterPro; IPR000051; SAM_bind.
CC Transferase; Methyltransferase; Cytoskeleton; Actin-binding;
KW Ribosomal frameshift.
FT INIT MET 0
SQ SEQUENCE 627 AA; 71354 MW; D4E55F9485412F39 CRC64;
Query Match 7.0%; Score 85; DB 1; Length 627;
Best Local Similarity 18.8%; Pred. No. 17;
Matches 41; Conservative 47; Mismatches 92; Indels 38; Gaps 7;
Qy 22 ELSLNPVNHGPOESCGSQLHNSGSPETSRLPAPQDNDFLSRKAQDCYFVKLHCP 81
Db 180 EEDADIEQNSGKRETAENASQAQNGSTSTTSKKNKKKKKKKKKKR- 229
Qy 82 GNHSWDSITSGSQRAAFCDHKTPCSSLINPLSTAGNSERLQP---GIAQQ---WIQS 134
Db 230 GNVTNANVDDSTKTGENDDTTGTTSITTSATQEVNDLEVDVDDSCLDGIDQHNREHLKA 289
Qy 135 KREDIVNMQTEACLNQSL-DALLSRDLIMKEDYELVSTKPTRTSK-----VRLDIT 186
Db 290 LTQDVKEETLENTAHEGRGDNQDQNAVEKSDFEKSDTEGSRIGRDLPFPGKRNLTES 349
Qy 187 DI-----QGEEPAKVIIVOKLKNQMGQLPYPE 214
Db 350 DVWDHNDVNDVWEEGEEQVQAEEKIKQPK---HPVPE 384
Search completed: March 29, 2004, 14:08:38
Job time : 19 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:03:30 ; Search time 45 Seconds  
(without alignments)  
1626.672 Million cell updates/sec

Title: US-09-771-161A-93

Perfect score: 1206

Sequence: 1 MISLQSQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	27.8	584	13 Q8JHU4	Q8jhu4 brachydanio
2	99	8.2	461	12 Q8J861	Q8j861 spodoptera
3	98.5	8.2	537	11 Q8R489	Q8r489 cavia porce
4	98	8.1	799	5 Q8IN63	Q8in63 drosophila
5	98	8.1	829	5 Q9VDR7	Q9vdr7 drosophila
6	98	8.1	830	5 Q45116	Q45116 mus musculus
7	98	8.1	830	5 Q44224	Q44224 drosophila
8	97.5	8.1	869	10 Q9FTV4	Q9ftv4 oryza sativ
9	97	8.0	285	13 Q8JFU4	Q8jfu4 brachydanio
10	96	8.0	1169	16 Q7ZAJ1	Q7zaj1 scaphylococ
11	95.5	7.9	791	16 Q8A9V6	Q8a9v6 bacteroides
12	95.5	7.9	2063	11 Q8QTB4	Q8qtb4 mus musculus
13	94.5	7.8	589	11 Q9QZC6	Q9qzc6 rattus norv
14	94.5	7.8	589	11 Q8ESE8	Q8ese8 rattus norv
15	94.5	7.8	896	11 Q91X10	Q91x10 mus musculus
16	93.5	7.8	571	16 Q87L04	Q87l04 vibrrio para

17	93.5	7.8	1229	16 Q8D169	Q8d169 yersinia pe
18	93	7.7	692	5 Q965M1	Q965m1 caenorhabdi
19	92.5	7.7	923	13 Q902T7	Q902t7 xenopus lae
20	90.5	7.5	241	10 Q9XHR9	Q9xhr9 nicotiana s
21	90	7.5	2315	5 Q95ZK3	Q95zk3 caenorhabdi
22	90	7.5	2396	5 Q23081	Q23081 caenorhabdi
23	89	7.4	212	10 Q7XBN6	Q7xbn6 antirrhinum
24	89	7.4	237	10 Q7XSS6	Q7xss6 oryza sativ
25	89	7.4	242	10 Q8LLR0	Q8llr0 vitis vinif
26	89	7.4	242	10 Q38733	Q38733 antirrhinum
27	89	7.4	738	4 Q9P2P8	Q9p2p8 homo sapien
28	89	7.4	1360	5 Q9TYK4	Q9tyk4 caenorhabdi
29	88.5	7.3	617	17 Q8PUY5	Q8puys methanosarc
30	88.5	7.3	2439	5 Q9VMS2	Q9vms2 drosophila
31	88	7.3	283	16 Q9JX61	Q9jx61 neisseria m
32	88	7.3	524	13 Q8JGL7	Q8jgl7 xenopus lae
33	88	7.3	777	12 Q7TFN7	Q7tfn7 rhesus cyto
34	88	7.3	1049	4 Q8WYL5	Q8wyl5 homo sapien
35	88	7.3	1135	13 Q9YHD3	Q9yhd3 xenopus lae
36	88	7.3	1762	2 Q9KWC9	Q9kwc9 agrobacteri
37	87.5	7.3	288	4 Q8N5S3	Q8n5s3 homo sapien
38	87.5	7.3	340	5 Q9XW80	Q9xw80 caenorhabdi
39	87.5	7.3	386	6 Q9N2H6	Q9n2h6 bos taurus
40	87.5	7.3	665	16 Q87JP9	Q87jp9 vibrrio para
41	87.5	7.3	1844	4 Q86QE3	Q86qe3 homo sapien
42	87	7.2	147	10 Q228J1	Q228j1 arabidopsis
43	87	7.2	1205	12 Q56300	Q56300 human herpe
44	87	7.2	1205	12 Q69513	Q69513 human herpe
45	86.5	7.2	210	10 Q7XBM3	Q7xbm3 lycopersico

#### ALIGNMENTS

#### RESULT 1

Q8JHU4	Q8JHU4	PRELIMINARY;	PRT;	584 AA.
AC	Q8JHU4;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Protein kinase RICK.			
GN	RICK.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98241596; PubMed=9575181;			
RA	Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;			
RT	"RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Muto A., Ruland J., McAllister-Lucas L.M., Lucas P.C., Yamaoka S.,			
RA	Chen F.F., Lin A., Mak T.W., Nunez G., Inohara N.;			
RT	"PKC mediates Bcl10-independent NF-kappa B activation induced by phorbol ester.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
DR	EMBL; AF487540; AAM76920.1;			
DR	GO; GO:0005622; C:intracellular;			
DR	GO; GO:0016329; P:apoptosis regulator activity; IEA.			
DR	GO; GO:0004674; P:apoptosis regulator activity; IEA.			
DR	GO; GO:0005524; P:ATP binding; IEA.			
DR	GO; GO:0004713; P:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0016740; P:transferase activity; IEA.			
DR	GO; GO:0006915; P:apoptosis; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR001315; CARD.			
DR	InterPro; IPR000719; Prot_Kinase.			

DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyKc; 1.  
 DR PROSITE; PS02029; CARD; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Transferase.  
 SQ SEQUENCE 584 AA; 66124 MW; 7A4EFFCB65DEB9C0 CRC64;  
 Query Match 27.8%; Score 335; DB 13; Length 584;  
 Best Local Similarity 39.4%; Pred. No. 4e-22;  
 Matches 84; Conservative 28; Mismatches 45; Indels 56; Gaps 7;  
 QY 21 MEISLIPVNHGPOEESGSSQLHNSGSP-----TSRSLP-----APQNDNDFLSRKA 69  
 DB 396 MSPLDPP---KPLMDCSPNNL-----SPYQTAQVVSDINIPFKAHAPQSSESLALAI 447  
 QY 70 QDCYFMKLHCPGNHNSWDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQ 129  
 DB 448 QP---LTLHPHPQDFV-----TAFDDQ-----GPAA 470  
 QY 130 QWIOGKREIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDDTTDQ 189  
 DB 471 RWTAAAREEVQRQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDDTTDQ 189  
 QY 190 GEEFAKIVQKLDNKMQLQPYPEILVWRSRP 222  
 DB 531 SEEFRCVVVRKLDNKMQLQPYPEILVWRSRP 563  
 RESULT 2  
 Q9J861 ID Q9J861 PRELIMINARY; PRT; 461 AA.  
 AC Q9J861;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE ORF76 cg30.  
 OS Spodoptera exigua nucleopolyhedrovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=10454;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20036646; PubMed=10567663;  
 RA Iukel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,  
 RA Goldbach R.W., Vlask J.M.;  
 RA "Sequence and organization of the spodoptera exigua multicapsid  
 RT nucleopolyhedrovirus genome.";  
 RL J. Gen. Virol. 80:3289-3304 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Iukel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.,  
 RA Goldbach R.W., Vlask J.M.;  
 RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -|- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL; AF169823; AAF33605.1;  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00097; zf-G3HC4; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 DR Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 461 AA; 50820 MW; 6C062A3B43DD5D06 CRC64;  
 Query Match 8.2%; Score 99; DB 12; Length 461;  
 Best Local Similarity 22.3%; Pred. No. 1.3;  
 Matches 46; Conservative 37; Mismatches 9; Indels 44; Gaps 7;

QY 49 SPETSRLPAPQDNDFLSRKA-----QDCYFMKLH-----HCPGNHNSWDSTI 90  
 DB 157 SPSS---PSKQNNKLYKOPTLRQVFNCFPPFKLELPKTKTSTSVTPSTSGPSTS 213  
 QY 91 SGSQRAAFCDHKTTPCSSAIINPLSTAGNS-----ERLQPGIAQWQIQS 134  
 DB 214 AGPSTSGPSTSGPSTSA--GPSTSGPSTSAEYQNNDNDDDLKQRLDAAIELSLIOY 271  
 QY 135 KREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDDTTDQEEPA 194  
 DB 272 EREKIIRKINDNFETO--DRINVTDLKNFRDMFKNEEIAKMTKDLENLKNKNDLV 329  
 QY 195 KVIV---QKLKONKQMLQPYPEILV 217  
 DB 330 KDIANLQSKLNEQKLKSTQDENIV 355  
 RESULT 3  
 Q8R489 ID Q8R489 PRELIMINARY; PRT; 537 AA.  
 AC Q8R489;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Syntaxin-interacting protein OCSYN.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Safieddine S., Ly D., Wang Y.-X., Wang C.-Y., Kachar B., Petralia R.,  
 RA Wenthold R.;  
 RT "OCSYN, A novel syntaxin-interacting protein enriched in the subapical  
 RT region of inner hair cells.";  
 RL Mol. Cell. Neurosci. 0:0-0 (2002).  
 DR EMBL; AF494296; AAM14616.1; -.  
 SQ SEQUENCE 537 AA; 58735 MW; EA9DFD9AADDECD4 CRC64;  
 Query Match 8.2%; Score 98.5; DB 11; Length 537;  
 Best Local Similarity 22.0%; Pred. No. 1.8;  
 Matches 51; Conservative 46; Mismatches 76; Indels 59; Gaps 12;  
 QY 30 NHGPOEESGSSQLHNSGSPETSRSLPAPQDNDFLSRKAQDCYF-MKLHHCPCGNHNSWD 88  
 DB 54 NRGPHGNSGAS-LHKPGSP-----PSPREKDLMLCRLNQLGPNVHPSTAPSSPS 106  
 QY 89 TISGQRAAFCDHKTTPCSSAIINP--LSTAGNSERLQPGIAQWQIQS-KREDIVNQWTE 145  
 DB 107 SNSGS-----YKESDCSPVMRRPGRVMSCGSHGVKPPNPQYLTPLOKEVTVRHLK 159  
 QY 146 ACLNQS-----LDALLSRDLIMKEDY-----ELVSTKPTRTSKVROL 183  
 DB 160 TLKESERLHERSEIVEIKSQLAR---MREDWIEECHRVEAQLKALKEAR-KEIKQL- 214  
 QY 184 DTTDQIEEFKIVQKLDN---KQMLQPYPEILVWRSRPSLNLIQKSM 232  
 DB 215 -----KQVIETMRDNLADKDKGIQYFVDINIQNKKLEALLQSMEM 255  
 RESULT 4  
 Q8IN63 ID Q8IN63 PRELIMINARY; PRT; 799 AA.  
 AC Q8IN63;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CG12249-PB (LDQ2989p).  
 GN MIRA OR CG12249.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;









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RESULT 10
Q7ZAJ1 PRELIMINARY; PRT; 1169 AA.
AC Q7ZAJ1; 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA translocase stage III sporulation prot.
GN S21414.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren Y., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016748; AAC05013.1; -
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR Pfam; PF01580; FtsK_SpoIIIE; 1.
DR PROSITE; PS50901; FtsK_SpoIIIE; 1.
KW Complete proteome.
SQ SEQUENCE 1169 AA; 133548 MW; 320DC7EDAA48E2C8 CRC64;

Query Match 8.0%; Score 96; DB 16; Length 1169;
Best Local Similarity 16.2%; Pred. No. 8.3;
Matches 49; Conservative 57; Mismatches 93; Indels 104; Gaps 10;

QY 17 DKKQK-----ELSLNIP-----VNHGPOESGSSQLHE----- 45
Db 559 DKKQMDQNHKVSVPKPEKQANANHRKSDSEKFEKQINTNRETDSNYESNGIE 618

QY 46 ---NSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPCGNHWD-----STISGQRAAF 98
Db 619 HDMNSSDEHVYETPSQDEQIQKQDDPHFENANAHAKINNSNETGNQSNISHSKRSQY 678

QY 99 CDHKTTPCSSAIINPLSTAGNSERLQPG-----IAQOWIOSKREDI- 139
Db 579 STNESKNIDQTSNSTSNQNFQIRGPNIKLPSYQLLEAPPEHKKQDQWIDNKKQELN 738

QY 140 -----VNQMTAC-----LNQSLDALLSRDLIMKED----- 165
Db 739 DALYFNVPAEVKNVTEGSPVTRPELSVEKGVKVSRTALQDDIKMALAAKDIRIEAIP 798

QY 166 -----YELVSTRKTRSKVRLDITDIOGEEFAKIVVQKLKDKQKQWGLQPYPEILVVS 219
Db 799 GTSLVGIEVQNQNPKNV-LRSIIESPKNKTESKLTVMAGYRINNE-----PLLMEDIA 851

QY 220 RSP 222
Db 852 KTP 854

RESULT 11
Q8A9V6 PRELIMINARY; PRT; 791 AA.
AC Q8A9V6; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN B70709.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RC STRAIN=VPI-5482 / ATCC 29148;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016928; AAC75816.1; -
DR InterPro; IPR001364; Hemagglutn.
DR ProDom; PD000225; Hemagglutn; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 791 AA; 88443 MW; 7C72011D0CD93232 CRC64;

Query Match 7.9%; Score 95.5; DB 16; Length 791;
Best Local Similarity 19.4%; Pred. No. 5.6;
Matches 48; Conservative 36; Mismatches 80; Indels 83; Gaps 9;

QY 2 YSLQLQSVSAIHLCDKKKWEISLNP-----VNHGPOESG 39
Db 452 YTLSLQAI-----RKNTAATNLPEPEPKLAPPLIPADISRAQLITHLINNQSCS 503

QY 40 SSQIHNSSPETSRLPAPQDNDFLSRKAQDCYFMKLHHCPCGNH-----SWDSTISG 92
Db 504 SLLTSTEASSVSTARNQDYGHFDDILCKAFEHLELISSSYKINGRHPKVEYPSLSAFLTG 563

QY 93 SQRAAFCDHKTTPCSSAIINPLSTAG-----NSERL-----OPGIAQOWIOSKREDIVN 141
Db 564 -----TPSSLLIFPTMETGLYNYRFLINTFLPAWQDVFAEKVRA--DDLFN 610

QY 142 QMTEACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLDITDIOGEEFAKIVVQKL 201
Db 611 ELSMRFAQMAL-----FLKDSPTPE-----VKLTDQKKEFNVRFTQLL 648

QY 202 KDNKQMG 208
Db 649 KDTDLG 655

RESULT 12
Q80TB4 PRELIMINARY; PRT; 2063 AA.
AC Q80TB4; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MKIAA1606 protein (Fragment).
GN MKIAA1606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
DR EMBL; AK122531; BAC65813.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR003822; PAH_
DR PROSITE; PS50090; MYB_3; 1.
FT NON_TER 1
SQ SEQUENCE 2063 AA; 227819 MW; 8AA6E1AA113B3899 CRC64;

Query Match 7.9%; Score 95.5; DB 11; Length 2063;
Best Local Similarity 21.2%; Pred. No. 19;
Matches 43; Conservative 35; Mismatches 84; Indels 41; Gaps 7;

QY 25 LNIPVNHGPOESGSSQLHNSSGSPETSRLPAPQDNDFLSRKAQDCYFMKLHHCPCGNH 84

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Db 1026 LTLFVTSIPEDKAQVCLDVAEGKNAFQNPESKLKQELTPL-----CTTVFSKEEP--K 1077
QY 85 SWDSTISGSGRAAFCDHKTTTPCSSALINPLSTAGNSERLQ-----PG 126
Db 1078 SHWSSADTGSQAFSE--SSACSWAVVKTESQSGSEKACGVTWVKTEDGGHVEPLPQ 1135
QY 127 IAQWITQSKREDIVNQ-----TRACL-----NQSLDALLSRDLIMKEDYELVSTKPTR 175
Db 1136 NLQDSLSPSKOLLNVMKMEADCMVEISSNLPKQDIGEVKECSMELDSESPQEKPSR 1195
QY 176 TSKV--RQLDITDIQEEFAKV 196
Db 1196 ASEMSKQTVLQREDTOAAKSPSV 1218

RESULT 13
Q9QZC6 PRELIMINARY; PRT; 589 AA.
AC Q9QZC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF190020; AAF04585.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW EMBL; AF190020; AAF04585.1; -.
SQ SEQUENCE 589 AA; 66777 MW; E6812FPE3EA34142 CRC64;

Query Match 7.8%; Score 94.5; DB 11; Length 589;
Best Local Similarity 25.5%; Pred. No. 4.7;
Matches 28; Conservative 21; Mismatches 48; Indels 13; Gaps 2;

QY 132 IQSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLDITDIQGE 191
Db 432 IRKNRMALFQQLT--CVIPILDLLEASVLTKEHDIIRQKQIPIQARELIDITLVKGN 489

QY 192 EFAKIVQKLKD-----NKGMLQPYPEILVWSRSPSLNLLQNK 230
Db 490 AAASFVKNLSKEVDSTLYEHLFVEKTKYIPTEDVSGLSLEQLRLQEE 539

RESULT 14
Q9ESE8 PRELIMINARY; PRT; 589 AA.
ID Q9ESE8;
AC Q9ESE8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Leu M., Ehler E., Perriard J.-C.;
RT "Cloning of an unknown protein.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040842; AAK84686.1; -.
DR Hypothetical protein.
KW EMBL; AY040842; AAK84686.1; -.
SQ SEQUENCE 589 AA; 66777 MW; E6812FPE3EA34142 CRC64;

Query Match 7.8%; Score 94.5; DB 11; Length 896;
Best Local Similarity 21.2%; Pred. No. 8.1;
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Query Match 7.8%; Score 94.5; DB 11; Length 896;
Best Local Similarity 21.2%; Pred. No. 8.1;
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Matches		43; Conservative	35; Mismatches	84; Indels	41; Gaps	7;
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Db	436	LTLPTVTSIPEDKAOVKLDVAEGKNAPONPESKLPQELTPL-----CTTVFPKKEP--K				
Qy	85	SWDSTTSGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ-----PG				
Db	488	SWHSSADTGSQEAFFE--SSACSWAVVVKTESQESSEKSACGWTVVVKTEGGHVEPLPQ				
Qy	127	IAQQWIOSKREDIVNQ-----TEACL-----NQSLDALLSRDLIMKEDYELVSTKPTR				
Db	546	NLQDSLSSPSKDLLNMVMEAECDMVEISSNLPKQDIGBEVKEECSELDSESPQKPSR				
Qy	176	TSKV--RQLLDTTDIQEEPAKV				
Db	606	ASEMSKQTVLQREDTQAAKSPSV				

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 12:09:03 ; Search time 105 Seconds  
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1226.177 Million cell updates/sec

Title: US-09-771-161A-93

Perfect score: 232

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Searched: 682709 seqs, 277475446 residues

Word size: 20

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Database :

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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	97.8	2501	4	US-09-920-663-3
2	227	97.8	2502	4	US-09-069-023-2
3	185	79.7	1060	4	US-09-023-655-684
4	128	55.2	1820	4	US-09-099-041A-3
5	128	55.2	1820	4	US-09-245-281-3
6	128	55.2	1820	4	US-09-207-359B-3
7	128	55.2	1620	4	US-09-340-620A-3
8	128	55.2	1620	4	US-09-865-364-3
9	128	55.2	1931	3	US-09-019-942-2
10	128	55.2	1931	4	US-09-099-041A-1
11	128	55.2	1931	4	US-09-245-281-1
12	128	55.2	1931	4	US-09-470-271-2

13	128	55.2	1931	4	US-09-207-359B-1	Sequence 1, Appli
14	128	55.2	1931	4	US-09-340-620A-1	Sequence 1, Appli
15	128	55.2	1931	4	US-09-865-364-1	Sequence 1, Appli
16	128	55.2	1931	4	US-09-748-537-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-920-663-3  
; Sequence 3, Application US/09920663  
; Patent No. 6426221  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION  
; FILE REFERENCE: RTS-0233  
; CURRENT APPLICATION NUMBER: US/09/920,663  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 3  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (225)...(1847)  
US-09-920-663-3

Alignment Scores:	2.61e-231	Length:	2501
Pred. No.:	227.00	Matches:	227
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	97.84%	Indels:	0
Query Match:	4	Gaps:	0
DB:			

US-09-771-161A-93 (1-232) x US-09-920-663-3 (1-2501)

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DB	1164	TTACAGAGTGTTCCTCAAGTGCCTTCCATATGTGACAGAGAAATGAATTAATCTCTG	1223
QY	26	AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	45
DB	1224	AACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA	1283
QY	46	AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	65
DB	1284	AATAGTGGTTCCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT	1343
QY	66	SerAspLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer	85
DB	1344	TCTAGAAAGCTCAAGACTGTTATTTATGAAGTGCATCATGTCTCGAATTCAGT	1403
QY	86	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro	105
DB	1404	TGGATAGCACCATTCTGGTTCTCAAGGGCTGCATTCTGTGATCACAAGACCCTCA	1463
QY	106	CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro	125
DB	1464	TGCTCTTCAGCAATAATAATCACTCTCACTGAGGAAACTCAGAACGCTCTGCAGCCT	1523
QY	126	GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu	145
DB	1524	GGTATAGCCACAGTGGATCCAGACAAAGGAGACATTTGTGAACCAATGACAGAA	1583
QY	146	AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp	165
DB	1584	GCCTGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGGAC	1643
QY	166	TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr	185

Db 1644 TATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACACT 1703  
QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
Db 1704 ACTGACATCCAGGAGGAAGAAATTGCGAAGTTATAGTACAAATAATGAAAGATACAAA 1763  
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225  
Db 1764 CAAATGGGCTTCAGCCTTACCGGAAATACCTTGTTCTAGATCACCATCTTTAAAT 1823  
QY 226 LeuLeuGlnAsnLysSerMet 232  
Db 1824 TTACTTCAAAATAAAAGCATG 1844  
RESULT 2  
US-09-069-023-2  
; Sequence 2, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2502  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-069-023-2  
Alignment Scores:  
Pred. No.: 2,61e-231 Length: 2502  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
DB: 4 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-069-023-2 (1-2502)  
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
Db 1165 TTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAAGAAATGGAAATATCTCTG 1224  
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
Db 1225 AACATACCTGTAATCATGTGTCACCAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1284  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
Db 1285 AATAGTGTTTCTCTGAAACTTCAAGCTCCCTGCGAGCTCCTCAAGCAATGATTTTITA 1344  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
Db 1345 TCTAGAAAGCTCAAGACTGTATTTATAGAGCTGCATCCTCTCTGGAATCAGT 1404  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
Db 1405 TGGGATAGCACCATTCTGGTTTCTCAAGGGCTGCTTCTGTGATCAAGAGCCTCCA 1464  
QY 106 CysSerSerAlaIleLeuAsnProLeuSerThrIleGlnSerGluArgLeuGlnPro 125  
Db 1465 TGCTCTTTCAGCAATTAATAATCCACTCTCACTCGAGGAACCTCAGAACGTTCTGACGCT 1524  
QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
Db 1525 GGTATAGCCCGAGCTGATCCAGAGCAAAAGGAGGAGACATTTGTGAACCAATGACAGAA 1584

QY 146 AlaCysLysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
Db 1585 GCCTGCTTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAGGAC 1644  
QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
Db 1645 TATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGACACT 1704  
QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
Db 1705 ACTGACATCCAGGAGGAAGAAATTGCGAAGTTATAGTACAAATAATGAAAGATACAAA 1764  
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225  
Db 1765 CAAATGGGCTTCAGCCTTACCGGAAATACCTTGTTCTAGATCACCATCTTTAAAT 1824  
QY 226 LeuLeuGlnAsnLysSerMet 232  
Db 1825 TTACTTCAAAATAAAAGCATG 1845  
RESULT 3  
US-09-023-655-684  
; Sequence 684, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 684:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1060 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: MPMGN03  
; CLONE: 445186  
US-09-023-655-684  
Alignment Scores:  
Pred. No.: 4.57e-187 Length: 1060  
Score: 185.00 Matches: 226  
Percent Similarity: 98.69% Conservative: 0

US-09-099-041A-3

Alignment Scores:

Pred. No.: 2,35e-126 Length: 1620

Score: 128.00 Matches: 226

Percent Similarity: 99.12% Conservative: 0

Best Local Similarity: 99.12% Mismatches: 1

Query Match: 55.17% Indels: 2

DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-099-041A-3 (1-1620)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25

DB 940 TTACAGAGTGTTCAGTGCCATTCACCTATGTGCAAGAGAAATGGAATATCTCTG 999

QY 26 AnileProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45

DB 1000 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1059

QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65

DB 1060 AATAGTGTTCCTCGAACTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTTTA 1119

QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85

DB 1120 TCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTCTCTGGAATACACAGT 1179

QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr-Thr-Pr 105

DB 1180 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCAT-TCC 1238

QY 105 OCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125

DB 1239 ATGCTCTTCAGCAATAAATCACTCTCACTCACTGAGGAACTCAGACGCTCTGCAGCC 1298

QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145

DB 1299 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGA 1358

QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuLeuMetLysGluAs 165

DB 1359 AGCCTGCCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGGA 1418

QY 165 pTyrGluLeuValSerThrLysProThrArgThr-SerLysValArgGlnLeuLeuAspTh 185

DB 1419 CTATGACTTGTGTAGTCAAGGCTCAGAGGACCTCAAAAGTCAAGCAATTTACTAGACAC 1478

QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsnL 205

DB 1479 TACTGACATCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1538

QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225

DB 1539 ACAAAATGGGTCTTCAGCCTTACCCGGAATAATCTGTGGTTTCTAGATCACCATCTTTAA 1598

QY 225 nLeuLeuGlnAsnLysSerMet 232

DB 1599 TTTACTTCAAAATAAAGCATG 1620

RESULT 5

US-09-245-281-3

; Sequence 3, Application US/09245281

; Patent No. 6369196

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: 07334/118001

; CURRENT APPLICATION NUMBER: US/09/245,281

; PRIOR FILING DATE: 1999-02-05

; EARLIER APPLICATION NUMBER: US 09/207,359

; EARLIER FILING DATE: 1998-12-08



Qy 225 nLeuLeuGlnAnLysSerMet 232  
 Db 1599 TTTACTTCAAAATAAAAGCATG 1620

RESULT 7  
 US-09-340-620A-3  
 ; Sequence 3, Application US/09340620A  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/340,620A  
 ; CURRENT FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-340-620A-3

Alignment Scores:  
 Pred. No.: 2,35e-126 Length: 1620  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-340-620A-3 (1-1620)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 Db 940 TTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGGAATTTATCTCTG 999

Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1000 AACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1059

Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1060 AATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGGAATTTATCTCTG 1119

Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 Db 1120 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTCTCTGGAATCAGAGT 1179

Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleThr-Thr-Pr 105  
 Db 1180 TGGGATAGCACCATTCTCGAATCTCAAGGGCTGCAATCTGTGATCACAAGACCAT-TCC 1238

Qy 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1239 ATGCTCTTCAGCAATAATAATCACTCTCACTGCAGGAATCAGAACTCAGAGCTCAGCC 1298

Qy 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG 145  
 Db 1299 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGCAACCAATGACAGA 1358

Qy 145 uAlaCysLeuAnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 Db 1359 AGCCTGCCTTAACAGTCGCTAGTGCCTCTGTCCAGGGACTTGCATCATGAAAGAGGA 1418

Qy 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 Db 1419 CTATGAACCTTTGTAGTACCAAGCCTCAAGAGCCTCAAAAGCTCAGACAAATTTACTAGACAC 1478

Qy 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsnLy 205  
 Db 1479 TACTGACATCCAGAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAA 1538

Qy 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225  
 Db 1539 ACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1598

Qy 225 nLeuLeuGlnAnLysSerMet 232  
 Db 1599 TTTACTTCAAAATAAAAGCATG 1620

RESULT 8  
 US-09-865-364-3  
 ; Sequence 3, Application US/09865364  
 ; Patent No. 6613521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/865,364  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-865-364-3

Alignment Scores:  
 Pred. No.: 2,35e-126 Length: 1620  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-865-364-3 (1-1620)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 Db 940 TTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGGAATTTATCTCTG 999

Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1000 AACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1059

Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1060 AATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGGAATTTATCTCTG 1119

Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 Db 1120 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTCTCTGGAATCAGAGT 1179

Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleThr-Thr-Pr 105  
 Db 1180 TGGGATAGCACCATTCTCGAATCTCAAGGGCTGCAATCTGTGATCACAAGACCAT-TCC 1238

Qy 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1239 ATGCTCTTCAGCAATAATAATCACTCTCACTGCAGGAATCAGAACTCAGAGCTCAGCC 1298

Qy 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG 145  
 Db 1299 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGCAACCAATGACAGA 1358

Qy 145 uAlaCysLeuAnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 Db 1359 AGCCTGCCTTAACAGTCGCTAGTGCCTCTGTCCAGGGACTTGCATCATGAAAGAGGA 1418

Db 1239 ATGCTCTTCAGCAATAATAATCACTCACTCACTGAGGAACTCAGAACGCTGCGAGCC 1298  
Qy 125 oGlyileAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145  
Db 1299 TGGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGTGAACCAATGACAGA 1358  
Qy 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
Db 1359 AGCTGCTTTAAACAGTCGCTAGATGCTCTGTCAGGAGCTTTGATCATGAAGAGGA 1418  
Qy 165 pTyrgluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
Db 1419 CTATGAACCTTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAGACAATTTACTAGAC 1478  
Qy 185 rThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
Db 1479 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAA 1538  
Qy 205 sGlnMetGlyLeuGlnProTyrgluIleLeuValValSerArgSerProSerLeuAs 225  
Db 1539 ACAAAATGGGTCTTCAGGCTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1598  
Qy 225 nLeuLeuGlnAsnLysSerMet 232  
Db 1599 TTTACTTCAAAATAAAAGCATG 1620  
RESULT 9  
US-09-019-942-2  
; Sequence 2, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA: US/09/019,942  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1931 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-09-019-942-2  
Alignment Scores: 2,78e-126 Length: 1931  
Pred. No.: 128.00 Matches: 226  
Score:

Percent Similarity: 99.12% Conservative: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 3 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-019-942-2 (1-1931)  
Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
Db 1153 TTACAGAGTGTTCAGAGTCCCATTCACCTATGTGACAGAGAAATGGAATTTATCTCTG 1212  
Qy 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
Db 1213 AACATACCTGTAAATCATGTCACCAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
Qy 46 AsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
Db 1273 AATAGTGGTTCCTCGAACTTCAAGGTCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1332  
Qy 66 SerArgLysAlaGlnAspCysTyrgluMetLysLeuHisHisCysProGlyAsnHisSer 85  
Db 1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTGGAATTCACAGT 1392  
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105  
Db 1393 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATCTCTGTGATCACAAGACCAT-TCC 1451  
Qy 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
Db 1452 ATGCTCTTTCAGCAATTAATTAATCCACTCTCACTGCAGGAACTCAGACCTGTGAGCC 1511  
Qy 125 oGlyileAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145  
Db 1512 TGCTATAGCCAGCAGCTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGA 1571  
Qy 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
Db 1572 AGCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGGA 1631  
Qy 165 pTyrgluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
Db 1632 CTATGAACCTTGTAGTACCAAGCTCAAGACCTCAAAAGTCAGACAATTTACTAGACAC 1691  
Qy 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
Db 1692 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAA 1751  
Qy 205 sGlnMetGlyLeuGlnProTyrgluIleLeuValValSerArgSerProSerLeuAs 225  
Db 1752 ACAAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1811  
Qy 225 nLeuLeuGlnAsnLysSerMet 232  
Db 1812 TTTACTTCAAAATAAAAGCATG 1833  
RESULT 10  
US-09-099-041A-1  
; Sequence 1, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA



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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-099-041A-1

Alignment Scores:
Pred. No.:      2,78e-126      Length:      1931
Score:          128.00         Matches:      226
Percent Similarity: 99.12%      Conservative: 0
Best Local Similarity: 99.12%      Mismatches:  1
Query Match:      55.17%      Indels:      2
DB:              4           Gaps:          0

US-09-771-161A-93 (1-232) x US-09-099-041A-1 (1-1931)

QY      6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
Db      1153 TTACAGAGTGTTCAGTGCCTTCACTTATGTAAGAGGAAATGGAATTTATCTCTG 1212

QY      26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db      1213 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272

QY      46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db      1273 AATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1332

QY      66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db      1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTCGTGGAAATCACAGT 1392

QY      86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105
Db      1393 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTATCACAAGACCAT-TCC 1451

QY      105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db      1452 ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTTCGAGCC 1511

QY      125 oGlyIleAlaGlnInTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db      1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGA 1571

QY      145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAs 165
Db      1572 AGCCTGCCTTACCAGTCCGTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAGGA 1631

QY      165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db      1632 CTATGAACCTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1691

QY      185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205
Db      1692 TACTGACATCCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAA 1751

QY      205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225
Db      1752 ACAAATGGGTCTTCAGCCCTTACCCGGAATACCTTGTGGTTCTTAGATCACCATCTTTAA 1811

QY      225 nLeuLeuGlnAsnLysSerMet 232
Db      1812 TTACTTCAAAATAAAAGCATG 1833

RESULT 11
US-09-245-281-1
; Sequence 1, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
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Qy 225 nLeuLeuGlnAsnLysSerMet 232
Db 1812 TTTACTTCAAAATAAAAGCATG 1833

RESULT 12
US-09-470-271-2
; Sequence 2, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-470-271-2

Alignment Scores:
Pred. No.: 2,78e-126 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-470-271-2 (1-1931)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
Db 1153 TTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAGAGAAATGGAAATTATCTCTG 1212

Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1213 AACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGATCTCTCAGCTCCATGAA 1272

Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1273 AATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCAGCTCCTCAAGACAATGATTTTAA 1332

Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db 1333 TCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCTGGAATTCACAGT 1392
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Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105
Db 1393 TGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCATTCTGTGATCACAAGACCAT-TCC 1451

Qy 105 oCysSerSerAlaIleAsnProIleSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db 1452 ATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCTGCAGCC 1511

Qy 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145
Db 1512 TGGTATAGCCACGACGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAATATGACAGA 1571

Qy 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db 1572 AGCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGGA 1631

Qy 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuaspTh 185
Db 1632 CTATGAACCTTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTTACTAGACAC 1691

Qy 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205
Db 1692 TACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAGATACAA 1751

Qy 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
Db 1752 ACAATGGGTCTTCAGCCTTACCCGGAATACTTTGTGGTTTCTAGATCACCATCTTTAA 1811

Qy 225 nLeuLeuGlnAsnLysSerMet 232
Db 1812 TTTACTTCAAAATAAAAGCATG 1833

RESULT 13
US-09-207-359B-1
; Sequence 1, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-207-359B-1

Alignment Scores:
Pred. No.: 2,78e-126 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-207-359B-1 (1-1931)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
Db 1153 TTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAGAGAAATGGAAATTATCTCTG 1212

Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1213 AACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGATCTCTCAGCTCCATGAA 1272

Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1273 AATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCAGCTCCTCAAGACAATGATTTTAA 1332

Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db 1333 TCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCTGGAATTCACAGT 1392
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QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1213 AACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
QY 46 AsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1273 AATAGTGGTCTCTCGAACTTCAAGTCCCTCCAGCTCCCTCAAGACAAATGATTTTAA 1332  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
DB 1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGTCTGGAATCACAGT 1392  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
DB 1393 TGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCAATCTGTGATCACAAGACCAT-TCC 1451  
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
DB 1452 ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCC 1511  
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
DB 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGA 1571  
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
DB 1572 AGCCTGCCTTAAACCAAGTCGTAGTCCCTTCTGTCAGGGACTTGTATCATGAAAGAGA 1631  
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
DB 1632 CTATGAACCTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAAATTTACTAGACAC 1691  
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205  
DB 1692 TACTGACATCCAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1751  
QY 205 sGlnMetGlyLeuGlnProTyProGluIleLeuValSerArgSerProSerLeuAs 225  
DB 1752 ACAAATGGGTCTTACGCTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTTAA 1811  
QY 225 nLeuLeuGlnAsnLysSerMet 232  
DB 1812 TTTACTTCAAAATAAAGCATG 1833

## RESULT 14

US-09-340-620A-1  
; Sequence 1, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-09-340-620A-1

Alignment Scores:  
Pred. No.: 2,78e-126 Length: 1931  
Score: 128.00 Matches: 226  
Percent Similarity: 99.12% Conservative: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 4 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-340-620A-1 (1-1931)  
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
DB 1153 TTACAGAGTGTTCCTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATTAATCTCTG 1212  
QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1213 AACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1273 AATAGTGGTCTCTCGAACTTCAAGGTCCCTGCCAGCTCTCTCAAGACAAATGATTTTAA 1332  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
DB 1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGTCTGGAATCACAGT 1392  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
DB 1393 TGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCAATCTGTGATCACAAGACCAT-TCC 1451  
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
DB 1452 ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCC 1511  
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
DB 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGA 1571  
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
DB 1572 AGCCTGCCTTAAACCAAGTCGTAGTCCCTTCTGTCAGGGACTTGTATCATGAAAGAGA 1631  
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
DB 1632 CTATGAACCTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAAATTTACTAGACAC 1691  
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205  
DB 1692 TACTGACATCCAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1751  
QY 205 sGlnMetGlyLeuGlnProTyProGluIleLeuValSerArgSerProSerLeuAs 225  
DB 1752 ACAAATGGGTCTTACGCTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTTAA 1811  
QY 225 nLeuLeuGlnAsnLysSerMet 232  
DB 1812 TTTACTTCAAAATAAAGCATG 1833  
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US-09-865-364-1  
; Sequence 1, Application US/09865364  
; Patent No. 6613521  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/865,364  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17

Job time : 116 secs

;; PRIOR APPLICATION NUMBER: US 09/019,942  
;; PRIOR FILING DATE: 1998-02-06  
;; NUMBER OF SEQ ID NOS: 47  
;; SOFTWARE: Fast-Seq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 1931  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (214)...(1833)  
US-09-865-364-1

Alignment Scores:  
Pred. No.: 2,78e-126 Length: 1931  
Score: 128.00 Matches: 226  
Percent Similarity: 99.12% Conservatives: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-865-364-1 (1-1931)

Qy	6	LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu	25
Db	1153	TTACAGAGTCTTTCAAGTGCATTACCTATGTGACAAAGAGAAATGGAATTATCTCTG	1212
Qy	26	AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	45
Db	1213	AACATCCTGTAATCATGTCCACAGAGGAATCAITGGATCCTCTCAGCTCCATGAA	1272
Qy	46	AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	65
Db	1273	AATAGTGGTTCCTCGAACTTCAAGCTCCCTGCCAGCTCCTCAAGACAAATGATTTT	1332
Qy	66	SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer	85
Db	1333	TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCTGGAAATCAGT	1392
Qy	86	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr	105
Db	1393	TGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTATCAAGACCAT-TCC	1451
Qy	105	OCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr	125
Db	1452	ATGCTTTACGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACGCTCGCAGCC	1511
Qy	125	oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl	145
Db	1512	TGSTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACAG	1571
Qy	145	uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs	165
Db	1572	AGCTGGCTTTACAGTCGGTAGTGCCTTCTGTCCAGGACTTGATCATGAAGAGGA	1631
Qy	165	pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuAspThr	185
Db	1632	CTATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACAC	1691
Qy	185	rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy	205
Db	1692	TACTGACATCCAAGGAGAAGAAATTGGCCAAAGTTATAGTACAAAATTTGAAGATACAA	1751
Qy	205	sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs	225
Db	1752	ACAAATGGGTCTTCAGGCTTACCCGGGAATACTTGTGGTTCTTAGATCACCACCTTTAAA	1811
Qy	225	nLeuLeuGlnAsnLysSerMet	232
Db	1812	TTTACTTCAAAATAAAAGCATG	1833

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 12:50:59 ; Search time 417 Seconds  
(without alignments)  
2080.611 Million cell updates/sec

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

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Word size: 20

Total number of hits satisfying chosen parameters: 15  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

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Database : Published Applications NA:

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- 2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:
- 3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq:
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- 11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	227	97.8	2501	10	US-09-981-397A-13	Sequence 13, Appl
4	227	97.8	2709	9	US-09-925-301-173	Sequence 173, App
5	128	55.2	1620	9	US-09-728-721-3	Sequence 3, Appli
6	128	55.2	1620	13	US-10-105-931-3	Sequence 3, Appli
7	128	55.2	1620	13	US-10-118-984-3	Sequence 3, Appli
8	128	55.2	1620	14	US-10-235-981-3	Sequence 3, Appli
9	128	55.2	1931	9	US-09-748-537-2	Sequence 2, Appli
10	128	55.2	1931	9	US-09-728-721-1	Sequence 1, Appli
11	128	55.2	1931	13	US-10-133-780-2	Sequence 2, Appli
12	128	55.2	1931	13	US-10-105-931-1	Sequence 1, Appli
13	128	55.2	1931	13	US-10-118-984-1	Sequence 1, Appli
14	128	55.2	1931	14	US-10-235-981-1	Sequence 1, Appli
15	120	51.7	491	10	US-09-918-995-20565	Sequence 20565, A

ALIGNMENTS

RESULT 1  
US-09-771-161A-2  
; Sequence 2, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1669  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: (1)..(1669)  
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'  
US-09-771-161A-2

Alignment Scores:  
Pred. No.: 8.03e-227 Length: 1669  
Score: 232.00 Matches: 232  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-771-161A-2 (1-1669)

QY	1	MetTyrSerLeuGlnLeuGlnSerValSerAlaIleHisLeuCysAspLysLys	20
DB	320	ATGTATTATTACAGTTACAGAGTGTTCAGTGCCATTCCTATGTGACAGAGAAA	379
QY	21	MetGluLeuSerLeuAsnIleProValAnHisGlyProGlnGluSerCysGlySer	40
DB	380	ATGGAATTATCTCTGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGATCC	439
QY	41	SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGln	60
DB	440	TCTCAGCTCCATGAAATAGTGGTTCTCTCTGAAACTTCAAGGTCCCTCCAGCTCTCAA	499
QY	61	AspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCys	80
DB	500	GACAAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCTGT	559

QY 81 ProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAsp 100  
Db 560 CTTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGGAT 619  
QY 101 HisIysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSer 120  
Db 620 CACAAGACCACTCCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACTCA 679  
QY 121 GluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleVal 140  
Db 680 GAAGCTGTGAGCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTG 739  
QY 141 AsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeu 160  
Db 740 AACCAATGACAGAGGCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTG 799  
QY 161 IleMetLysGluAspTyrGluLeuValSerThrIysProThrArgThrSerLysValArg 180  
Db 800 ATCATGAAGAGGACTATGAATGTTAGTACCAAGCCTACAAAGGACCTCAAAAGTCAGA 859  
QY 181 GlnLeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLys 200  
Db 860 CAATTACTAGACACTACTGATCCAGAGGAAGAATTTGCCAAAGTTATAGTACAAAA 919  
QY 201 LeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluLeuLeuValSerArg 220  
Db 920 TTCAAGATAAACAACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGA 979  
QY 221 SerProSerLeuAsnLeuGlnAsnLysSerMet 232  
Db 980 TCACCATCTTTAAATTTACTTCAAAATAAAAGCATG 1015  
RESULT 2  
US-10-342-887-957  
; Sequence 957, Application US/10342887  
; Publication No. US20040058340A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van 't Veer, Laura Johanna  
; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 60/298,918  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/380,710  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 957  
; LENGTH: 1623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-342-887-957  
Alignment Scores:  
Pred. No.: 9,91e-222 Length: 1623  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
DB: 12 Gaps: 0  
US-09-771-161A-93 (1-232) x US-10-342-887-957 (1-1623)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25

Db 940 TTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAAAATGGAATTTATCTCTG 999  
QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
Db 1000 AACATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1059  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
Db 1060 AATAGTGGTTCCTCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1119  
QY 66 SerArgGlyAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
Db 1120 TCTAGAAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGCTCTGGAATCAAGT 1179  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105  
Db 1180 TGGGACAGACCCANTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCCTCCA 1239  
QY 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
Db 1240 TGCTCTTACGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCCT 1299  
QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
Db 1300 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACAGAA 1359  
QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
Db 1360 GCCTGCTTAAACGATCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGGAC 1419  
QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
Db 1420 TATGAACCTTGTAGTACCAAGCCTCAGAGCCTCAAAAGTCAAGACAATTTACTAGACACT 1479  
QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsnLys 205  
Db 1480 ACTGACATCCAAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1539  
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225  
Db 1540 CAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTAAT 1599  
QY 226 LeuLeuGlnAsnLysSerMet 232  
Db 1600 TTAATTTCAAAATAAAAGCATG 1620  
RESULT 3  
US-09-981-397A-13  
; Sequence 13, Application US/09981397A  
; Publication No. US20030082519A1  
; GENERAL INFORMATION:  
; APPLICANT: Axxima Pharmaceuticals AG  
; APPLICANT: Schubart, Daniel  
; APPLICANT: Habenberger, Peter  
; APPLICANT: Stein-Gerlach, Matthias  
; APPLICANT: Bevec, Dorian  
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
; TITLE OF INVENTION: Inhibition  
; FILE REFERENCE: AXM-004.1 US  
; CURRENT APPLICATION NUMBER: US/09/981,397A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/240,750  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-981-397A-13  
Alignment Scores:

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Pred. No.: 1.47e-221 Length: 2501
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.84% Indels: 0
DB: 10 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-981-397A-13 (1-2501)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
Db 1164 TTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAGAGAAATGGAATTAATCTCTG 1223
Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1224 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1283
Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1284 AATAGTGGTTCCTCGAACTTCAAGTCCCTGCGAGCTCCTCAAGACAAATGATTTTAA 1343
Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db 1344 TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCGAATACACAGT 1403
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrPro 105
Db 1404 TGGGATAGCACCATTTCTGGTTCTCAAGGGGTGCATTTCTGTGATCACAAGACCCTCCA 1463
Qy 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
Db 1464 TGCCTCTTACAGCAATTAATAATCACTCTCACTGAGGAACTCAGAAAGCTCTGAGGCT 1523
Qy 126 GlyIleAlaGlnGlnTriPleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
Db 1524 GGTATAGCCAGAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACAAATGACAGAA 1583
Qy 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
Db 1584 GCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGCACTTGATCATGAAAGAGGAC 1643
Qy 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
Db 1644 TATGAACCTTGTATGACCAAGCTCAAGGACCTCAAAAGTCTGATCAACAAATTAACACT 1703
Qy 186 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
Db 1704 ACTGATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATTAACAAA 1763
Qy 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225
Db 1764 CAAATGGGTCTTCAGCCTTACCCTGGAATATCTTGTGGTTCTAGATCACCATCTTTAAAT 1823
Qy 226 LeuLeuGlnAsnLysSerMet 232
Db 1824 TTACTTCAAAATAAAGCATG 1844

RESULT 4
US-09-925-301-173
; Sequence 173, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 173
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2595)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2622)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2659)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2670)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-173

Alignment Scores:
Pred. No.: 1.58e-221 Length: 2709
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.84% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-925-301-173 (1-2709)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
Db 1206 TTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAGAGAAATGGAATTAATCTCTG 1265
Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1266 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1325
Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1326 AATAGTGGTTCCTCGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1385
Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLysLeuHisCysProGlyAsnHisSer 85
Db 1386 TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAATACACAGT 1445
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrPro 105
Db 1446 TGGGATAGCACCATTTCTGGATCTCAAGGGGTGCATTTCTGTGATCACAAGACCCTCCA 1505
Qy 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
Db 1506 TGCTCTTCAGCAATTAATAATCCACTCTCACTGAGGAACTCAGAAAGCTCTGAGGCT 1565
Qy 126 GlyIleAlaGlnGlnTriPleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
Db 1566 GGTATAGCCAGAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACAAATGACAGAA 1625
Qy 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
Db 1626 GCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGCACTTGATCATGAAAGAGGAC 1685
Qy 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
Db 1686 TATGAACCTTGTATGACCAAGCTCAAGGACCTCAAAAGTCTGATCAACAAATTAACACT 1745
Qy 186 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
Db 1746 ACTGATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATTAACAAA 1805
Qy 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225
Db 1806 CAAATGGGTCTTCAGCCTTACCCTGGAATATCTTGTGGTTCTAGATCACCATCTTTAAAT 1865
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QY 226 LeuLeuGlnAsnLysSerMet 232  
 |||||  
 Db 1866 TTACTTCARATTAAGCATG 1886  
 |||||  
 RESULT 5  
 US-09-728-721-3  
 ; Sequence 3, Application US/09728721  
 ; Patent No. US20020061845A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/728,721  
 ; CURRENT FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 09/340,620  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-728-721-3  
 Alignment Scores:  
 Pred. No.: 1,07e-120 Length: 1620  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 9 Gaps: 0  
 US-09-771-161A-93 (1-232) x US-09-728-721-3 (1-1620)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 |||||  
 Db 940 TTACAGAGTGTTCCTGAACTTCAAGTCCCTGCAAGCAATGATTTTCTG 999  
 |||||  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 |||||  
 Db 1000 AACATACCTGTAATCATGTGTCACAAAGAGATCATGTGATCCTCTCAGCTCCATGAA 1059  
 |||||  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 |||||  
 Db 1060 AATAGTGGTTCCTGAACTTCAAGTCCCTGCAAGCAATGATTTTCTG 1119  
 |||||  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 |||||  
 Db 1120 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCGAAATCAGAT 1179  
 |||||  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrThr-Pr 105  
 |||||  
 Db 1180 TGGATAGACCATTTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCAT-TCC 1238  
 |||||  
 QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 |||||  
 Db 1239 ATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCC 1298  
 |||||  
 QY 125 oGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
 |||||  
 Db 1299 TGGTATAGCCAGCAGTGGATCCAGACCAAGGAAGACATTTGTGAACCAATGCAGAA 1358  
 |||||  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGluAs 165  
 |||||  
 Db 1359 AGCCTGCCTTAACAGTCGCTAGATGCCCCTCTGTCCAGGGACTTGTATCATGAAGAGGA 1418  
 |||||  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 |||||

Db 1419 CTATGAACCTGTAGTACCAGCCTACAAGGACCTCAAAGTACAGACAATTACTAGACAC 1478  
 |||||  
 QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspPheNly 205  
 |||||  
 Db 1479 TACTGACATCCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAA 1538  
 |||||  
 QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225  
 |||||  
 Db 1539 ACMAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTTAGATCACCATCTTTAA 1598  
 |||||  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 |||||  
 Db 1599 TTACTTCAAAATAAAAGCATG 1620  
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 RESULT 6  
 US-10-105-931-3  
 ; Sequence 3, Application US/10105931  
 ; Publication No. US20020150987A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE REFERENCE: 07334-076001  
 ; CURRENT APPLICATION NUMBER: US/10/105,931  
 ; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-105-931-3  
 Alignment Scores:  
 Pred. No.: 1,07e-120 Length: 1620  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 13 Gaps: 0  
 US-09-771-161A-93 (1-232) x US-10-105-931-3 (1-1620)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 |||||  
 Db 940 TTACAGAGTGTTCCTGAACTTCAAGTCCCTGCAAGCAATGATTTTCTG 999  
 |||||  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 |||||  
 Db 1000 AACATACCTGTAATCATGTGTCACAAAGAGATCATGTGATCCTCTCAGCTCCATGAA 1059  
 |||||  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 |||||  
 Db 1060 AATAGTGGTTCCTGAACTTCAAGTCCCTGCAAGCAATGATTTTCTG 1119  
 |||||  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 |||||  
 Db 1120 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCGAAATCAGAT 1179  
 |||||  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrThr-Pr 105  
 |||||  
 Db 1180 TGGATAGACCATTTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCAT-TCC 1238  
 |||||  
 QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 |||||  
 Db 1239 ATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCC 1298  
 |||||  
 QY 125 oGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
 |||||  
 Db 1299 TGGTATAGCCAGCAGTGGATCCAGACCAAGGAAGACATTTGTGAACCAATGCAGAA 1358  
 |||||  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGluAs 165  
 |||||  
 Db 1359 AGCCTGCCTTAACAGTCGCTAGATGCCCCTCTGTCCAGGGACTTGTATCATGAAGAGGA 1418  
 |||||  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 |||||



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Db 1299 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACAGA 1358
Qy 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db 1359 AGCCTGCCTTACCAGTCCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGA 1418
Qy 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db 1419 CTATGAACCTTGTATGACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1478
Qy 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsnLys 205
Db 1479 TACTGACATCCAAAGGAGAAGATTTCGCAAGATTATAGTACAAAATTGAAAGATAACAA 1538
Qy 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
Db 1539 ACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1598
Qy 225 nLeuLeuGlnAsnLysSerMet 232
Db 1599 TTTACTTCAAAATAAAAGCATG 1620

RESULT 7
US-10-118-984-3
; Sequence 3, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US/09/245,281
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-02-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-12-08
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-02-06
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-984-3

Alignment Scores:
Pred. No.: 1,07e-120 Length: 1620
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-118-984-3 (1-1620)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
Db 940 TTACAGAGTGTTCAGAGTGCCATTCACCTATGTGACAAAGAAATGGAATATCTCTG 999
Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1000 AACATACCTGTTAAATCATGTGTCACAAAGAGGAATCATGTGGATCCCTCAGTCCATGAA 1059
Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1060 AATAGTGGTTCCTCGAAATCTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTTAA 1119
Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
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Db 1120 TCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCACTGCTCTCGAAATCACAGT 1179
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrThr-Pr 105
Db 1180 TGGGATAGACACCATTTCTGGATCTCAAAGGGCTGCATCTTGATGATCACAAGACCAT-TCC 1238
Qy 105 oCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db 1239 ATGCTCTTTCAGCAATAATAATCCACTCTCAACTCAGGAAACTCAGAACGCTCTGCAGCC 1298
Qy 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db 1299 TGGTATAGCCCAAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACAGA 1358
Qy 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db 1359 AGCCTGCCTTAAACCAAGTCCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGA 1418
Qy 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db 1419 CTATGAACCTTGTATGACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1478
Qy 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsnLys 205
Db 1479 TACTGACATCCAAAGGAGAAGATTTCGCAAGATTATAGTACAAAATTGAAAGATAACAA 1538
Qy 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
Db 1539 ACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1598
Qy 225 nLeuLeuGlnAsnLysSerMet 232
Db 1599 TTTACTTCAAAATAAAAGCATG 1620

RESULT 8
US-10-295-981-3
; Sequence 3, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3

Alignment Scores:
Pred. No.: 1,07e-120 Length: 1620
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-295-981-3 (1-1620)
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QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 Db 940 TTACAGAGTGTTCACAGTGCATTCACATATGTGACAGAGAAATGGATATATCTCTG 999  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1000 AACATACCTGTAATCATGTGTCACAAAGAGGAATCATGTGATCTCTCAGCTCCATGAA 1059  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1060 AATAGTGGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1119  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 Db 1120 TCTAGAAAAGCTCAAGACTGTATTTATGAGCTGCATCTACTGTCTCTGGAATCACAGT 1179  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
 Db 1180 TGGGATAGCACCATTTCTGGATCTCAAAAGGCTGCATTTCTGTGATCACAAAGACCAT-TCC 1238  
 QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1239 ATGCTCTTTCAGCAATAATAATCAACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCC 1298  
 QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145  
 Db 1299 TGGTATAGCCACAGCTGGATCCAGACAAAGGAGAGACATTTCTGAAACCAATGACAGA 1358  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGluAs 165  
 Db 1359 AGCCTGCTTAAACAGTTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAGGA 1418  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 Db 1419 CTATGAACCTTGTATGATACCAAGCTTCAAGAGCTCAAAAGTACAGAAATTTACTAGAC 1478  
 QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
 Db 1479 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAA 1538  
 QY 205 sGlnMetGlyLeuGlnProThrProGluIleLeuValValSerArgSerProSerLeuAs 225  
 Db 1539 ACAAAATGGGTCTTCAGCCTTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1598  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 Db 1599 TTTACTTCAAAATAAAAGCATG 1620  
 RESULT 9  
 US-09-748-537-2  
 ; Sequence 2, Application US/09748537  
 ; Patent No. US20020061833A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; APPLICANT: Chao, Moses V.  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-316001  
 ; CURRENT APPLICATION NUMBER: US/09/748,537  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-748-537-2  
 Alignment Scores:  
 Pred. No.: 1.25e-120 Length: 1931

Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 9 Gaps: 0  
 US-09-771-161A-93 (1-232) x US-09-748-537-2 (1-1931)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 Db 1153 TTACAGAGTGTTCACAGTGCATTCACATATGTGACAGAGAAATGGATATATCTCTG 1212  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1213 AACATACCTGTAATCATGTGTCACAAAGAGGAATCATGTGATCTCTCAGCTCCATGAA 1272  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1273 AATAGTGGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1332  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 Db 1333 TCTAGAAAAGCTCAAGACTGTATTTATGAGCTGCATCTACTGTCTCTGGAATCACAGT 1392  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
 Db 1393 TGGGATAGCACCATTTCTGGATCTCAAAAGGCTGCATTTCTGTGATCACAAAGACCAT-TCC 1451  
 QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1452 ATGCTCTTTCAGCAATAATAATCAACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCC 1511  
 QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145  
 Db 1512 TGGTATAGCCACAGCTGGATCCAGACAAAGGAGAGACATTTGTGAACCAATGACAGA 1571  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGluAs 165  
 Db 1572 AGCCTGCTTAAACAGTTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAGGA 1631  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 Db 1632 CTATGAACCTTGTATGATACCAAGCTTCAAGAGCTTCAAAAGTACAGAAATTTACTAGAC 1691  
 QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
 Db 1692 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAA 1751  
 QY 205 sGlnMetGlyLeuGlnProThrProGluIleLeuValValSerArgSerProSerLeuAs 225  
 Db 1752 ACAAAATGGGTCTTCAGCCTTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1811  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 Db 1812 TTTACTTCAAAATAAAAGCATG 1833  
 RESULT 10  
 US-09-728-721-1  
 ; Sequence 1, Application US/09728721  
 ; Patent No. US20020061845A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/728,721  
 ; CURRENT FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 09/340,620  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942

;; PRIORITY FILING DATE: 1998-02-06  
;; NUMBER OF SEQ ID NOS: 71  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 1931  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (214)...(1833)  
US-09-728-721-1

Alignment Scores:  
Pred. No.: 1.25e-120 Length: 1931  
Score: 128.00 Matches: 226  
Percent Similarity: 99.12% Conservative: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-728-721-1 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
DB 1153 TTACAGAGTGTTCAGTCCCAATTCACCTATGTGACAGAGAAATGAATATCTCTG 1212  
QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1213 AACATACCTGTAAATCAATGCTCCACAGAGAGAAATCATGTGGATCTCTCAGCTCCATGAA 1272  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1273 AATAGTGGTTCCTCGAAACTTCAAGGTCCCTGCCAGCTCCCTCAAGACAATGATTTTAA 1332  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
DB 1333 TCTAGAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTGCTGGAATCACAGT 1392  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105  
DB 1393 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAGACCAT-TCC 1451  
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
DB 1452 ATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAGCC 1511  
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrCl 145  
DB 1512 TGGTATAGCCCGCAGCTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGA 1571  
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
DB 1572 AGCCTGCTTACCAGTCGTAGATGCCCTTCTGTCCAGGACTGTGATCATGAAGAGA 1631  
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValaGlnLeuLeuAspThr 185  
DB 1632 CTATGAACCTGTGTAGTACCAGCTACAGGACCTCAAAAGTCAGACAATTAAGTACAC 1691  
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205  
DB 1692 TACTGACATCCCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAA 1751  
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225  
DB 1752 ACAATGGTCTTACGCTTACCGGAATACTTGTGGTTTCTAGATCACCATCTTTAA 1811  
QY 225 nLeuLeuGlnAsnLysSerMet 232  
DB 1812 TTACTTCAAAATAAAGCATG 1833

RESULT 11

US-10-133-780-2

; Sequence 2, Application US/10133780

;; Publication No. US20020123115A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bertin, John  
;; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
;; DOMAIN POLYPEPTIDES  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson P.C.  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows 95  
;; SOFTWARE: FastSeq for Windows Version 2.0b  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/133,780  
;; FILING DATE: 26-Apr-2002  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/019,942  
;; FILING DATE: 06-FEB-1998  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MeikieJohn, Ph.D., Anita L.  
;; REGISTRATION NUMBER: 35,283  
;; REFERENCE/DOCKET NUMBER: 07334/068001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617/542-5070  
;; TELEFAX: 617/542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1931 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-133-780-2

Alignment Scores:  
Pred. No.: 1.25e-120 Length: 1931  
Score: 128.00 Matches: 226  
Percent Similarity: 99.12% Conservative: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-133-780-2 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
DB 1153 TTACAGAGTGTTCAGTCCCAATTCACCTATGTGACAGAGAAATGAATATCTCTG 1212  
QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1213 AACATACCTGTAAATCAATGCTCCACAGAGAGAAATCATGTGGATCTCTCAGCTCCATGAA 1272  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1273 AATAGTGGTTCCTCGAAACTTCAAGGTCCCTGCCAGCTCCCTCAAGACAATGATTTTAA 1332  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
DB 1333 TCTAGAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTGGAATCACAGT 1392  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105  
DB 1393 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAGACCAT-TCC 1451  
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125

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Db 1452 ATGCTTTTCAGCAATTAATAATCCATCTCACTGAGGAACTCAGAACGCTGCAGCC 1511
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACAGA 1571
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db 1572 AGCCTGCTTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGA 1631
QY 165 pTyrgluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db 1632 CTATGAACTTTAGTACCAAGCTCACAAGACCTCAAAAGTCAGACAATTACTAGACAC 1691
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205
Db 1692 TACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAGATAACAA 1751
QY 205 sGlnMetGlyLeuGlnProTyrgluIleLeuValSerArgSerProSerLeuAs 225
Db 1752 ACAAATGGGCTTCAGCCTTACCGGAAATACTTGGTTCCTAGATCACCATCTTTAA 1811
QY 225 nLeuLeuGlnAsnLysSerMet 232
Db 1812 TTTACTTCAAAATAAAGCAATG 1833

RESULT 12
US-10-105-931-1
; Sequence 1, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 05/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-105-931-1

Alignment Scores:
Pred. No.: 1.25e-120 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-105-931-1 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
Db 1153 TTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTCTG 1212
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1213 AACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1272
QY 46 AnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPheLeu 65
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Db 1273 AATAGTGGTTCCTCGAAACTTCAAGGTCCTGCAGCTCCTCAAGACAATGATTTTAA 1332
QY 66 SerArgLysAlaGlnAspCysTyrrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db 1333 TCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTTGGAATCACAGT 1392
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaLalaPheCysAspHisLysThrThr-Pr 105
Db 1393 TGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCAT-TCC 1451
QY 105 cCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db 1452 ATGCTCTTCAGCAATAATAAATCCACTCTCAACTCCAGGAACTCAGAACGCTCTGCAGCC 1511
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACAGA 1571
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db 1572 AGCCTGCTTTAACAGCTCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACAGA 1631
QY 165 pTyrgluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db 1632 CTATGAACTTTAGTACCAAGCTCACAAGACCTCAAAAGTCAGACAATTACTAGACAC 1691
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205
Db 1692 TACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAGATAACAA 1751
QY 205 sGlnMetGlyLeuGlnProTyrgluIleLeuValSerArgSerProSerLeuAs 225
Db 1752 ACAAATGGGCTTCAGCCTTACCGGAAATACTTGGTTCCTAGATCACCATCTTTAA 1811
QY 225 nLeuLeuGlnAsnLysSerMet 232
Db 1812 TTTACTTCAAAATAAAGCAATG 1833

RESULT 13
US-10-118-984-1
; Sequence 1, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-118-984-1

Alignment Scores:
Pred. No.: 1.25e-120 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
DB: 13 Gaps: 0
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Query Match: 55.17% Indels: 2
DB: 13 Gaps: 0
US-09-771-161A-93 (1-232) x US-10-118-984-1 (1-1931)
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
DB 1153 TTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGAATATCTCTG 1212
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 45
DB 1213 AACATACCTGTTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1272
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB 1273 AATAGTGGTCTCCTGAAATCTCAAGGTCCTCCAGAGGCTCCTCAAGACAATGATTTTAA 1332
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
DB 1333 TCTAGAAAGCTCAAGACGTGTTATTTATGAAGTGCATCTCTCAAGACAATGATTTTAA 1392
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105
DB 1393 TGGGATAGCACCATTTCTGATCTCAAGGGCTGCATTCCTGATCACAAGACCAT-TCC 1451
QY 105 cCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
DB 1452 ATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCC 1511
QY 125 cGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrCl 145
DB 1512 TGGTATAGCCCAAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACAGA 1571
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DB 1632 CTATGAACCTTGTATGATCAAGCTTACAGGACCTCAAGGACCTCAAGGACCAATGACACAC 1691
QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205
DB 1692 TACTGACATCCAAAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1751
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
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; Sequence 1, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-295-981-1
Alignment Scores:
Pred. No.: 1,258-120 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 14 Gaps: 0
US-09-771-161A-93 (1-232) x US-10-295-981-1 (1-1931)
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
DB 1153 TTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGAATATCTCTG 1212
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 45
DB 1213 AACATACCTGTTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1272
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB 1273 AATAGTGGTCTCCTGAAATCTCAAGGTCCTCCAGAGGCTCCTCAAGACAATGATTTTAA 1332
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
DB 1333 TCTAGAAAGCTCAAGACGTGTTATTTATGAAGTGCATCTCTCAAGACAATGATTTTAA 1392
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105
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QY 105 cCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
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QY 125 cGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrCl 145
DB 1512 TGGTATAGCCCAAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACAGA 1571
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGluAs 165
DB 1572 AGCCTGCCTTAACCAAGTCCAGTCCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCC 1631
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
DB 1632 CTATGAACCTTGTATGATCAAGCTTACAGGACCTCAAGGACCTCAAGGACCAATGACACAC 1691
QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205
DB 1692 TACTGACATCCAAAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1751
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
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QY 225 nLeuLeuGlnAsnLysSerMet 232
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US-09-918-995-20565
; Sequence 20565, Application US/09918995
; Publication No. US20030073623A1
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; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20565
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-20565

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Alignment Scores:
Pred. No.: 5.24e-113 Length: 491
Score: 120.00 Matches: 120
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.72% Indels: 0
DB: Gaps: 10

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US-09-771-161A-93 (1-232) x US-09-918-995-20565 (1-491)

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Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
Db 131 TTACAGAGTGTTCAGAGTGCCATTACGCTATGTGACAAAGAGAAATGGAATTTATCTCTG 190
Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 191 AACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 250
Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 251 AATAGTGTTCCTCGTAACCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 310
Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db 311 TCTAGAAAAGCTCAAGACTGTATTATTAAGAGCTGCATCACTGTCTGGAAATCACAGT 370
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105
Db 371 TGGGATAGACCAATTTCTGGATCTCAAAGGGCTGCATTTCTGTATCAAGACCACTCCA 430
Qy 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
Db 431 TGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCCTGAGCCT 490

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Search completed: April 1, 2004, 14:59:43  
Job time : 426 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 12:07:21 ; Search time 2694 Seconds  
(without alignments)  
2571.650 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MSLQLQSVSSAIHLCDKKK.....PEILVVSRSPLNLQNKSM 232

Scoring table:  
OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 20

Total number of hits satisfying chosen parameters: 108

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV=xlh  
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-DB=EST -QFMT=fastap -SUPFIX=oli20p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=quality -THR MIN=20 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CN 1 1 1906 @runat 29032004 124851 19870 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :  
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1: em estba.\*  
2: em esthum.\*  
3: em estin.\*  
4: em estmu.\*  
5: em estov.\*  
6: em estpl.\*  
7: em estro.\*  
8: em htc.\*  
9: gb est1.\*  
10: gb est2.\*  
11: gb htc.\*  
12: gb est3.\*  
13: gb est4.\*  
14: gb est5.\*  
15: em estfun.\*  
16: em estom.\*  
17: em gas hum.\*  
18: em gas inv.\*  
19: em gas pin.\*  
20: em gas vrt.\*  
21: em gas fun.\*  
22: em gas mam.\*  
23: em gas mus.\*  
24: em gas pro.\*  
25: em gas rod.\*  
26: em gas phg.\*  
27: em gas vri.\*  
28: gb gas1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	195	84.1	883	14	CB852764	CB852764 UI-CF-FNO
3	186	80.2	938	13	BQ670832	BQ670832 AGENCOURT
4	184	79.3	656	12	BM973770	BM973770 UI-CF-ECL
5	184	79.3	660	12	BM840808	BM840808 K-EST0117
6	184	79.3	715	14	CB851847	CB851847 UI-CF-FNO
7	184	79.3	734	12	BQ008463	BQ008463 UI-H-ED1-
8	181	78.0	592	9	AI745575	AI745575 WC34112.X
9	178	76.7	852	12	BG757422	BG757422 602711061
10	175	75.4	811	12	BG170405	BG170405 602322736
11	167	72.0	667	13	BQ773811	BQ773811 UI-H-E21-
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13	167	72.0	744	14	CD365404	CD365404 UI-H-F72-
14	165	71.1	672	14	CA314123	CA314123 UI-CF-FNO
15	165	71.1	709	14	CA413941	CA413941 UI-H-E20-
16	165	71.1	1623	29	AY415527	AY415527 Homo sapi
17	161	69.4	647	10	AW960501	AW960501 EST372572
18	154	66.4	1623	29	AY415528	AY415528 Pan trogl
19	153	65.9	636	10	BE551615	BE551615 7a43g06.X
20	153	65.9	812	12	BI257472	BI257472 602367861
21	153	65.9	870	10	BE877822	BE877822 601486392
22	147	63.4	564	12	BM796243	BM796243 K-EST0078
23	145	62.5	606	9	AW085560	AW085560 wy67C04.X
24	144	62.1	479	12	BM855477	BM855477 K-EST0138
25	144	62.1	505	13	EX280487	EX280487 BX280487
26	138	59.5	610	13	BQ623654	BQ623654 UI-H-FG1-
27	137	59.1	423	9	AA574167	AA574167 nl78801.S
28	137	59.1	483	9	AI343247	AI343247 tb94804.X
29	137	59.1	624	14	CD368863	CD368863 UI-H-F71-
30	136	58.6	476	14	CF528565	CF528565 UI-H-BC1-
31	133	57.3	455	9	AI343850	AI343850 qp07401.X
32	130	56.0	828	10	BE875947	BE875947 601486423
33	129	55.6	476	9	AA913804	AA913804 ol35d11.S
34	129	55.6	499	12	BQ011550	BQ011550 UI-H-BC1P
35	128	55.2	496	12	BQ011702	BQ011702 UI-H-BC1P
36	126	54.3	628	12	BQ000991	BQ000991 UI-H-DH1-
37	116	50.0	350	10	BF754627	BF754627 QV3-CT055
38	116	50.0	432	9	AA723533	AA723533 zg73g08.S
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43	108	46.6	615	9	AI801150	AI801150 t085h04.X
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ALIGNMENTS

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DEFINITION mRNA sequence.  
ACCESSION BG393551  
VERSION BG393551.1 GI:13286999  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 883)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM10471 row: e column: 12  
High quality sequence stop: 767.  
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Pred. No.: 1,78e-193 Length: 883  
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Query Match: 87.93% Indels: 0  
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QY 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148  
DB 302 CAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGGCTGCTT 361  
QY 149 AsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168  
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QY 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 188  
DB 422 GTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACATTTACTAGACACTACTGACATC 481  
QY 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208

Db 482 CAAGGAGAAGAAATTTGCCAAGTTATAGTACAAAATTCGAAGATACAAACAAATGGGT 541  
QY 209 LeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsnLeuGln 228  
Db 542 CTTGAGCCTTACCCGGAATACCTTGGTTCCTAGATCACCATCTTTAAATTTACTTCAA 601  
QY 229 AsnLysSerMet 232  
Db 602 AATAAAGCATG 613  
RESULT 2  
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VERSION CB852764  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics ([www.resgen.com](http://www.resgen.com)) or from Open Biosystems ([www.openbiosystems.com](http://www.openbiosystems.com)).  
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POLYA=Yes.  
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Alignment Scores:  
Pred. No.: 1,42e-184 Length: 683  
Score: 195.00 Matches: 195  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 84.05% Indels: 0  
DB: 14 Gaps: 0



```

US-09-771-161A-93 (1-232) x CB852764 (1-683)
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QY 44 HisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsp 63
Db 601 CATGAAATAGTGGTTCTCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGAT 542
QY 64 PheLeuSerArgGlyAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsn 83
Db 541 TTTTATCTAGAAAAGCTCAAGACTGTATTTATGAACTGCATCCTGCTGGAAT 482
QY 84 HisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 103
Db 481 CACAGTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTATCACAAGACC 422
QY 104 ThrProCysSerSerAlaIlelelelelelelelelelelelelelelelelelele 123
Db 421 ACTCCATGCTCTCTAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGTTTG 362
QY 124 GlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMet 143
Db 361 CAGCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAATG 302
QY 144 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleleMetLys 163
Db 301 ACAGAGCTGCTGTTAACCACTGCTAGATGCCCTCTCTGTCAGGACTTGATCATGAA 242
QY 164 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 183
Db 241 GAGGACTATGAATGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAAGCAATTACTA 182
QY 184 AspThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAsp 203
Db 181 GACACTACTGATCCAGGAGAAATTTGCCAAGTTATAGTCAAAATTTGAAAGAT 122
QY 204 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValVal 218
Db 121 ACAAACAATGGCTTTCAGCTTACCCGGAATACTTGTGTT 77

RESULT 3
LOCUS BM973770
DEFINITION AGENCOURT_8191703 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6257019
5', mRNA sequence.
ACCESSION BM973770
VERSION BM973770.1 GI:21781666
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2410 row: k column: 04
High quality sequence stop: 659.
Location/Qualifiers
i. .938
/organism="Homo sapiens"

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/mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6257019"  
 /tissue\_type="epidermoid carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 102"  
 /note="Organ: salivary gland; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed  
 by Ling Hong in the laboratory of Gerald M. Rubin  
 (University of California, Berkeley) using ZAP-cDNA  
 synthesis kit (Stratagene) and Superscript II RT (Life  
 Technologies). Note: this is a NIH\_MGC Library."

Alignment Scores:  
 Pred. No.: 1,99e-175 Length: 938  
 Score: 186.00 Matches: 199  
 Percent Similarity: 99.50% Conservative: 0  
 Best Local Similarity: 99.50% Mismatches: 1  
 Query Match: 80.17% Indels: 1  
 DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x BQ670832 (1-938)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 Db 139 TTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAGAAATGAAATATCTCTG 198  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 199 AACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 258  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 259 AATAGTGGTTCCTCGAAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATTTTTTA 318  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 Db 319 TCTAGAAAAGCTCAAGACTGTTATTTTAAAGCTGCATCCTCTCTGGAATCACAGT 378  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 Db 379 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCTCTGTGATCACAAGACCCTCCA 438  
 QY 106 CysSerSerAlaIle 125  
 Db 439 TGCTCTTACGCAATTAATATCCACTCTCACTGAGGAACTCAGAACTCTGAGCCT 498  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 Db 499 GGTATAGCCAGCAGCTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAGAA 558  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaAlaPheCysAspHisLysThrPro 165  
 Db 559 GCCTGCCTTAACCACTGCTAGATCCCTCTCTGTCAGGAGCTTGCATCATGAAAGAGGAC 618  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 Db 619 TATGAACCTTTGTAGTACCAGCTCAAGGACCTCAAAAGTCAAGCAATATTACTAGACAT 678  
 QY 186 ThrAspIleGln-GlyGluGluPheAlaLysValIleValGlnLysLysLysAspAsn 204  
 Db 679 ACTGACATCCAGGAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAAC 736

RESULT 4  
 BM973770/c  
 LOCUS BM973770  
 DEFINITION UI-CF-EC1-ach-1-07-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone  
 UI-CF-EC1-ach-1-07-0-UI 3', mRNA sequence.  
 ACCESSION BM973770  
 VERSION BM973770.1 GI:19591361

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Bernaldo.M.F., Lennon.G. and Soares.M.B.
Normalizaton and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.
FEATURES Location/Qualifiers
source 1..656
/mol_type="mRNA"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-ach-1-07-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/name="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bernaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTGCCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCCTTAC"
ORIGIN
Alignment Scores: 1.41e-173 Length: 656
Pred. No.: 184.00 Matches: 184
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 79.31% Gaps: 0
DB: 12
US-09-771-161A-93 (1-232) x BM973770 (1-656)
Oy 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 68
Db 625 TCTCTGGAACCTTCAGGTCCTGCCAGCTCTCTCAAGACATGATTTTATCTAGAAA 566
69 AlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAspSer 88
565 GCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCTGGAAATCACAGTTGGGATAGC 506
89 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSer 108
505 ACCATTTCGATCTCAAGAGGCTGCTTCTGTGATCAAGACCACCTCCATGCTCTTCA 446
109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128
445 GCATTAATAATCCACTCTCAACTGCAGAAATCAGAACTGAGAGCTGGTATAGCC 386
129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148
385 CAGCAGTGCATCCAGAGCAAAAGGGAAGACATTGTGAACAAATGACAGAGCGTCGCTT 326
149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168
325 AACCAAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGACTATGAACTT 266
169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 188
265 GTTAGTACCAAGCTCAAGAGACCTCAAAAGTCAGACAACTACTAGACACTACTGACATC 206
189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208
205 CAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAAGATAACAAACAAATGG 146
209 LeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsnLeuLeuGln 228
145 CTTCAAGCTTACCCGGAATATCTTGTGGTTTCTAGATCCACTCTTTAAATTTACTTCAA 86
229 AsnLysSerMet 232
85 AATAAAGCATG 74
RESULT 5
BM840808
LOCUS K-EST0117952 S12SNU216 Homo sapiens cDNA clone S12SNU216-38-G08 5',
DEFINITION mRNA sequence.
ACCESSION BM840808.1 GI:19197217
VERSION BM840808
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 38 row: G column: 08
High quality sequence stop: 660.
FEATURES Location/Qualifiers
source 1..660
/mol_type="mRNA"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S12SNU216-38-G08"
/sex="F"
/tissue_type="Lymph node"
/cell_type="Epithelial"
/cell_line="SNU-216"

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/lab\_host="Top10P"  
 /clone\_lib="S12NU216"  
 /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;  
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10P, by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.42e-173 Length: 660  
 Score: 184.00 Matches: 184  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 79.31% Indels: 0  
 DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BM840808 (1-660)

QY 6 LeuGlnSerValSerSerLalleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 67 TTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATATCTCTG 126  
 QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 127 AACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 186  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 187 ATATGTTGTTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 246  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 DB 247 TCTAGAAAGCTCAGACACTGTTATTTATGAAGCTGCATCACTGTCTCGAAATCACAGT 306  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105  
 DB 307 TGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAGACCACTCCA 366  
 QY 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 367 TGCTCTTCAGCAATAATAATCCATCTCACTGAGGAACTCAGAGCTCTGAGCT 426  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 427 GGTATAGCCAGCAGTGGATCCAGACAAAGGAAGACATTGTGAACCAATGACAGAA 486  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 487 GCCTGCTTAAACAGTCGGTAGTCCCTTCTGTCAGGGACTTGATCATGAAGAGGAC 546  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 DB 547 TATGAACTGTGTATACCAAGCTACAGGACTCAAGAGTCAAGCAATATACAGACT 606  
 QY 186 ThrAspIleGln 189  
 DB 607 ACTGATACCAA 618

RESULT 6

CB851847/c

LOCUS

715 bp mRNA linear EST 22-APR-2003

## DEFINITION

UI-CF-FNO-aem-o-20-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
 UI-CF-FNO-aem-o-20-0-UI 3', mRNA sequence.

ACCESSION CB851847  
 VERSION CB851847.1 GI:30046667

KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 715)

## AUTHORS

Bonaldo, M.F., Lennon, G. and Soares, M.B.

## TITLE

Normalization and subtraction: two approaches to facilitate gene

## JOURNAL

Genome Res. 6 (9), 791-806 (1996)

## MEDLINE

97044477

## PUBMED

8889548

## COMMENT

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.reagen.com) or from Open Biosystems

(www.openbiosystems.com).

The following repetitive elements were found in this cDNA

sequence: 1-24, >AT rich#Low\_complexity (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

source

1..715

/location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-CF-FNO-aem-o-20-0-UI"

/tissue\_type="Human Lung Epithelial cells"

/lab\_host="DH10B (life technologies) (T1 phage resistant)"

/clone\_lib="UI-CF-FNO"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-CF-FNO is a subtracted cDNA library derived from two

normalized Human lung epithelial cell libraries (EN1 and

DUI) The library was subtracted according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. For additional information, contact:

bento-soares@uiowa.edu

TAG\_SEQ=None found"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.53e-173 Length: 715  
 Score: 184.00 Matches: 208  
 Percent Similarity: 99.52% Conservative: 0  
 Best Local Similarity: 99.52% Mismatches: 1  
 Query Match: 79.31% Indels: 1  
 DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CB851847 (1-715)

QY 24 SerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeu 43

DB 691 TCTCTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTC 632

QY 44 HisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsn 63

DB 631 CATGAAATAGTGT-TCTCTGAAACTTCAGAGTCCCTGCCAGCTCCTCAAGACATGAT 573

QY 64 PheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsn 83

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Db 572 TTTTATCTAGAAAGCTCAAGACTGTATTTATGAAGCTGATCCTGTCTCTGGAAT 513
Qy 84 HisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 103
Db 512 CACAGTTGGATAGACCACTTTCTGGATCTCAAGAGGCTGCATCTGTGTATCAAGACC 453
Qy 104 ThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 123
Db 452 ACTCCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGAACGTCG 393
Qy 124 GlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMet 143
Db 392 CAGCCTGGTATAGCCAGCAGTGGATCTCAGAGCAAAAGGGAAGACATTTGTGAACCAATG 333
Qy 144 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLys 163
Db 332 ACAGAGCCTGCTTACCAAGTCGTAGTGCCTCTGTCAGAGGACTTGATCATGAAA 273
Qy 164 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 183
Db 272 GAGGACTATGAACCTGTGTAGTACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTACTA 213
Qy 184 AspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsp 203
Db 212 GACACTACTGACATCCAGAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGAT 153
Qy 204 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSer 223
Db 152 AACAAACAATAGGTCTTACGCTTACCCGGAATACTTGTGTGTTCTTAGATCACCATCT 93
Qy 224 LeuAsnLeuLeuGlnAsnLysSerMet 232
Db 92 TTTAAATTTACTTCAAAATAAAGCATG 66

RESULT 7
BQ008463/c 734 bp mRNA linear EST 26-MAR-2002
LOCUS UI-H-ED1-avk-k-19-0-UI.s1 NCI CGAP_ED1 Homo sapiens cDNA clone
DEFINITION IMAGE:5840010 3', mRNA sequence.
ACCESSION BQ008463
VERSION BQ008463.1 GI:19733364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 734)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..734
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5840010"
/tissue_type="Chondrosarcoma"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac"

FEATURES
source
```

(Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP\_ED1 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma cell line C55. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.

TAG\_TISSUE=Chondrosarcoma

TAG\_LIB=UI-H-ED1

TAG\_SEQ=CGTCAAGGCT"

#### ORIGIN

##### Alignment Scores:

Pred. No.: 1.57e-173 Length: 734  
Score: 184.00 Matches: 184  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 79.31% Indels: 0  
DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BQ008463 (1-734)

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Qy 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 68
Db 681 TCTCCTGGAACCTTCAAGGTCCTCCAGGCTCTTCAAGACATGATTTTATCTAGAAA 622
Qy 69 AlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSer 88
Db 621 GCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCTGGAATCACAGTTGGATAGC 562
Qy 89 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrTrpProCysSerSer 108
Db 561 ACCATTCTGGATCTCAAAAGGCTGCATTTCTGTGATCACAAGACCCTCCATGCTCTTCA 502
Qy 109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128
Db 501 GCAATTAATAATCCATCTCACTCGAGGAACCTCAGACCTCGAGCTGGTATAGCC 442
Qy 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148
Db 441 CACGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGCAACCAATGACAGAAGCTGCTT 382
Qy 149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168
Db 381 AACCACTGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAAGAGGACTATGAACCT 322
Qy 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrAspIle 188
Db 321 GTTAGTACCAAGCTCAGAGGACCTCAAAAGTCAGACATTTACTAGACACTACTGACATC 262
Qy 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208
Db 261 CAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAACAAACAAATGGGT 202
Qy 209 LeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuGln 228
Db 201 CTTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAA 142
Qy 229 AsnLysSerMet 232
Db 141 AATAAAAGCATG 130
```

#### RESULT 8

AI745575/c

LOCUS

DEFINITION

AI745575 592 bp mRNA linear EST 17-DEC-1999  
wc34f12.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2317103 3',  
similar to TR:Q43353 043353 SERINE/THREONINE KINASE RICK. ; mRNA

```

sequence.
AI745575
VERSION AI745575.1 GI:5113863
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 592)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 673 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
FEATURES
source
1..592
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2317103"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 1,29e-170 Length: 592
Score: 181.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.02% Indels: 0
DB: 9 Gaps: 0
US-09-771-161A-93 (1-232) x AI745575 (1-592)
QY 52 ThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLyAlaGlnAep 71
Db ATTTCAAGTCTCCTGCCACTCTCTCAAGCAATGATTTTATCTAGAAAAGCTCAAGAC 533
QY 72 CysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSerThrIleSer 91
Db TGTATTATTAAGAGTGCATCACTGCTCTGGAATACAGTTGGATAGCACCATTCT 473
QY 92 GlySerGlnArgAlaAlaPheCysAspHisLysThrProCysSerSerAlaIlelle 111
Db GGATCTCAAAAGGCTGTCATCTGTGTATCAACAGACCACTCCATGCTCTTCAGCAATAATA 413
QY 112 AsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnInTrp 131
Db ATTCACCTCTCACTGACAGAACTCAGAACGCTCTGCAGCCTGGTATATGCCAGCAGTGG 353

```

sequence.

AI745575

VERSION AI745575.1 GI:5113863

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 592)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 673 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 459.

FEATURES

source

1..592

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2317103"

/sex="male"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP Pr28"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 1.29e-170 Length: 592

Score: 181.00 Matches: 181

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 78.02% Indels: 0

DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x AI745575 (1-592)

QY 52 ThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLyAlaGlnAep 71

Db ATTTCAAGTCTCCTGCCACTCTCTCAAGCAATGATTTTATCTAGAAAAGCTCAAGAC 533

QY 72 CysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSerThrIleSer 91

Db TGTATTATTAAGAGTGCATCACTGCTCTGGAATACAGTTGGATAGCACCATTCT 473

QY 92 GlySerGlnArgAlaAlaPheCysAspHisLysThrProCysSerSerAlaIlelle 111

Db GGATCTCAAAAGGCTGTCATCTGTGTATCAACAGACCACTCCATGCTCTTCAGCAATAATA 413

QY 112 AsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnInTrp 131

Db ATTCACCTCTCACTGACAGAACTCAGAACGCTCTGCAGCCTGGTATATGCCAGCAGTGG 353

QY 132 IleGlnSerLysArgGluAspIleValaenGlnMetThrGluAlaCysLeuAenGlnSer 151

Db ATCCAGAGCAAAAGGGAAGACATTGTGAACCAATACAGAAAGCCTGCCTTAACCAAGTCG 293

QY 152 LeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThr 171

Db CTAGATGCCCTTCTGTCAGGACCTTGATCATGAAGAGGACTATGAACCTTGTAGTACC 233

QY 172 LysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGlu 191

Db AGCCTACAAGGACCTCAAAAGTCAGACAACTTACTAGACACTTACTGACATCCAAAGGAGAA 173

QY 192 GluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnPro 211

Db GAAATTTGCCAAAGTTATATAGTACAAAATTTGAAGATAACAAACAAATGGTCTTTCAGCCT 113

QY 212 TyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuGlnAsnLysSer 231

Db TACCCGGAATACTTGTGTTTCTAGATCACCATCTTTAAATTTACTTCAAATAAAGC 53

QY 232 Met 232

Db 52 ATG 50

RESULT 9

BG757422 852 bp mRNA linear EST 15-MAY-2001

LOCUS 602711061F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4851542 5';

DEFINITION mRNA sequence.

ACCESSION BG757422

VERSION BG757422.1 GI:14068075

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 852)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM1694 row: i column: 15

High quality sequence stop: 814.

FEATURES

source

1..852

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4851542"

/tissue\_type="primary B-cells from tonsils (cell line)"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_48"

/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.85e-167 Length: 852

Score: 178.00 Matches: 178  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 76.72% Indels: 0  
 DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BG757422 (1-852)

QY 6 LeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 121 TTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTCTG 180  
 QY 26 AsnIleProValAsnHisGlyProGlnGluLeuSerCysGlySerSerGlnLeuHisGlu 45  
 DB 181 AACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCCTCTCAGCTCCATGAA 240  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 241 AATAGTGGTTCCTCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACCAATGATTTTAA 300  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 301 TCTAGAAAGCTCAAGACTGTATTTATGAAGCTGCATCCTCTCTGGAATCAGT 360  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 DB 361 TGGATAGCACCATTTCTGGATCTCAAAGGCTGCAATTCGTGATCACAAGACCACTCCA 420  
 QY 106 CysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 421 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAGCCT 480  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 481 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAGAA 540  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 541 GCCTGCCTTAACCACTCGCTAGATGCCCTTCTGTCAGGACCTTGATCATGAAAGGAC 600  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 183  
 DB 601 TATGAACCTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAAGACCAATTA 654

RESULT 10  
 BG170405 811 bp mRNA linear EST 06-FEB-2001  
 LOCUS 60232736F1 NIH\_MGC\_89 Homo sapiens cDNA clone IMAGE:4426016 5',  
 DEFINITION mRNA sequence.

ACCESSION BG170405  
 VERSION BG170405.1 GI:12677108

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 811)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

NIH-MGC <http://mgi.nci.nih.gov/>.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM10172 row: g column: 09

High quality sequence stop: 721.

Location/Qualifiers

1. .811

FEATURES

source

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4426016"  
 /tissue\_type="hypernephroma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_89"  
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

# ORIGIN

## Alignment Scores:

Pred. No.: 1-78e-164 Length: 811  
 Score: 175.00 Matches: 175  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 75.43% Indels: 0  
 DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BG170405 (1-811)

QY 6 LeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 168 TTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTCTG 227  
 QY 26 AsnIleProValAsnHisGlyProGlnGluLeuSerCysGlySerSerGlnLeuHisGlu 45  
 DB 228 AACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCCTCTCAGCTCCATGAA 287  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 288 AATAGTGGTTCCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACCAATGATTTTAA 347  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 348 TCTAGAAAGCTCAAGACTGTATTTATGAAGCTGCATCCTCTCTGGAATCAGT 407  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 DB 408 TGGATAGCACCATTTCTGGATCTCAAAGGCTGCAATTCGTGATCACAAGACCACTCCA 467  
 QY 106 CysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 468 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAGCCT 527  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 528 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAGAA 587  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 588 GCCTGCCTTAACCACTCGCTAGATGCCCTTCTGTCAGGACCTTGATCATGAAAGGAC 647  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArg 180  
 DB 648 TATGAACCTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAAGACCAATTA 692

RESULT 11  
 BQ773811/c 667 bp mRNA linear EST 26-JUL-2002  
 LOCUS BQ773811  
 DEFINITION UI-H-EZ1-bbz-f-10-0-UI.s1 NCI CGAP\_Ch2 Homo sapiens cDNA clone  
 UI-H-EZ1-bbz-f-10-0-UI 3', mRNA sequence.  
 ACCESSION BQ773811  
 VERSION BQ773811.1 GI:21982287  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 667)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 JOURNAL Tumor Gene Index  
 COMMENT Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of  
 Orthopaedics  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 source  
 1. .667  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-E21-bbz-f-10-0-UI"  
 /tissue\_type="Chondrosarcoma Grade II"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI\_CGAP\_Ch2"  
 /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCAGCTT.  
 TAG\_TISSUE=grade-2-chondrosarcoma  
 TAG\_LIB=UI-H-E21  
 TAG\_SEQ=ATCTAATG"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.5e-156 Length: 667  
 Score: 167.00 Matches: 167  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.98% Indels: 0  
 DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x BQ773811 (1-667)

QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 |||||  
 Db 630 TCTAGAAAAGCTCAGACTGTTATTATTATGAAGCTGCATCTGCTCGAATACACT 571  
 |||||

QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 |||||  
 Db 570 TGGATAGACCATTTCTGGATCTCAAGGGCTGCATTTCTGTATCACAAGACCACTCCA 511  
 |||||

QY 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 |||||  
 Db 510 TGCCTCTTCAGCAATATTAATCCATCTCACTGACAGAAATCAGAACTGTGAGCT 451  
 |||||

QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 |||||  
 Db 450 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAACATTGTGCAACCAATGACAGAA 391  
 |||||

QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 |||||  
 Db 390 GGCTGCTTTAAGCAGTGCCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAGAGGAC 331  
 |||||

QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 |||||  
 Db 330 TATGAACCTTGTGTAGTACCAAGCCTCAAAAGCTCAGACAATTACTAGCACT 271  
 |||||

QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 |||||  
 Db 270 ACTGACATCCAAAGGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAAA 211  
 |||||

QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 |||||  
 Db 210 CAAATGGGCTCTCAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAT 151  
 |||||

QY 226 LeuLeuGlnAsnLysSerMet 232  
 |||||  
 Db 150 TTACTTCAAAATAAAGCATG 130  
 |||||

RESULT 12  
 BQ774940/c  
 BQ774940/LOCUS  
 DEFINITION UI-H-FHO-bcd-1-20-0-UI.s1 NCI CGAP FHO Homo sapiens cDNA clone  
 UI-H-FHO-bcd-1-20-0-UI 3', mRNA sequence.  
 ACCESSION BQ774940  
 VERSION BQ774940.1 GI:21983416  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 721)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: James Martin  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 The following repetitive elements were found in this cDNA  
 sequence: 1-22, >AT rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 Location/Qualifiers  
 1..721  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-FHO-bcd-1-20-0-UI"  
 /tissue\_type="Human Chondrosarcoma Cell Line"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI\_CGAP\_FHO"  
 /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FHO is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCCGCG. The cell line was provided by Dr James Martin from University of Iowa  
 TAG\_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1  
 Chondrosarcoma



Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/cgap.html  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
1..744  
/location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bj1-h-03-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_FT2"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT2 is a subcloned cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa."  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_LIB=UI-H-FT2  
TAG\_SEQ=GGCCATGCCG"

ORIGIN  
Alignment Scores:  
Pred. No.: 1,678-156 Length: 744  
Score: 167.00 Matches: 208  
Percent Similarity: 99.05% Conservative: 0  
Best Local Similarity: 99.05% Mismatches: 1  
Query Match: 71.98% Indels: 2  
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x BQ774940 (1-721)

ORIGIN  
Alignment Scores:  
Pred. No.: 1,678-156 Length: 744  
Score: 167.00 Matches: 208  
Percent Similarity: 99.05% Conservative: 0  
Best Local Similarity: 99.05% Mismatches: 1  
Query Match: 71.98% Indels: 2  
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CD365404 (1-744)

ORIGIN  
Alignment Scores:  
Pred. No.: 1,628-156 Length: 721  
Score: 167.00 Matches: 167  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.98% Indels: 0  
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x BQ774940 (1-721)

ORIGIN  
Alignment Scores:  
Pred. No.: 1,678-156 Length: 744  
Score: 167.00 Matches: 208  
Percent Similarity: 99.05% Conservative: 0  
Best Local Similarity: 99.05% Mismatches: 1  
Query Match: 71.98% Indels: 2  
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CD365404 (1-744)

ORIGIN  
Alignment Scores:  
Pred. No.: 1,628-156 Length: 721  
Score: 167.00 Matches: 167  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.98% Indels: 0  
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x BQ774940 (1-721)

ORIGIN  
Alignment Scores:  
Pred. No.: 1,678-156 Length: 744  
Score: 167.00 Matches: 208  
Percent Similarity: 99.05% Conservative: 0  
Best Local Similarity: 99.05% Mismatches: 1  
Query Match: 71.98% Indels: 2  
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CD365404 (1-744)

ORIGIN  
Alignment Scores:  
Pred. No.: 1,628-156 Length: 721  
Score: 167.00 Matches: 167  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 71.98% Indels: 0  
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x BQ774940 (1-721)



QY 203 p8nlysglnMetGlyLeuGlnProTyPrOglluLeuValSerArgSerProse 223  
 DB 123 TAACAACAAATGGGCTTACCCGAAATACCTGTGGTTCTAGATCACCATC 64  
 QY 223 rLeuAenLeuGlnAenLysSerMet 232  
 DB 63 TTTAATTTACTTCAAATAAAGCATG 36

CA314123 672 bp mRNA linear EST 04-NOV-2002  
 UI-CF-FNO-a2-o-11-0-UI s1 UI-CF-FNO Homo sapiens cDNA clone  
 UI-CF-FNO-a2-o-11-0-UI 3', mRNA sequence.  
 CA314123  
 ACCESSION CA314123.1 GI:24532221  
 VERSION 1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 1 (bases 1 to 672)  
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com) or from Open Biosystems  
 (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 source Location/Qualifiers  
 1..672  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-FNO-a2-o-11-0-UI"  
 /tissue\_type="Human Lung Epithelial cells"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-FNO"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-CF-FNO is a subtracted cDNA library derived from two  
 normalized Human lung epithelial cell libraries (ENI and  
 DU1) The library was subtracted according to according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. For additional information, contact:  
 bento-soares@uiowa.edu  
 TAG\_TISSUE=Lung Epithelial Cells Tissue nos 359-368  
 TAG\_LIB=UI-CF-FNO  
 TAG\_SEQ=GGCTGTAGGC"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.52e-154 Length: 672  
 Score: 165.00 Matches: 165  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.12% Indels: 0  
 DB: 14 Gaps: 0

## FEATURES

source

Location/Qualifiers  
 1..709  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"

US-09-771-161A-93 (1-232) x CA314123 (1-672)

QY 68 LysAlaGlnAspCyTyPrPheMetLysLeuHisCysProGlyAsnHisSerTrpAsp 87  
 DB 546 AAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCTGGAAATCACAGTTGGGAT 487  
 QY 88 SerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSer 107  
 DB 486 AGCACCATTCTGGATCTCAAGAGGCTCATTTCTGTGATCAACAGACCACTCCATGCTCT 427  
 QY 108 SerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIle 127  
 DB 426 TCAGCAATATATATCCACTCTCACTCAGAGAACTCAGAACGCTGCGAGCTGGTATA 367  
 QY 128 AlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCys 147  
 DB 366 GCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAGCCTGC 307  
 QY 148 LeuAsnGlnSerLeuAspAlaIleLeuSerArgAspLeuIleMetLysGluAspTrpGlu 167  
 DB 306 CTTAACCAAGTGCCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAGACTATGAA 247  
 QY 168 LeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAsp 187  
 DB 246 CTTGTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACAAATTACTAGACACTACTGAC 187  
 QY 188 IleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMet 207  
 DB 186 ATCCAAGGAGAGAAGATTGTCACAAAGTTATAGTACAAAAATTGAAAGATAACAAACAATG 127  
 QY 208 GlyLeuGlnProTyPrOglluLeuValSerArgSerProSerLeuAsnLeuLeu 227  
 DB 126 GGTCTTCAGCCCTTACCCCGAAATACTTGTGGTTTCTAGATCACCATTCTTTAAATTTACTT 67

QY 228 GlnAsnLysSerMet 232  
 DB 66 CAAATAAAGCATG 52

## RESULT 15

CA413941/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA413941 709 bp mRNA linear EST 07-NOV-2002  
 UI-H-EZ0-bau-f-07-0-UI s1 NCI CGAP Chl Homo sapiens cDNA clone  
 UI-H-EZ0-bau-f-07-0-UI 3', mRNA sequence.

CA413941.1 GI:24776592

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 709)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of  
 OrthopaedicscDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.eduThe following repetitive elements were found in this cDNA  
 sequence: 1-64, >AT rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

Location/Qualifiers

1..709

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/clone="UI-H-EZO-bau-f-07-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ch1"
/notes="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch1 is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZO
TAG_SEQ=ATCTAATATG"

```

# ORIGIN

Alignment Scores:

Pred. No.:	1.6e-154	Length:	709
Score:	165.00	Matches:	165
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	71.12%	Indels:	0
DB:	14	Gaps:	0

US-09-771-161A-93 (1-232) x CA413941 (1-709)

Qy	68	LysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAsp	87
Db	708	AAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCGAAATCACAGTTGGAT	649
Qy	88	SerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSer	107
Db	648	AGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGATCACAGACCCTCCATGCTCT	589
Qy	108	SerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIle	127
Db	588	TCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACTGTGCGAGCCTGGTATA	529
Qy	128	AlaGlnGlnTrpIleGlnSerIysArgGluAspIleValAsnGlnMetThrGluAlaCys	147
Db	528	GCCACGACGTGGATCCAGAGAAAGGGAAGACATTGTGAACCAATGACAGAACCTGC	469
Qy	148	LeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGlu	167
Db	468	CTTAACCAAGTCGTAGATGCCCTTCTGTCAGGACCTTGATCATGAAAGAGGACTATGAA	409
Qy	168	LeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrAsp	187
Db	408	CTTGTTAGTACCAGCCTACAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGAC	349
Qy	188	IleGlnGlyGluGluPheAlaIleValGlnLysLeuLysAspAsnLysGlnMet	207
Db	348	ATCCAAGGAGAGAAGATTGGCCAAAGTTATAGTACAAAATTGAAAGATACAAACAATG	289
Qy	208	GlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsnLeuLeu	227
Db	288	GGTCTTCAGCCTTACCCGAAATACCTTGTGGTTCTAGATCACCACATCTTTAAATTTACTT	229
Qy	228	GlnAsnLysSerMet	232
Db	228	CAAAATAAAGCATG	214

Search completed: April 1, 2004, 14:50:52  
Job time : 2712 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 08:35:52 ; Search time 4002 Seconds  
(without alignments)  
2512.640 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLOQSVSSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh  
-O=/cgn2.1/USPTO spoal/US09771161/runat\_29032004.124819.19493/app query fasta\_1.391  
-DB=GenEmbl -OFT=fastap -SURFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CGN 1.1 2496 @runat\_29032004.124819.19493 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sv.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*

29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rtd.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1182	98.0	1623	9	AF078530 Homo sapi
2	1182	98.0	1623	12	AY335645 Synthetic
3	1182	98.0	1886	9	AY358813 Homo sapi
4	1182	98.0	1889	9	BC004553 Homo sapi
5	1182	98.0	1902	9	AF064824 Homo sapi
6	1182	98.0	2024	6	BD251808 Phosphory
7	1182	98.0	2033	6	BD127583 Primer fo
8	1182	98.0	2033	9	AK075213 Homo sapi
9	1182	98.0	2098	6	AB277777 Sequence 2
10	1182	98.0	2098	6	BD106658 Modulator
11	1182	98.0	2501	6	AR221453 Sequence
12	1182	98.0	2501	6	AX429236 Sequence
13	1182	98.0	2501	9	AF027706 Homo sapi
14	1182	98.0	2502	6	AR194318 Sequence
15	1182	98.0	2521	9	AY358814 Homo sapi
16	1176	97.5	1620	6	AR183235 Sequence
17	1176	97.5	1620	6	AR205635 Sequence
18	1176	97.5	1620	6	AR241237 Sequence
19	1176	97.5	1620	6	AR256253 Sequence
20	1176	97.5	1620	6	AR391600 Sequence
21	1176	97.5	1620	6	AX082201 Sequence
22	1176	97.5	1620	6	BD123999 Novel mol
23	1176	97.5	1931	6	AR183234 Sequence
24	1176	97.5	1931	6	AR205634 Sequence
25	1176	97.5	1931	6	AR216112 Sequence
26	1176	97.5	1931	6	AR241236 Sequence
27	1176	97.5	1931	6	AR256252 Sequence
28	1176	97.5	1931	6	AR391599 Sequence
29	1176	97.5	1931	6	AX082199 Sequence
30	1176	97.5	1931	6	BD123998 Novel mol
31	1165	96.6	1060	6	AR380139 Sequence
32	839.5	69.6	1620	10	AF461040 Mus muscu
33	839.5	69.6	1620	10	AF487539 Mus muscu
34	726	60.2	116650	9	AC004003 Homo sapi
35	726	60.2	320187	9	AF117829 Homo sapi
36	569.5	47.2	173259	2	AC117336 Rattus no
37	514.5	42.7	186519	10	AL807379 Mouse DNA
38	417.5	34.6	575	6	BD126039 Primer fo
39	371	30.8	61099	2	AC139421 Homo sapi
40	335	27.8	1755	5	AF487540 Danio rer
41	125	10.4	1400	6	AR205645 Sequence
42	125	10.4	1400	6	AR241247 Sequence
43	125	10.4	1400	6	AR256263 Sequence
44	125	10.4	1400	6	AR391610 Sequence
45	125	10.4	1400	6	AX082238 Sequence

ALIGNMENTS

RESULT 1

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AF078530      1623 bp      mRNA      linear      PRI 28-JUL-1998
LOCUS      Homo sapiens receptor interacting protein 2 (RIP2) mRNA, complete
DEFINITION
ACCESSION      AF078530
VERSION      AF078530.1
KEYWORDS      GI:3342909
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1623)
AUTHORS      McCarthy, J.V., Ni, J. and Dixit, V.M.
TITLE      RIP2 is a novel NF-kappaB-activating and cell death-inducing kinase
JOURNAL      J. Biol. Chem. 273 (27), 16968-16975 (1998)
MEDLINE      98307936
PUBMED      9642260
REFERENCE      2 (bases 1 to 1623)
AUTHORS      McCarthy, J.V., Ni, J. and Dixit, V.M.
TITLE      Direct Submission
JOURNAL      Submitted (15-JUL-1998) Molecular Oncology, Genentech Inc, 1 DNA
Way, South San Francisco, CA 94080, USA
FEATURES
source
1. .1623
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1. .1623
/genes="RIP2"
/function="activates NF-kappaB"
/function="induces cell death"
/notes="RIP2; serine/threonine kinase homolog; contains
CARD motif"
/codon_start=1
/product="receptor interacting protein 2"
/protein_id="AAC27722.1"
/db_xref="GI:3342910"
/translation="MGEAICSLPTIPYHKLADLYLNGASGTVSSARHADRVQV
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LNELLHKKTEYDPAWPLFRILHEIALGVNLYHNTPPLHLDLKTQILLDNEFHV
KIADFLGSKWRMSLSQSRSSKSAPEGGTIIYMPENYEPGQKSRASIKHDIYSYAVI
TWEVLRKQPFEDVNTPLQIMYSVQOHRPVINEESLPYDI PHARMISILIESGWAQN
PDRPSFLKCLILEPVTFRBITLEAVIOLKTKLOSVAIHLCKKKWELSLN
IPVNHGPEQSCSSQLHENSQSPETSRSLPAQDNDFLSRKQDCYFWKLHHCPCGNH
SWDTISGQRAFCBKHKTTPCSAIIINPLSTAGNSERLQPGIAQQWISKRREDIVNQ
MTEACLNQLDALLSRDLINKEDYELVSTKPTSKVRQLLDTTDIOGBEFKVIQVK
LKDNKQMGLOPYEILLVSRSPSLNLLQKSM"
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Alignment Scores:

Pred. No.:	4.96e-104	Length:	1623
Score:	1182.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	98.01%	Indels:	0
DB:	9	Gaps:	0

US-09-771-161A-93 (1-232) x AF078530 (1-1623)

```
QY      5 GlnLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db      :
937 AAGTTACAGAGTGTTCAGTGCCATTACCTAATGTCACAGAGAAATGGAATTATCT 996

QY      25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db      :
997 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCAT 1056

QY      45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db      :
1057 GAAATAGTGTTCTCTCTGAACTTCAAGTTCCTGCCAGCTCTCTCAAGCAATGATTTT 1116
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65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
1117 TTATCTAGAAAAGCTCAAGACTGTTATTATTTATGAAGCTGCATCACTGTCTCTGAAATCAC 1176

85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleThrThr 104
1177 AGTTGGGACAGCACCATTTCTGGATCTCAAGGGCTGCAATTCCTGTGATCACAGACCAT 1236

105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
1237 CCANGCTCTTCAGCAATAATAATCACTCTCACTGCGAGAACTCAGAACGCTCTGCAG 1296

125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 1356

145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
1357 GAAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAG 1416

165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
1417 GACTATGAACCTGTTAGTACCAAGCTCAAGAGCTCAAAAGTCAGACAAATTACTAGAC 1476

185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
1477 ACTACTGACATCCAGGAGAGAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAAC 1536

205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
1537 AAACAAATGGGTCTTCAGCCTTACCCGGAATACTTTGTGGTTTCTAGATCACCATCTTTA 1596

225 AsnLeuLeuGlnAsnLysSerMet 232
1597 AATTACTTCAAAATTAAGCATG 1620
```

RESULT 2

LOCUS	AY335645	1623 bp	mRNA	linear	SYN 15-OCT-2003
DEFINITION	Synthetic construct Homo sapiens serine/threonine kinase 2 (RIP2) mRNA, partial cds.				
ACCESSION	AY335645				
VERSION	AY335645.1	GI:33303916			
KEYWORDS	FLI CDNA.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 1623)				
AUTHORS	Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jenson, D., Harlow, E., LaBaer, J., and Brizuela, L.				
TITLE	Cloning of human full-length CDS FLEXGene kinases in recombinational vector system				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1623)				
AUTHORS	Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jenson, D., Harlow, E., LaBaer, J., and Brizuela, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA				
COMMENT	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last 'codon' and before HindIII site to maintain reading frame.				
FEATURES	Location/Qualifiers				
source	1. .1623				

Alignment Scores:		
Pred. No.:	5.98e-104	Length: 1886
Score:	1182.00	Matches: 227

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Query Match: 98.01% Indels: 0
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DEFINITION
AF064824
ACCESSION AF064824
VERSION AF064824.1 GI:3290171
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1902)
AUTHORS Thome,M., Hofmann,K., Burns,K., Martinon,F., Bodmer,J.-L.,
Mattmann,C. and Tschopp,J.
Identification of CARDIAC, a RIP-like kinase that associates with
caspase-1
CURR. BIOL. 8 (1998) In press
REFERENCE 2 (bases 1 to 1902)
AUTHORS Thome,M., Hofmann,K., Burns,K., Martinon,F., Bodmer,J.-L.,
Mattmann,C. and Tschopp,J.
Direct Submission
TITLE Submitted (12-MAY-1998) Institute of Biochemistry, University of
Lausanne, Chemin des Boveresses, 155, Epalinges, CH 1066,
Switzerland
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Pred. No.: 6, 05e-104 Length: 1902
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DB: 9 Gaps: 0
US-09-771-161A-93 (1-232) x AF064824 (1-1902)
QY 5 GlnLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 24
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QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
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RESULT 6
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LOCUS BD251808
DEFINITION Phosphorylation effectors.
ACCESSION BD251808
VERSION BD251808.1 GI:33061578
KEYWORDS JP 2002526035-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2024)
Hillman,J.L., Lal,P., Tang,T.Y., Corley,N.C., Guegler,K.J.,
Baughn,M.R., Patterson,C., Bandman,O., Young,J.A., Gorgone,G.A.,
Yue,H., Azimzai,Y., Reddy,R., Lu,D.A.M. and Shih,L.L.
Phosphorylation effectors
Patent: JP 2002526035-A 6 20-AUG-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002526035-A/6
PD 20-AUG-2002
PF 28-JUL-1999 JP.2000562510
PR 28-JUL-1998 US 60/155213,14-SEP-1998 US 60/155196 PR
14-OCT-1998 US 60/155239,03-NOV-1998 US 60/106889 PR
19-NOV-1998 US 60/109093,22-DEC-1998 US 60/113796 PR
12-JAN-1999 US 60/155233
PI JENNIFER L HILLMAN, PREETI LAL, TOM Y TANG, NEIL C CORLEY, KARL J
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PI GUEGLER,
PI MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDMAN, JANICE AU
YOUNG.
PI GINA A GORGONE, HENRY YUE, YALDA AZIMZAI, ROOPA REDDY, DYUNG AINA
PI M LU,
PI LEO L SHIH
PC C12N15/09, A61K38/00, A61K45/00, A61P1/04, A61P1/16, A61P3/10 PC
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A61P21/04,
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PC 12, C12N9/16,
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Conservative: 1
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 ACCESSION BD127583  
 VERSION BD127583.1 GI:23222528  
 KEYWORDS JP 2002017375-A/3014.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 REFERENCE 1 (bases 1 to 2033)  
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
 Koga,H.  
 TITLE Primer for synthesizing full-length cDNA and use thereof  
 JOURNAL Patent: JP 202017375-A 3014 22-JAN-2002;  
 COMMENT OS Homo sapiens (human)  
 PN JP 202017375-A/3014  
 PD 22-JAN-2002  
 PF 07-JUL-2000 JP 2000253172  
 PI TOSHIO OTA, FETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO  
 PI ISHII,  
 PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI  
 SHINICHI KOJIMA,  
 PI TETSUJI OTSUKI, HISASHI KOGA  
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 VERSION AK075213.1 GI:22761157  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,  
 Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,  
 Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,  
 Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,  
 Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and  
 Ninomiya,K.  
 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 2033)  
 Isogai,T. and Otsuki,T.  
 Direct Submission  
 TITLE  
 JOURNAL  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,  
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology; cDNA library construction:  
 Institute of Medical Science, University of Tokyo, Laboratory of  
 Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass  
 sequencing and clone selection: Helix Research Institute (supported  
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QY		5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	24	
DB		1196	AGATTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAGAAATGGAATTATCT	1255	
QY		25	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	44	
DB		1256	CTGAACATACCTGTAATCATGTGCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT	1315	
QY		45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe	64	
DB		1316	GAATAAGTAGGTCTCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACCAATGATTTT	1375	
QY		65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	84	
DB		1376	TTATCTAGAAAAGCTCAAGACTGTATTATTTATGAGCTGCATCCTCTCGAAATCAC	1435	
QY		85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr	104	
DB		1436	AGTTGGGATAGCACCACTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT	1495	
QY		105	ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124	
DB		1496	CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACCTCTGCAG	1555	
QY		125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144	
DB		1556	CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTGTGACCAATGACA	1615	
QY		145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu	164	
DB		1616	GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG	1675	
QY		165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184	
DB		1676	GACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACATTTACTAGAC	1735	
QY		185	ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn	204	
DB		1736	ACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC	1795	
QY		205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224	
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ORIGIN				Patent: WO 9855507-A 2 10-DEC-1998;	
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				Location/Qualifiers	
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DB		1155	AAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAGAAATGGAATTATCT	1214	
QY		25	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	44	
DB		1215	CTGAACATACCTGTAATCATGTGCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT	1274	
QY		45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe	64	
DB		1275	GAATAAGTAGGTCTCTCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACCAATGATTTT	1334	
QY		65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	84	
DB		1335	TTATCTAGAAAAGCTCAAGACTGTATTATTTATGAGCTGCATCCTCTCGAAATCAC	1394	
QY		85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr	104	
DB		1395	AGTTGGGATAGCACCACTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT	1454	
QY		105	ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124	
DB		1455	CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACCTCTGCAG	1514	
QY		125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144	
DB		1515	CCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTGTGAACCAATGACA	1574	
QY		145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu	164	
DB		1575	GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG	1634	
QY		165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184	
DB		1635	GACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACATTTACTAGAC	1694	
QY		185	ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn	204	
DB		1695	ACTACTGACATCCAAAGGAGAGAAATTTGCTAAAGTTATAGTACAAAATTTGAAGATAAC	1754	
QY		205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224	
DB		1755	AAACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA	1814	
QY		225	AsnLeuLeuGlnAsnLysSerMet	232	
DB		1815	AAATTTACTTCAAAATAAAGCATG	1838	

RESULT 9		A82777		2098 bp		linear		PAT 21-JAN-2000	
LOCUS		A82777		2098 bp		linear		PAT 21-JAN-2000	
DEFINITION		Sequence 2 from Patent WO9855507.		2098 bp		linear		PAT 21-JAN-2000	

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QY 225 AsnLeuGlnAsnLysSerMet 232
DB 1856 AATTTACTTCAAAATAAAAGCATG 1879

RESULT 10
LOCUS BD106658
DEFINITION Modulators of intracellular inflammation, cell death and cell survival pathways.
ACCESSION BD106658
VERSION BD106658.1 GI:23201476
KEYWORDS JP 2002502258-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 2098)
AUTHORS Wallach,D., Boldin,M. and Malinin,N.
TITLE Modulators of intracellular inflammation, cell death and cell survival pathways
JOURNAL Patent: JP 2002502258-A 1 22-JAN-2002;
COMMENT YEDA RESEARCH AND DEVELOPMENT CO LTD
PN JP 2002502258-A/1
PD 22-JAN-2002
PF 01-JUN-1998 JP 1999501993
PR 03-JUN-1997 IL 121011,30-JUN-1997 IL 121199 PR
11-SEP-1997 IL 121746
PI DAVID WALLACH,MARK BOLDIN,NIKOLAI MALININ
PC C12N15/12,C07K14/47,C07K16/18,C12Q1/68,A61K38/17,G01N33/68 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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ORIGIN
Alignment Scores:
Pred. No.: 6.84e-104 Length: 2098
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x BD106658 (1-2098)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 1196 AAGTTACAGAGTGTTCAGAGTGCCATTACCTATGTGACAGAAGAAAATGGAATTATCT 1255

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1256 CTGAACATACCTGTAAATCATGTGTCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 1315

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1316 GAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1375

QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1376 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCGGAATAC 1435

QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1436 AGTTGGATAGACCACTTCTGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCACT 1495

QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1496 CCATGCTCTTCAGCAATAATAATCACTCTCACTGCAAGGAACATCAGAAGCTCTGCAG 1555

QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144

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DB 1556 CCTGTATAGCCACGACGTGGATCCAGAACGGAAGACATTTGTGAACCAATGACA 1615
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1616 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1675
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1676 GACTATGAATGTTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 1735
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsn 204
DB 1736 ACTACTGCATCCAAAGGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1795
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
DB 1796 AAACAATAATGGTCTTCAGCCCTACCCGGGAAATACCTTGTTTCTAGATCACCACATCTTA 1855
QY 225 AsnLeuGlnAsnLysSerMet 232
DB 1856 AATTTACTTCAAAATAAAAGCATG 1879

RESULT 11
LOCUS AR221453
DEFINITION Sequence 3 from patent US 6426221.
ACCESSION AR221453
VERSION AR221453.1 GI:23328503
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2501)
AUTHORS Ward,D.T. and Cowsert,L.M.
TITLE Antisense modulation of RIP2 expression
JOURNAL Patent: US 6426221-A 3 30-JUL-2002;
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Alignment Scores:
Pred. No.: 8.52e-104 Length: 2501
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 6 Gaps: 0

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QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1221 CTGAACATACCTGTAAATCATGTGTCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 1280

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1281 GAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1340

QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1341 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCGGAATAC 1400

QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
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105 ProCysSerSerAlaIleIleLeuProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
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125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 1521 CCTGGTATAGCCAGCAGTGATCCAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1580

145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 1581 GAAGCTCGCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAGAG 1640

165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 1641 GACTATGAACCTTGTAGTACCAAGCCTCAGGACCTCAAAAGTCAACAATTTGAAAGATAAC 1700

185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 1701 ACTACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAAC 1760

205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
 1761 AAACAAATGGCTCTTACGCTTACCCGAAATATCTTGTGGTTTCTAGATCACCATCTTTA 1820

225 AsnLeuLeuGlnAsnLysSerMet 232  
 1821 AATTACTTCAAAATAAAGCATG 1844

RESULT 12  
 AX429236 2501 bp DNA linear PAT 21-JUN-2002  
 LOCUS Sequence 13 from Patent EP1201765.  
 DEFINITION AX429236  
 ACCESSION AX429236.1 GI:21540548  
 VERSION  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE  
 1 Schubart,D., Habenberger,P., Stein-Gerlach,M. and Bevec,D.  
 AUTHORS Cellular kinases involved in cytomegalovirus infection and their  
 TITLE inhibition  
 JOURNAL Patent: EP 1201765-A 13 02-MAY-2002;  
 Axxima Pharmaceuticals Aktiengesellschaft (DE)

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 Pred. No.: 1182.00 Matches: 227  
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 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 99.56% Indels: 0  
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US-09-771-161A-93 (1-232) x AX429236 (1-2501)

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25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
 1221 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGGATCCCTCTCAGTCCAT 1280

45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 1281 GAAATAGTGGTTCTCTGAACTTCAAGGTCCTCCAGCTCCTCAAGACAATGATTTT 1340

65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 1341 TTAATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGCTCTCGAAATCAC 1400

85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 1401 AGTTGGGATAGACCACTTCTGGTTCCTCAAGGGCTGCATTTCTGTGATCAGAACCACT 1460

105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 1461 CCATGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGCTGCGAG 1520

125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
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145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
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165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
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205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
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225 AsnLeuLeuGlnAsnLysSerMet 232  
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RESULT 13  
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 DEFINITION cds.  
 ACCESSION AF027706 GI:3123886  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 2501)  
 Inohara,N., del Peso L., Koseki,T., Chen,S. and Nunez,G.  
 RICK, a novel protein kinase containing a caspase recruitment  
 domain, interacts with CLARP and regulates CD95-mediated apoptosis  
 J. Biol. Chem. 273 (20), 12296-12300 (1998)  
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 2 (bases 1 to 2501)  
 Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.  
 Direct Submission  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.  
 Submitted (01-OCT-1997) Dept. Pathology, Comprehensive Cancer &  
 Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr, Ann Arbor,  
 MI 48109, USA

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ORIGIN
Alignment Scores:
Pred. No.: 8 52e-104 Length: 2501
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x AF027706 (1-2501)
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DB 1221 CTGAACATACCTGTAAATCATGTCTCACAAAGGAATCATGTGATCCTCTCAGTCCAT 1280
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1281 GAAATAGTGTTCCTCAAGTTCACAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1340
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DB 1341 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCCTCTCGAAATCAC 1400
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DB 1401 AGTTGGATAGCACCACTTCCTGTTCTCAAGGGCTGCATTCCTGATCACAGACCACT 1460
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
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QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
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QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1581 GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTCTCCAGGACCTGATCATGAAAGAG 1640
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1641 GACTATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAACAAATTTACTAGAC 1700
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DB 1761 AAACAAATGGGTCTTCACGCTTACCCGGANATACCTTGTGTTCTAGATCACCATCTTTA 1820
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1821 AATTTACTTCAAAATAAAGCATG 1844

RESULT 14
ARI94318
LOCUS
DEFINITION Sequence 2 from patent US 6348573.
ACCESSION ARI94318
VERSION ARI94318.1 GI:20240910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2502)
AUTHORS Nunez, G., Inohara, N. and Koseki, T.
TITLE Compositions and methods for identifying apoptosis signaling
JOURNAL Pathway inhibitors and activators
FEATURES Patent: US 6348573-A 2 19-FEB-2002;
Location/Qualifiers
source 1..2502
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Alignment Scores:
Pred. No.: 8 53e-104 Length: 2502
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x ARI94318 (1-2502)
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DB 1162 AAGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCT 1221
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1222 CTGAACATACCTGTAAATCATGTCTCACAAAGGAATCATGTGATCCTCTCAGTCCAT 1281
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1282 GAAATAGTGTTCCTCAAGTTCCTGCCAGCTCCTCAAGACAAATGATTTT 1341
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
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QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIlySerThr 104
DB 1402 AGTTGGATAGCACCACTTCCTGTTCTCAAGGGCTGCATTCCTGATCACAGACCACT 1461
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1462 CCATGCTCTTCAGCAATATAATCCACTCTCAAGGGCTGCATTCCTGATCACAGACCACT 1521
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1522 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 1581
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
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QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184

Db 1642 GACTATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACAAATTACTAGAC 1701

QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204

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QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224

Db 1762 AAACAAATGGGTCTTACGCTTACCGGAAATATTGTGGTTTCTAGATCACCATCTTTA 1821

QY 225 AsnLeuLeuGlnAsnLysSerMet 232

Db 1822 AATTACTTCAAAATAAAGCATG 1845

RESULT 15

AY358814

LOCUS AY358814 2521 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA43305 RIPK2 (UNQ277) mRNA, complete cds.

ACCESSION AY358814

VERSION AY358814.1 GI:37182745

KEYWORDS FLI CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2521)

Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J.S., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.V., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment

Genome Res. 13 (10), 2265-2270 (2003)

12975309

2 (bases 1 to 2521)

Clark, H.F.

Direct Submission

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

Location/Qualifiers

1. .2521

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DNA43305"

1. .2521

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252. .1874

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ORIGIN

Alignment Scores:

8 61e-104 Length: 2521

1182.00 Matches: 227

Percent Similarity: 100.00%

Best Local Similarity: 99.56%

Query Match: 98.01%

Indels: 0

Gaps: 0

US-09-771-161A-93 (1-232) x AY358814 (1-2521)

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Db 1188 AAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAAAAATGATATATCT 1247

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 44

Db 1248 CTGAACATACCTGTAAATCATGGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1307

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64

Db 1308 GAAATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1367

QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84

Db 1368 TTATCTAGAAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTGTCTCGAAATCAC 1427

QY 85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104

Db 1428 AGTGGGATAGACCACTTCTGGAATCTCAAGGGCTGCATTTCTGTGATCACAAGACCCT 1487

QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124

Db 1488 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCTGCAG 1547

QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144

Db 1548 CCTGGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGTGAACCAAAATGACA 1607

QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164

Db 1608 GAAGCTCGCTTAACCAAGCTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAAG 1667

QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184

Db 1668 GACTATGAACCTTCTTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAGACAAATTACTAGAC 1727

QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204

Db 1728 ACTACTGACATCCACAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1787

QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224

Db 1788 AAACAAATGGGTCTTACGCTTACCGGAAATATTGTGGTTTCTAGATCACCATCTTTA 1847

QY 225 AsnLeuLeuGlnAsnLysSerMet 232

Db 1848 AATTACTTCAAAATAAAGCATG 1871

Search completed: April 1, 2004, 11:22:01

Job time : 4018.secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 06:43:21 ; Search time 473 Seconds  
(without alignments)  
2083.683 Million cell updates/sec

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Perfect score: 1206  
Sequence: 1 MYSLQLQSVSAIH/CDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: BLASUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
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6: Geneseqn2002s.\*  
7: Geneseqn2003as.\*  
8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182	98.0	2024	3	Aaz46143
2	1182	98.0	2033	4	Aak94554
3	1182	98.0	2098	2	Aax02558
4	1182	98.0	2501	6	ABK51169
5	1182	98.0	2501	6	Aad45172
6	1182	98.0	2502	3	Aaz48762
7	1182	98.0	2709	3	AAC77779
8	1176	97.5	1620	7	ABX75870

9	1176	97.5	1931	2	Aaz09246	Aaz09246	Human	CAR
10	1176	97.5	1931	4	Aaf30001	Aaf30001	Human	CAR
11	1176	97.5	1931	6	ABK89280	ABK89280	Human	CAR
12	1176	97.5	1931	6	AAL40752	AAL40752	cDNA of h	
13	1176	97.5	1931	7	ABX75869	ABX75869	Human	CAR
14	1176	97.5	1931	9	AD881363	AD881363	Human	CAR
15	1149	95.3	1619	6	AAL40753	AAL40753	DNA of hu	
16	1027	85.2	1959	9	ADC99131	ADC99131	Human	KPP
17	650	53.9	491	8	ACH33353	ACH33353	Human	end
18	436	36.2	762	7	ACD96414	ACD96414	Human	col
19	417.5	34.6	575	4	AAK93010	AAK93010	Human	CAR
20	125	10.4	1400	2	Aaz09250	Aaz09250	Human	CAR
21	125	10.4	1400	4	Aaf30005	Aaf30005	Human	CAR
22	125	10.4	1400	6	ABK89283	ABK89283	Human	CAR
23	125	10.4	1400	6	AAL40763	AAL40763	cDNA of h	
24	125	10.4	1400	7	ABX75880	ABX75880	Human	CAR
25	125	10.4	1400	8	ABT44225	ABT44225	Human	nuc
26	125	10.4	3382	4	Aaf30002	Aaf30002	Human	CAR
27	125	10.4	3382	6	ABK89281	ABK89281	Human	CAR
28	125	10.4	3382	6	AAL40754	AAL40754	cDNA of h	
29	125	10.4	3382	7	ABX75871	ABX75871	Human	CAR
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31	125	10.4	4302	4	Aaf30004	Aaf30004	Human	CAR
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33	125	10.4	4302	6	AAL40762	AAL40762	cDNA of h	
34	125	10.4	4302	7	ABX75879	ABX75879	Human	CAR
35	125	10.4	4302	8	ABT44224	ABT44224	Human	nuc
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38	125	10.4	4570	4	AAK51622	AAK51622	Human	pol
39	125	10.4	4610	4	AH181313	AH181313	Human	CAR
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41	125	10.4	5250	4	AAK52606	AAK52606	Human	pol
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43	122.5	10.2	2859	7	ABX75872	ABX75872	Human	Cas
44	122.5	10.2	3789	3	AAa95798	AAa95798	Apoptosis	
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ALIGNMENTS

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DT	16-MAY-2000 (first entry)
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DE	cDNA sequence encoding a human phosphorylation effector PHSP-6.
XX	XX
KW	Human; phosphorylation effector; PHSP; proliferative disorder;
KW	immune disorder; neuronal disorder; ss.
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OS	Homo sapiens.
XX	XX
FH	Key
FT	CDS
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FT	/*tag= a
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XX	XX
PN	WO200006728-A2.
XX	XX
PD	10-FEB-2000.
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PF	28-JUL-1999; 99WO-US017132.
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PR	28-JUL-1998; 98US-0155213P.
PR	14-SEP-1998; 98US-0155196P.
PR	14-OCT-1998; 98US-0155239P.
PR	03-NOV-1998; 98US-0106889P.
PR	19-NOV-1998; 98US-0109093P.
PR	22-DEC-1998; 98US-0113796P.



PR	12-JAN-1999;	99US-0155233P.	
XX	(INCY-)	INCYTE PHARM INC.	
PA	Hillman JL,	Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;	
XX	Patterson C,	Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;	
PI	Reddy R,	Lu DWM, Shin LL;	
PI	WPI;	2000-183125/16.	
XX	P-PSDB;	AAV68774.	
DR	New human phosphorylation effectors useful for the diagnosis, treatment		
XX	and prevention of proliferative, immune and neuronal disorders.		
PT	Claim 9;	Page 121-122; 142pp; English.	
XX	AAZ46138-246168	encode human phosphorylation effectors (PHSP), designated	
XX	PHSP1-PHSP31	(the protein sequence for PHSP28 is not given in the	
CC	specification). The sequences were isolated from cDNA libraries prepared		
CC	from various human tissues. The PHSP proteins are useful for the		
CC	diagnosis, treatment and prevention of proliferative disorders, immune		
CC	disorders and neuronal disorders. The PHSP proteins form pharmaceutical		
CC	compositions which useful for treating or preventing disorders associated		
CC	with decreased PHSP expression/activity. PHSP antagonists are useful for		
CC	treating or preventing disorders associated with increased PHSP		
CC	expression/activity		
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SQ	Alignment Scores:		
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	Percent Similarity:	100.00%	Conservative: 1
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	DB:	3	Gaps: 0
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PI	:	:	:
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OY	25	LeuSerIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	44
DB	1199	CTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCCAT	1258
OY	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
DB	1259	GAAATAGTGTTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT	1318
OY	65	LeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisCysProGlyAsnHis	84
DB	1319	TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAATCAC	1378
OY	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr	104
DB	1379	AGTTGGATAGACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACT	1438
OY	105	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
DB	1439	CCATGCTCTTCAGCAATAATAATCACTCAACTGCAGGAAACTCAGAACGCTGCAG	1498
OY	125	ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
DB	1499	CTGGTATAGCCAGAGTGGATCAGAGCAAAAGGAGACATTTGTGAACCAATGACA	1558
OY	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164
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OY	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
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1678

185

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205

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1822

RESULT 2

AAK94554

ID

AAK94554

standard; cDNA; 2033 BP.

XX

AAK94554;

XX

06-NOV-2001

(first entry)

DT

Human full-length cDNA, SEQ ID NO: 3453.

XX

Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX

Homo sapiens.

OS

EP1130094-A2.

XX

05-SEP-2001.

XX

07-JUL-2000; 2000EP-00114089.

XX

08-JUL-1999; 99JP-00194486.

PR

11-JAN-2000; 2000JP-00118774.

PR

02-MAY-2000; 2000JP-00183765.

PR

(HELI-) HELIX RES INST.

XX

Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;

XX

Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

WPI; 2001-524255/58.

DR

P-PSDB; AAM93621.

XX

830 Primers useful for synthesizing full length cDNA clones and their use

XX

in genetic manipulation.

PT

Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.

PS

The invention relates to primers for synthesising full length cDNA

CC

clones. 830 cDNA molecules encoding a human protein have been isolated

CC

and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

CC

been determined. Primers for synthesising the full length cDNA are useful

CC

for clarifying the function of the protein encoded by the cDNA. The full

CC

length clones were obtained by construction of full length enriched cDNA

CC

libraries that were synthesised by the oligo-capping method. The primers

CC

enable the production of the full length cDNA easily without any special

CC

methods. The present sequence is a full length human cDNA of the

CC

invention. Note: The sequence data for this patent did not form part of

CC

the printed specification, but was obtained in CD-ROM format directly

CC

from EPO

XX

Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.:

1,8e-108

Length: 2033

Score:

1182.00

Matches: 227

Percent Similarity:

100.00%

Conservative: 1

Best Local Similarity:

99.56%

Mismatches: 0

Query Match:

98.01%

Indels: 0

DB:

4

Gaps: 0



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US-09-771-161A-93 (1-232) x AAX94554 (1-2033)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 1155 AAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAAGAAATGAATATCT 1214
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 1215 CTGAACATACCTGTAAATCATGGTCACAGAAGGAATCATGTGGATCCTCTCAGCTCCAT 1274
QY 45 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1275 GAAATAGTGGTTCCTCGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1334
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1335 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGTCGATCCTCTCGAATATCAC 1394
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 1395 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT 1454
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
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Db 1575 GAAGCCTGCCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAG 1634
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QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
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RESULT 3
AAX02558
ID AAX02558 standard; cDNA; 2098 BP.
AC AAX02558;
XX
XX
XX 07-MAY-1999 (first entry)
DE Human B1 cDNA.
XX
KW B1 protein; intracellular mediator; modulator; inflammation; cell death;
KW cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.
XX
OS Homo sapiens.
XX
PN WO9855507-A2.
XX
PD 10-DEC-1998.
XX
PF 01-JUN-1998; 98WO-IL000255.
XX
PR 05-JUN-1997; 97IL-00121011.

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PR 30-JUN-1997; 97IL-00121199.
XX
XX 11-SEP-1997; 97IL-00121746.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
PI Wallach D, Boldin M, Malinin N;
XX
DR WPI; 1999-070258/06.
DR P-PSDB; AAW92795.
XX
PT New B1 protein regulates cell death and cell survival pathways -
PT derivatives, DNA and antibodies, also regulate intracellular inflammation
PT ; for treating AIDS, cancer.
XX
PS Claim 4; Fig 3B; 90pp; English.
XX
CC This invention describes the isolation of a novel human B1 protein which
CC can interact with, intracellular mediators or modulators of inflammation,
CC cell death and/or cell survival pathways, directly or indirectly. Cells
CC can be modulated or mediated in inflammation, cell death or cell survival
CC pathways or another intracellular signalling activity using B1.
CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,
CC oligonucleotides and ribozymes can also be used to regulate the above
CC pathways
XX
SQ Sequence 2098 BP; 649 A; 452 C; 449 G; 539 T; 0 U; 9 Other;

Alignment Scores:
Pred. No.: 1,89e-108 Length: 2098
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 2 Gaps: 0

US-09-771-161A-93 (1-232) x AAX02558 (1-2098)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 1196 AAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAAGAAATGAATATCT 1255
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 1256 CTGAACATACCTGTAAATCATGGTCCAGAAGGAATCATGTGGATCCTCTCAGCTCCAT 1315
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1316 GAAATAGTGGTTCCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1375
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db 1376 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTGTCTCGAAATCAC 1435
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 1436 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAAGACCACT 1495
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1496 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTGTGCAG 1555
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1556 CTGTGTATAGCCAGCAGTGGATCCAGACGAAAAGGAAGACATTTGTGAACCAATGACA 1615
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 164
Db 1616 GAAGCCTGCCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAG 1675
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1676 GACTATGAACCTTGTAGTACCAGGCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 1735

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185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 1736 ACTACTGACATCCAGGAGAGAAATTGGCAAGTTATAGTACAAATAATTGAAGATAC 1795  
 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
 1796 AAACAAATGGGTCTTCAGCCTTACCGGAATACTTGTGGTCTTAGATCACCATCTTTA 1855  
 225 AsnLeuLeuGlnAsnLysSerMet 232  
 1856 AATTACTTCAAAATAAAGCATG 1879  
 RESULT 4  
 ABK51169  
 ID ABK51169 standard; cDNA; 2501 BP.  
 XX  
 AC ABK51169;  
 DT 30-JUL-2002 (first entry)  
 DE cDNA encoding human cellular kinase RICK protein.  
 XX  
 KW Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;  
 KW RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 225..1847  
 FT /\*tag= a  
 FT /product= "Human cellular kinase RICK"  
 XX  
 PN EPI201765-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 15-OCT-2001; 2001EP-00124604.  
 XX  
 PR 16-OCT-2000; 2000US-0240750P.  
 XX  
 PA (AXXI-) AXXIMA PHARM AG.  
 XX  
 PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;  
 XX  
 DR WPI: 2002-373930/41.  
 DR P-PSDB; AAU80369.  
 XX  
 XX Identifying agents for treatment or prevention of cytomegalovirus  
 PT infection, comprises contacting test compound with cellular kinase and  
 PT detecting change in cellular kinase activity.  
 XX  
 PS Disclosure; Page 20-23; 49pp; English.  
 XX  
 CC The present invention relates to a new method for identifying compounds  
 CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
 CC related diseases. The method of the invention comprises contacting a test  
 CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
 CC Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
 CC activity. The method of the invention can be used to treat and/or prevent  
 CC CMV infections and related diseases. Oligonucleotides that can detect the  
 CC specified kinases can also be used for diagnosis of infection. The  
 CC present nucleic acid sequence encodes the human cellular kinase RICK  
 CC protein of the invention, as described above  
 XX  
 SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.41e-108 Length: 2501  
 Score: 1182.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.56% Mismatches: 0  
 Query Match: 98.01% Indels: 0  
 DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x ABK51169 (1-2501)  
 QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24  
 DB :::::|||||  
 1161 AAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAAATGAATTAICT 1220  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
 DB |||||  
 1221 CTGAACATACCTGTAATCATGTCTCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1280  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 DB |||||  
 1281 GAAATAGTGGTCTCTCAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1340  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 DB |||||  
 1341 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTCTCTGGAAATCATC 1400  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleThrThr 104  
 DB |||||  
 1401 AGTTGGATAGCACCATTTCTGTTCTCAAGGGTGCATTCTGTGATCACAAGACCACT 1460  
 QY 105 ProCysSerSerAlaIleHisProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 DB |||||  
 1461 CCATGCTCTTCAGCAATAATAAATCACTCTCACTGCAGGAACTCAGAACGTCTGCAG 1520  
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 DB |||||  
 1521 CTGGTATAGCCAGCAGTGGATCCAGCAAAAGGAGACATTTGTGAACCAATGACA 1580  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 DB |||||  
 1581 GAAGCTGCTTAACCCAGTCTGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAG 1640  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuAsp 184  
 DB |||||  
 1641 GACTATGAATCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGAAATTTACTAGAC 1700  
 QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 DB |||||  
 1701 ACTACTGACATCCAGGAGAGAAATTGGCAAGTTATAGTACAAATAATTGAAGATAAC 1760  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
 DB |||||  
 1761 AAACAAATGGGTCTTCAGCCTTACCGGAATACTTGTGGTCTTAGATCACCATCTTTA 1820  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 DB |||||  
 1821 AATTACTTCAAAATAAAGCATG 1844  
 RESULT 5  
 AAD45172  
 ID AAD45172 standard; DNA; 2501 BP.  
 XX  
 AC AAD45172;  
 DT 27-DEC-2002 (first entry)  
 XX  
 DE Human receptor interacting protein (RIP) 2 DNA.  
 XX  
 KW Human; receptor interacting protein; RIP2; antisense; gene therapy; gene;  
 KW ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 225..1847  
 FT /\*tag= a  
 FT /product= "Human RIP2 protein"  
 XX  
 PN US6426221-B1.  
 XX

```
PD 30-JUL-2002.
XX
PF 01-AUG-2001; 2001US-00920663.
XX
PR 01-AUG-2001; 2001US-00920663.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Cowser LM;
XX WPI; 2002-673017/72.
DR P-PSDB; AAE27882.
XX
PT New antisense oligonucleotide that targets regions of a nucleic acid
PT encoding human receptor interacting protein (RIP)2, for treating diseases
PT associated with RIP2 expression.
XX
XX Claim 1; Col 49-54; 35pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding human receptor interacting protein (RIP)2 to inhibit its
CC expression. Antisense compounds are used for treating diseases associated
CC with RIP2 expression. They are also useful in antisense gene therapy. The
CC present sequence is human RIP2 DNA
XX
SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2, 41e-108 Length: 2501
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 6 Gaps: 0
US-09-771-161A-93 (1-232) x AAD45172 (1-2501)
QY 5 GlnLeuGlnSerValSerSerLalleHleHisLeuCysAspLysLysMetGluLeuSer 24
DB 1161 AAGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCT 1220
QY 25 LeuAenlleProValAenHleGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
DB 1221 CTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 1280
QY 45 GluAenSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1281 GAAATAGTGTTCCTCAAGTTCACAGTCCCTGCCAGCTCCTCAAGACATGATTTT 1340
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAenHis 84
DB 1341 TTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCTCTCTGGAATCAC 1400
QY 85 SerTrpAspSerThrIleSerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1401 AGTTGGATAGCACCATTCTGTGTTCTCAAGGGCTGCATCTGTGATCACAAGACCAT 1460
QY 105 ProCysSerSerAlaIleAenProLeuSerThrAlaGlyAenSerGluArgLeuGln 124
DB 1461 CCATGCTCTTCAGCAATATATATCACTCTCACTGCGAGGAACCTCAAGACGTCTGAG 1520
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAenGlnMetThr 144
DB 1521 CCTGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTGTGAACCAATGACA 1580
QY 145 GluAlaCysLeuAenGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 164
DB 1581 GAAGCTGCTTTAAACAGTCGTAGATGCCCTTCTGTCCAGGAGCTGATCATGAAAGAG 1640
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1641 GACTATGAACCTTGTAGTACCAGGCTTCAAGACCTCAAAAGTCAACAATTAATCTAGAC 1700
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QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1701 ACTACTGCATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1760
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1761 AACCAAAATGGTCTTCAGCCTTACCCGGAATACATTGTGGTTCTAGATCACCATCTTTA 1820
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1821 AATTACTTCAAAATAAAGCATG 1844
RESULT 6
AAZ48762
ID AAZ48762 standard; cDNA; 2502 BP.
XX
AC AAZ48762;
XX
DT 21-MAR-2000 (first entry)
XX
DE Human RICK coding sequence.
XX
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;
KW CIDE-A; CIDE-B; DRBP-1; diagnosis; cell growth; apoptosis dysregulation;
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.
XX
OS Homo sapiens.
XX
PN WO9555134-A2.
XX
PD 04-NOV-1999.
XX
PF 27-APR-1999; 99WO-US009183.
XX
PR 27-APR-1999; 98US-00069023.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Nunez G, Inohara N, Koseki T;
XX WPI; 2000-072163/06.
DR P-PSDB; AAY59404.
XX
Compositions for identifying apoptosis signaling pathway inhibitors
useful for treating diseases.
Claim 8; Fig 7b; 93pp; English.
XX
This sequence encodes the human RICK (RIP-like interacting CLARP kinase)
protein of the invention. The RICK protein acts as a positive regulator
of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10
during CD95 signalling. The invention provides methods for identifying
apoptosis signalling pathway inhibitors and activators, and methods and
compositions for screening compounds which will modulate the interactions
of the various compositions identified: ARC, RICK, and the CIDE family of
activators (CIDE-A, CIDE-B and DRBP-1). RICK is useful in screening
assays for agents, useful in the diagnosis, prognosis or treatment of
disease associated with excess cell growth and dysregulation of
apoptosis. Complexes containing RICK and CLARP can be used in drug
screening assays to identify inhibitor molecules blocking CD95-mediated
apoptosis. Overexpression of ARC in an in vitro cell system can be used
to identify inhibitors of the enzymatic activity of caspase-8.
Identification of ARC-like inhibitory compounds may be useful for gene
therapy treatment of disease with increased cell death in muscle tissue
and cardiac disorders. Therapeutic compositions of CIDEs can be used to
treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,
ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies
can be used as reagents for the preparation or affinity chromatography
media, and for diagnostically measuring RICK levels. A specific inhibitor
of an essential step in the biochemistry of apoptosis is needed. RICK
interaction with intracellular factors such as CLARP and FADD appears to
```

CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
CC apoptosis factors are potential drug candidates  
XX  
SQ Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other;

Alignment Scores:		
Pred. No.:	2,418-108	2502
Score:	1182.00	Matches: 127
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	99.58%	Mismatches: 1
Query Match:	98.01%	Indels: 0
DB:	3	Gaps: 0

US-09-771-161A-93 (1-232) x AAZ48762 (1-2502)

Qy	5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer	24
Db	1162	AAAGTTACAGAGTGTTCCTCAAGTGGCCATTACGCTATGTGACAAAGAAGAAATGGAAATATATCT	1221
Qy	25	LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis	44
Db	1222	CTGNAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCAT	1281
Qy	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
Db	1282	GAAATAATAGTGGTTCCTCTGAAACTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTT	1341
Qy	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	84
Db	1342	TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCTGGAAATCAC	1401
Qy	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	104
Db	1402	AGTTGGGATAGCACCAATTTCTGGTTCTCAAAAGGGCTGCATTTCTGTGATCAACAAGACCACT	1461
Qy	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
Db	1462	CCATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGAAACTCAGAACGTCCTCGAG	1521
Qy	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
Db	1522	CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACA	1581
Qy	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164
Db	1582	GAAGCCTCGCCTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGGGACTTGTATCATGAAAGAG	1641
Qy	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
Db	1642	GACTATGAACCTTGTATTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGAC	1701
Qy	185	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204
Db	1702	ACTACTGACATCCAAAGAGAGAATTTGCCAAAGTTATAGTACAAAAAATTTGAAAGATAAC	1761
Qy	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224
Db	1762	AAACAATGGGTCTTCAGCCTTACCCGGAAATACTTTGTGGTTTCTAGATCAACCAATCTTTA	1821
Qy	225	AsnLeuLeuGlnAsnLysSerMet	232
Db	1822	AATTTACTTCAAAATAAAGCATG	1845

## RESULT 7

AAC77779

ID AAC77779 standard; cDNA; 2709 BP.

AAC77779:

08-FEB-2001 (first entry)

DE Human cancer associated gene sequence SEQ ID NO:173.

XX

KW	Human; cancer associated gene; cancer antigen; detection; cancer;
KW	diagnosis; cytostatic; proliferative; cancer; immunomodulator;
KW	antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW	antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
KW	dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW	vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;
KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW	allergic reaction; graft versus host disease; organ rejection;
KW	haemostatic; thrombolytic; cardiovascular disorder; infection;
KW	neurological disease; drug screening; ss.
XX	
XX	Homo sapiens.
OS	
XX	WO200005350-A1.
PN	
XX	21-SEP-2000.
PD	
XX	
XX	08-MAR-2000; 2000WO-US005882.
PF	
XX	
XX	12-MAR-1999; 99US-0124270P.
XX	
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	
XX	
XX	Rosen CA, Ruben SM;
PI	
XX	
XX	WPI; 2000-587533/55.
DR	
DR	P-PSDB; AAB43570.
XX	
XX	Novel isolated nucleic acids comprising sequences encoding peptides
PT	useful for treating or diagnosing e.g. cancer.
PT	

Alignment Scores:		
Pred. No.:	2,698-108	Length: 2709
Score:	1182.00	Matches: 227
Percent Similarity:	100.00%	Conservative: 1
Best Local Similarity:	99.56%	Mismatches: 0
Query Match:	98.01%	Indels: 0
DR:	3	Gaps: 0

US-09-771-161A-93 (1-232) x AAC77779 (1-2709)

Qy	5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer	24
	:	:	
Db	1203	AAGTTACAGAGTGTTCCTATGTCACGAAGAATAATGGAATTATCT	1262
Qy	25	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	44



Db 1297 CCTGGTATAGCCAGCAGTGGATCCAGACCAAGGGAAGACATTGTGACCAATGACA 1356  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetIleMetIleGlu 164  
 Db 1357 GAAGCCTGCTTAAACCAAGTGGTATGATGCTTCTGTCAGGAGCTTGTATGATGAAGAG 1416  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 Db 1417 GACTATGAATCTTGTAGTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAG 1476  
 QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 Db 1477 ACTACTGACATCCAGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAC 1536  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224  
 Db 1537 AAACAAATGGTCTTTCAGCCTTACCCGGAATATCTTGTGGTTCTAGATCACCATTCTTA 1596  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 Db 1597 AATTTACTTCAAAATAAAGCATG 1620

RESULT 9  
 AAZ09246  
 ID AAZ09246 standard; cDNA; 1931 BP.  
 XX  
 AC AAZ09246;  
 XX  
 DT 25-OCT-1999 (first entry)  
 XX  
 DE Human CARD-3 cDNA.

XX CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
 KW caspase activation; detection; screening; therapy; diagnosis; disease;  
 KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
 KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
 KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;  
 KW myelodysplastic syndrome; myocardial infarction; cell proliferation;  
 KW cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;  
 KW human; ds.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH 214..1836  
 CDS /\*tag= a  
 FT /product= "CARD-3"  
 FT

XX WO9940102-A1.  
 XX 12-AUG-1999.  
 XX 05-FEB-1999; 99WO-US002544.  
 XX 06-FEB-1998; 98US-00019942.  
 XX 17-JUN-1998; 98US-00099041.  
 XX 08-DEC-1998; 98US-00027359.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Bertin J;  
 XX WPI; 1999-494269/41.  
 XX P-PSDB; AAY31140.  
 XX Novel CARD-3 and CARD-4 genes and polypeptides used or treating  
 PT regulation of cellular proliferation and differentiation and cell  
 PT survival.  
 XX

Example 2; Fig 1; 181pp; English.

PS This invention describes the isolation of novel human caspase recruitment  
 XX domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial  
 CC murine CARD-4L protein and genes. The genes and proteins of the invention  
 CC are involved in the regulation of caspase activation. The caspase  
 CC recruitment domain (CARD) polynucleotides, polypeptides, homologues and  
 CC antibodies can be used in screening assays, detection assays, predictive  
 CC medicine and therapeutic and prophylactic methods of treatment. The  
 CC methods may be used to diagnose and treat patients which are suffering  
 CC from a disorder associated with abnormal level or rate of apoptotic cell  
 CC death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
 CC activity of the TNF receptor complex, or abnormal activity of a caspase.  
 CC Diseases that may be treated include cancer (particularly follicular  
 CC lymphoma, carcinomas associated with mutations in p53 and hormone-  
 CC dependent tumours), autoimmune disorders (e.g. systemic lupus  
 CC erythematosus, immune-mediated glomerulonephritis), viral infections,  
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
 CC retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,  
 CC anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.  
 CC CARD-3 protein interacts with other cellular proteins, and so can be used  
 CC for regulation of cellular proliferation and differentiation and cell  
 CC survival. The CARD proteins may also be used to for screen drugs or  
 CC compounds which modulate their activity. The CARD-4 gene can express a  
 CC long transcript that encodes CARD-4L, a short transcript that encodes  
 CC CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence  
 CC encodes the human CARD-3 protein described in the method of the invention  
 XX  
 SQ Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6,72e-108 Length: 1931  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 0  
 Query Match: 97.51% Indels: 0  
 DB: 2 Gaps: 0

US-09-771-161A-93 (1-232) x AAZ09246 (1-1931)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
 Db 1150 AAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAAATGGAATTATCT 1209  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
 Db 1210 CTGAACATACCTGTAATATGTCCTCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64  
 Db 1270 GAAATAGTGGTTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 1329  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
 Db 1330 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACCTGTCTCGAAATCAC 1389  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 Db 1390 AGTTGGGATAGCACCATTCTGGATCTCAAGAGGCTGCTGCTGATCAAGACCAT 1449  
 QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 Db 1450 CCATGCTCTTCAGCATATTAATCCACTCTCACTGCAGAGAAATCAGAACGCTCTGCAG 1509  
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 Db 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 1569  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 Db 1570 GAAGCCTGCCTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGACCTGATCATGAAAGAG 1629  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184

Db 1630 GACTATGAACCTTTAGTACCAAGCTCAAGAGCTCAAAAGTCAGACAAATTACTAGAC 1689  
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1690 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAAC 1749  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
Db 1750 AAACAATAGGGTCTTTCAGCTTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA 1809  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1810 AATTACTTCAAAATAAAGCATG 1833  
RESULT 10  
AAF30001  
ID AAF30001 standard; cDNA; 1931 BP.  
XX  
AC AAF30001;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Human CARD-3 cDNA.  
XX  
KW CARD-3; caspase recruitment domain; human; cancer; infection;  
KW autoimmune disease; neurological disease; haematological disease;  
KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
KW antiinflammatory; apoptosis; diagnosis; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 214..1826  
FT /tag= a  
FT /note= "the open reading frame is also specifically  
FT claimed in Claim 1(a)"  
XX  
PN WO200100826-A2.  
XX  
XX 04-JAN-2001.  
XX  
XX 28-JUN-2000; 2000WO-US017691.  
XX  
XX 28-JUN-1999; 99US-00340620.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Bertin J;  
XX  
XX WPI; 2001-061973/07.  
XX P-PSDB; AAB20079.  
XX  
XX Isolated intracellular proteins predicted to be involved in regulating  
XX caspase activation are used for diagnosis and treatment of e.g. cancer,  
XX viral infections, autoimmune diseases, neurological diseases and  
XX hematological disorders.  
XX  
XX Claim 1(a); Fig 1; 208pp; English.  
XX  
XX The present sequence is that of cDNA encoding human caspase recruitment  
XX domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a  
XX database search using known CARD sequences. Plasmid pXEL17A containing  
XX CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular  
XX protein predicted to be involved in regulating caspase activation. It is  
XX useful as a modulating agent in regulating cellular processes include  
XX cell growth and cell death. Methods of diagnosing and treating patients  
XX suffering from a disorder associated with an abnormal level or rate of  
XX apoptotic cell death, abnormal activity of the Fas/APO-1 receptor  
XX complex, abnormal activity of the tumour necrosis factor receptor complex  
XX or abnormal activity of a caspase involve administering a compound that  
XX modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6  
XX e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide.

CC Such disorders include cancer, viral infection, autoimmune disorders,  
CC neurological diseases, haematological disorders, inflammatory disorders  
CC and immune disorders. CARD nucleic acids can be used to express CARD  
CC proteins in a host cell e.g. for gene therapy applications, to detect a  
CC genetic lesion and to modulate CARD activity  
XX  
SQ Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 6,72e-108 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 4 Gaps: 0  
US-09-771-161A-93 (1-232) x AAF30001 (1-1931)  
Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24  
Db 1150 AAGTTACAGAGTGTTCAGTGCCTATTCACCTATGTGCAAGAGAAAATGGAATATATCT 1209  
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
Db 1210 CTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269  
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
Db 1270 GAAATAGTGGTTCCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTGTCTCGAAATCAC 1389  
Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 1390 AGTTGGGATAGACCATTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAGACCATT 1449  
Qy 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 1509  
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1510 CCTGGTATAGCCACAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569  
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
Db 1570 GAAGCTCGCTTTACACGATCGTAGTCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1629  
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1630 GACTATGAACCTTTAGTACCAAGCTCAAGAGCTTCAAAAGTCAGACAAATTACTAGAC 1689  
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1690 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAAC 1749  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
Db 1750 AAACAATAGGGTCTTTCAGCTTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA 1809  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1810 AATTACTTCAAAATAAAGCATG 1833  
RESULT 11  
ID AAF30001 standard; cDNA; 1931 BP.  
XX  
XX ABK89280  
XX  
XX ABK89280;  
XX  
DT 21-OCT-2002 (first entry)







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XX OS Homo sapiens.
XX PN US6369196-B1.
XX PD 09-APR-2002.
XX PF 05-FEB-1999; 99US-00245281.
XX PR 06-FEB-1998; 98US-00019942.
XX PR 17-JUN-1998; 98US-00099041.
XX PR 08-DEC-1998; 98US-00207359.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Bertin J;
XX DR WPI: 2002-391988/42.
XX DR N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.
XX PT Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD
XX PT -4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's
XX PT disease, cancers and viral infections.
XX PS Example 2; Fig 1; 116pp; English.
XX CC The invention relates to novel isolated Caspase Recruitment Domain (CARD)
XX CC polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may
XX CC be used to treat disorders associated with decreased CARD expression by
XX CC supplementing the patient's own production of CARD. Disorders associated
XX CC with the expression and activity of CARD include cancers (particularly
XX CC follicular lymphomas, carcinomas associated with mutations in p53, and
XX CC hormone-dependent tumours such as breast cancer, prostate cancer, and
XX CC ovarian cancer), autoimmune disorders (such as systemic lupus
XX CC erythematosus, immune-mediated glomerulonephritis), viral infections
XX CC (such as those caused by herpes viruses, poxviruses, and adenoviruses),
XX CC neurological diseases (such as Alzheimer's disease, Parkinson's disease,
XX CC amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal
XX CC muscular atrophy, and various forms of cerebellar degeneration), anaemia
XX CC associated with chronic disease, aplastic anaemia, chronic neutropenia,
XX CC and the myelodysplastic syndromes. This polynucleotide sequence
XX CC represents the cDNA of a human CARD relating to the invention
XX SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,72e-108 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x AAL40752 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 1150 AAGTTACAGAGTGTTCCTCAAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 1210 CTGAACATACCTGTAAATCATGGTCACAGAGGAATCATGTGGATCTCTCAGTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1270 GAATATAGTGGTCTCTCTCAAACTTCAAGTCCCTGCCAGCTCTCTCAAGACATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCAGTCTCTCGAATATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104

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Db 1390 AGTTGGGATAGCACCAATTTCTGGATCTCAAAAGGGCTGCAATCTCTGTGATCACAAGACCATT 1449
QY 105 ProCysSerSerAlaIleAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1450 CCATGCTCTTCAGCAATTAATAATCCACTCTCAACTGTCAGGAAACTCAGAACGCTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1510 CCTGGTATAGCCACGACGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1570 GAAGCTGCTCTTAACCACTGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1630 GACTATGAACCTGTTAGTACCAAGCCTACAAGGCTCAAAAGCTCAGACAAATTACTAGAC 1689
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsn 204
Db 1690 ACTACTGACATCCAAAGGAGAAGATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
Db 1750 AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGTTCTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1810 AATTTACTTCAAAATAAAAGCATG 1833
RESULT 13
ABX75869
ID ABX75869 standard; cDNA; 1931 BP.
XX AC ABX75869;
XX DT 30-APR-2003 (first entry)
XX DE Human cDNA encoding Caspase recruitment domain protein, CARD-3.
XX KW Human; ss; gene; caspase recruitment domain; CARD; CARD-3; CARD-4;
XX KW CARD-4L; CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS;
XX KW autoimmune disorder; systemic lupus erythematosus; viral infection;
XX KW immune related glomerulonephritis; acquired immunodeficiency syndrome;
XX KW neurotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
XX KW amyotrophic lateral sclerosis; retinitis pigmentosa;
XX KW spinal muscular atrophy; cerebellar degeneration; haematological disease;
XX KW anaemia; neutropenia; myelodysplastic syndrome; myocardial infarction;
XX OS Homo sapiens.
XX PN US6469140-B1.
XX PD 22-OCT-2002.
XX PF 08-DEC-1998; 98US-00207359;
XX PR 06-FEB-1998; 98US-00019942.
XX PR 17-JUN-1998; 98US-00099041.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Bertin J;
XX DR WPI: 2003-147109/14.
XX DR P-PSDB; ABUS6269.
XX PT Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z
XX PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,
XX PT detection assays, predictive medicine, and in therapeutic applications.
XX PS Example 2; Fig 1; 99pp; English.

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XX The invention relates to an isolated polypeptide, comprising at least 25  
CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,  
CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)  
CC polypeptide. Also included is an isolated fusion protein, comprising the  
CC CARD polypeptide covalently linked by a peptide bond to a heterologous  
CC polypeptide. The CARD polypeptide is useful in screening assays,  
CC detection assays (e.g. chromosomal mapping, tissue typing and forensic  
CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,  
CC monitoring clinical trials and pharmacogenomics), and in therapeutic and  
CC prophylactic treatments (in diseases associated with apoptotic cell death  
CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and  
CC immune related glomerulonephritis), viral infections, AIDS (acquired  
CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's  
CC disease, Parkinson's disease, neurotrophic lateral sclerosis, retinitis  
CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),  
CC haematological diseases (e.g. anaemia, neutropenia and myelodysplastic  
CC syndromes), myocardial infarction and stroke). The CARD polypeptide is  
CC useful as bait protein in a two-hybrid assay or three hybrid assay to  
CC identify other proteins, which bind to or interact with other CARD  
CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
CC human CARD-4 is located on chromosome 7. The present sequence is a human  
CC CARD cDNA  
XX  
SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.72e-108 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 7 Gaps: 0  
  
US-09-771-161A-93 (1-232) x ABX75869 (1-1931)  
  
QY 5 GlnLeuGlnSerValSerSerAlaHisLeuCysAspLysLysLysMetGluLeuSer 24  
DB 1150 AAGTTACAGAGTGTTCCTCAAGTCCATTACCTATGTGACAGAGAAATGGAATTATCT 1209  
  
QY 25 LeuAsnIleProValAsnHisGlyProGluGluSerCysGlySerSerGlnLeuHis 44  
DB 1210 CTGAACATACCTGTAATCATGTTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269  
  
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
DB 1270 GAAATAGTGGTTCCTCTCAAGTCCCTCCAGTCCCTCTCAAGACATGATTTT 1329  
  
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
DB 1330 TTATCTAGAAAGCTCAAGACTGTATTTATGAAAGCTGCATCACTGTCTGGAAATCAC 1389  
  
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
DB 1390 AGTTGGATAGACCATTTCTGGATCTCAAGGGCTGCTGTGTATCATCAGACCAT 1449  
  
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
DB 1450 CCATGCTCTTCAGCAATTAATCACTCTCACTCAGGAACTCAGAACGCTCTGCAG 1509  
  
QY 125 ProGlyIleAlaGlnInTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
DB 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAAGACATTTGTGAACCAATGACA 1569  
  
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164  
DB 1570 GAAGCCCTGCCTTACCACTGCTAGTCCCTCTCTGTCAGGACCTTGTATCATGAAAGAG 1629  
  
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
DB 1630 GACTATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACAATTACTAGAC 1689  
  
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204

DB 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAC 1749  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
DB 1750 AAACAAATGGGTCTTCAGCCTTACCGGAATACCTGTGGTTCTAGATCACCACCTTTA 1809  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
DB 1810 AATTTACTTCAAAATAAAGCATG 1833  
  
RESULT 14  
ADB811363  
ID ADB81363 standard; cDNA; 1931 BP.  
XX  
AC ADB81363;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human caspase recruitment domain 3 (CARD-3) cDNA.  
XX  
KW human; ss; gene; CARD-3; CARD-4; caspase recruitment domain; apoptosis;  
KW p75; tumour necrosis factor; TNF; neutrophin receptor; cancer;  
KW autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;  
KW viral infection; neurological; retinitis pigmentosa; haematologic;  
KW chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.  
XX  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
CDS 214..1836  
FT /\*tag= a  
FT /product= "CARD-3 protein"  
XX  
XX US2002061833-A1.  
XX  
XX PD 23-MAY-2002.  
XX  
XX PF 26-DEC-2000; 2000US-00748537.  
XX  
XX PR 06-FEB-1998; 98US-00019942.  
XX PR 17-JUN-1998; 98US-00099041.  
XX  
XX PA (BERT/) BERTIN J.  
XX PA (CHAO/) CHAO M V.  
XX  
XX PI Bertin J, Chao MV;  
XX  
XX DR WPI; 2003-657125/62.  
XX DR P-PSDB; ADB81362.  
XX  
XX PT Detecting compounds which alter binding of the caspase recruitment domain  
XX PT (CARD) of CARD-3 polypeptide to the neutrophin receptor p75 is useful  
XX PT to provide compounds for treating CARD-3 mediated disorders.  
XX  
XX PS Disclosure; Fig 2; 40pp; English.  
XX  
XX This invention relates to two novel genes CARD-3 and CARD-4 (caspase  
XX recruitment domains), which are mediators of apoptosis and are useful in  
XX the identification of compounds that modulate apoptosis. Specifically,  
XX CARD-3 (also known as RIP2, RICK and CARDIAK) is known to be a mediator  
XX of p75 (a member of the tumour necrosis factor (TNF) family), and is  
XX believed to provide the switch for cell survival and cell death decisions  
XX mediated by this p75 neutrophin receptor. Accordingly these genes, and  
XX the proteins encoded thereof, are linked to certain disorders associated  
XX with an increased number of cells surviving and proliferating when  
XX apoptosis is inhibited. These include cancer, autoimmune disorders e.g.  
XX systemic lupus and immune mediated glomerulonephritis, viral infections  
XX such as those caused by the herpesvirus, neurological disorders such as  
XX retinitis pigmentosa, haematologic diseases including chronic  
XX neutropenia, as well as myocardial infarction and strokes. The present  
XX invention further describes a novel method for determining whether a test  
XX compound alters the binding of CARD-3 to p75, which comprises measuring

CC the binding of a polypeptide containing the CARD domain of CARD-3 to a  
CC polypeptide comprising the death domain of p75 in the presence and  
CC absence of the test compound, and determining if binding is altered. This  
CC polynucleotide is the human CARD-3 cDNA sequence of the invention.  
XX  
SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 6,72e-108 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservativity: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x ADB81363 (1-1931)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuValLeuMetGluLeuSer 24  
DB 1150 AAGTTACAGAGTGTTCAGAGTCCCATTCACCTATGTGCAAGAGAAATGGAATTATCT 1209  
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
DB 1210 CTGAACATACCTGTAATCATGCTCCCAAGAGGAAATCATGTGGATCCTCTCAGCTCCAT 1269  
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
DB 1270 GAAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329  
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
DB 1330 TTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCTGCTCGGAATCAC 1389  
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
DB 1390 AGTTGGATAGACCATTTCTGATCTCAAGGGGTGCAATCTGTGATCACAGACCATT 1449  
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
DB 1450 CCATGCTCTTACGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACCTCTGCAG 1509  
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
DB 1510 CTTGTATAGCCAGCAGTGGATCCAGAACAAAGGAGACATTTGTGAACCAATGACA 1569  
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
DB 1570 GAAGCTGCTTAAACAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAAGAG 1629  
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
DB 1630 GACTATGAATCTGTGTAGTACCAAGCTACAGGACCTCAAAAGTCAGACAAATTACTAGAC 1689  
QY 185 ThrThrAspIleGlnGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
DB 1690 ACTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAC 1749  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
DB 1750 AAACAATGGGTCTTCAGCTTACCCTCGGAAATACTTGTGGTTTCTAGATCACCATTCTTA 1809  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
DB 1810 AATTTACTTCAAAATAAAGCATG 1833

RESULT 15

AAAL40753

ID: AAL40753 standard; DNA; 1619 BP.

XX AC

AC AAL40753;

XX XX

DT 27-SEP-2002 (first entry)

XX

DE DNA of human CARD-3 SEQ ID No 3.

XX Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;  
XX cerebroprotective; antiparkinsonian; antischlerotic; ophthalmological;  
KW neotropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;  
KW cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;  
KW hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;  
KW systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;  
KW anaemia; neutropenia; myelodysplastic syndrome; human; ds.

OS Homo sapiens.

XX US6369196-B1.

XX 09-APR-2002.

XX 05-FEB-1999; 99US-00245281.

XX 06-FEB-1998; 98US-00019942.

PR 17-JUN-1998; 98US-00099041.

PR 08-DEC-1998; 98US-00207359.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J;

XX WPI; 2002-391988/42.

DR N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.

XX Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.

XX Disclosure; Col 75-78; 116pp; English.

XX The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and hormone-dependent tumours such as breast cancer, prostate cancer, and ovarian cancer), autoimmune disorders (such as systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections (such as those caused by herpes viruses, poxviruses, and adenoviruses), neurological diseases (such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, and the myelodysplastic syndromes. This polynucleotide sequence represents the DNA of a human CARD relating to the invention

SQ Sequence 1619 BP; 516 A; 360 C; 320 G; 423 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,69e-105 Length: 1619

Score: 1149.00 Matches: 225

Percent Similarity: 99.12% Conservativity: 1

Best Local Similarity: 98.68% Mismatches: 2

Query Match: 95.27% Indels: 1

DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x AAL40753 (1-1619)

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DB 937 AAGTTACAGAGTGTTCAGTGGCCATTACCTATGTGCAAGAGAAATGGAATTATCT 996

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44

DB 997 CTGAACATACCTGTAATCATGCTCCCAAGAGGAAATCATGTGGATCCTCTCAGCTCCAT 1056

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64

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Db 1057 GAAATAGTGGTTCTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAGACAAATGATTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysIyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1117 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTCATCACTGTCTCGAAAATCAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 1177 AGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCAATTCGTGATCACAAGACCATT 1236
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1237 CCAATGCTTTCAGCAATATATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCGTGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 1356
QY 145 GluAlaCysIleAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1357 GAAGCCTGCGCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1417 GACTATGAACCTTGTAGTACCAAGCCTACAAGGACCTCAAAAGCTCAGACAAATTACTAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1477 ACTACTGACATCCCAAGGAGAAGATTTCCTCAAAAGTTATAGTACAAAATTTGAAAGATAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1537 AAACAAATGGGTCTTCAGCCTTACCCGGAATA-CTTGTGGTTTCTAGATCACCATCTTTA 1595
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1596 AATTTACTTCAAAAATAAAAGCATG 1619
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Search completed: April 1, 2004, 10:15:08  
Job time : 487 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 09:56:07 ; Search time 105 Seconds  
(without alignments)  
1226.177 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLOQSVSAIHLCDKKK.....PEILVVRSPSLNLLQKSM 232

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues  
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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Database : Issued Patents\_NA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182	98.0	2501	4	US-09-920-663-3
2	1182	98.0	2502	4	US-09-069-023-2
3	1176	97.5	1620	4	US-09-099-041A-3
4	1176	97.5	1620	4	US-09-245-281-3
5	1176	97.5	1620	4	US-09-207-359B-3
6	1176	97.5	1620	4	US-09-340-620A-3
7	1176	97.5	1620	4	US-09-865-364-3
8	1176	97.5	1931	3	US-09-019-942-2
9	1176	97.5	1931	4	US-09-099-041A-1
10	1176	97.5	1931	4	US-09-245-281-1
11	1176	97.5	1931	4	US-09-470-271-2
12	1176	97.5	1931	4	US-09-207-359B-1

13	1176	97.5	1931	4	US-09-340-620A-1	Sequence 1, Appli
14	1176	97.5	1931	4	US-09-865-364-1	Sequence 1, Appli
15	1176	97.5	1931	4	US-09-748-537-2	Sequence 2, Appli
16	1165	96.6	1060	4	US-09-023-655-684	Sequence 684, Appl
17	125	10.4	1400	4	US-09-245-281-40	Sequence 40, Appl
18	125	10.4	1400	4	US-09-207-359B-40	Sequence 40, Appl
19	125	10.4	1400	4	US-09-340-620A-40	Sequence 40, Appl
20	125	10.4	1400	4	US-09-865-364-40	Sequence 40, Appl
21	125	10.4	3382	4	US-09-099-041A-7	Sequence 7, Appli
22	125	10.4	3382	4	US-09-245-281-7	Sequence 7, Appli
23	125	10.4	3382	4	US-09-207-359B-7	Sequence 7, Appli
24	125	10.4	3382	4	US-09-340-620A-7	Sequence 7, Appli
25	125	10.4	3382	4	US-09-865-364-7	Sequence 7, Appli
26	125	10.4	4302	4	US-09-245-281-38	Sequence 38, Appl
27	125	10.4	4302	4	US-09-207-359B-38	Sequence 38, Appl
28	125	10.4	4302	4	US-09-340-620A-38	Sequence 38, Appl
29	125	10.4	4302	4	US-09-865-364-38	Sequence 38, Appl
30	122.5	10.2	2859	4	US-09-099-041A-9	Sequence 9, Appli
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32	122.5	10.2	2859	4	US-09-207-359B-9	Sequence 9, Appli
33	122.5	10.2	2859	4	US-09-340-620A-9	Sequence 9, Appli
34	122.5	10.2	2859	4	US-09-865-364-9	Sequence 9, Appli
35	104.5	8.7	626	3	US-09-019-942-4	Sequence 4, Appli
36	104.5	8.7	626	4	US-09-470-271-4	Sequence 4, Appli
37	104.5	8.7	626	4	US-09-748-537-4	Sequence 4, Appli
38	104.5	8.7	1470	4	US-09-099-041A-27	Sequence 27, Appl
39	104.5	8.7	1470	4	US-09-245-281-27	Sequence 27, Appl
40	104.5	8.7	1470	4	US-09-207-359B-27	Sequence 27, Appl
41	104.5	8.7	1470	4	US-09-340-620A-27	Sequence 27, Appl
42	104.5	8.7	1470	4	US-09-865-364-27	Sequence 27, Appl
43	104.5	8.7	3080	4	US-09-099-041A-25	Sequence 25, Appl
44	104.5	8.7	3080	4	US-09-245-281-25	Sequence 25, Appl
45	104.5	8.7	3080	4	US-09-207-359B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-09-920-663-3  
; Sequence 3, Application US/09920663  
; Patent No. 6426221  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION  
; FILE REFERENCE: RTS-0233  
; CURRENT APPLICATION NUMBER: US/09/920,663  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 3  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (225)...(1847)  
US-09-920-663-3

Alignment Scores:			
Pred. No.:	3,11e-134	Length:	2501
Score:	1182.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	98.01%	Indels:	0
DB:	4	Gaps:	0

US-09-771-161A-93 (1-232) x US-09-920-663-3 (1-2501)

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Db	1161	AAAGTTACAGAGTGTTCAGTCCATTCACCTATGTGCAAGAGAAATGAATTATCT 1220
Qy	25	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44

Db 1221 CTGAACATACCTGTAATCATGTCACCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1280  
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGluAspAsnAspPhe 64  
Db 1281 GAAAAATAGTGGTCTCTCTGAACTTCAAGGTTCCTGCCAGCTCCTCAAGACAAATGATTTT 1340  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
Db 1341 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATAC 1400  
Qy 85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 1401 AGTTGGGATAGCACCATTCTGTTCTCAAGAGGCTGCATCTCTGATCACAAGACCAT 1460  
Qy 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1461 CCATGCTCTTCAGCAATATAATCACTCTCACTGCAGGAACTCAGAACGCTCTGCAG 1520  
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1521 CCTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGGAAGACATTTGTAACCAAAATGACA 1580  
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164  
Db 1581 GAAGCCTGCCTTAACCAAGTCGATAGTGCCTTCTGTCCAGGACTTGATCATGAAGAG 1640  
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1641 GACTATGAACCTGTTAGTACCAAGCCTTACCAAGGACCTCAAAAGTCAAGACAAATTAAGTAC 1700  
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1701 ACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1760  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
Db 1761 AAACAAATGGGTCTTCAGCCTTACCGGAAATACCTTGTGGTTCTAGATCACCATCTTTA 1820  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1821 AATTACTTCAAAATAAAAGCATG 1844

RESULT 2  
US-09-069-023-2  
; Sequence 2, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Nachiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2502  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-069-023-2  
Alignment Scores:  
Pred. No.: 3,12e-134 Length: 2502  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 98.01% Indels: 0  
DB: 4 Gaps: 0  
US-09-771-161a-93 (1-232) x US-09-069-023-2 (1-2502)

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Db 1162 AAGTTACAGAGTGTTCCTCAGTGCATTCACCTATGTGACAGAGAAATGGAATATATCT 1221  
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 1222 CTGAACATACCTGTAATCATGTCACCAAGAGGAATCATGTGGATCCTCTCAGTCCAT 1281  
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
Db 1282 GAAAAATAGTGGTCTCTCTGAACTTCAAGGTTCCTGCCAGCTCCTCAAGACAAATGATTTT 1341  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
Db 1342 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATAC 1401  
Qy 85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 1402 AGTTGGGATAGCACCATTCTGTTCTCAAGAGGCTGCATCTCTGATCACAAGACCAT 1461  
Qy 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1462 CCATGCTCTTCAGCAATATAATCACTCTCACTGCAGGAACTCAGAACGCTCTGCAG 1521  
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1522 CCTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGGAAGACATTTGTAACCAAAATGACA 1581  
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164  
Db 1582 GAAGCCTGCCTTAACCAAGTCGATAGTGCCTTCTGTCCAGGACTTGATCATGAAGAG 1641  
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1642 GACTATGAACCTGTTAGTACCAAGCCTTACCAAGGACCTCAAAAGTCAAGACAAATTAAGTAC 1701  
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1702 ACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1761  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
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Db 1822 AATTACTTCAAAATAAAAGCATG 1845

RESULT 3  
US-09-099-041A-3  
; Sequence 3, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-099-041A-3  
Alignment Scores:  
Pred. No.: 8,39e-134 Length: 1620  
Score: 1176.00 Matches: 226

APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

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; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-207-359B-3

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Score:          1176.00      Matches:      226
Percent Similarity: 99.56%      Conservative: 1
Best Local Similarity: 99.12%      Mismatches: 1
Query Match:      97.51%      Indels:      0
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US-09-771-161A-93 (1-232) x US-09-207-359B-3 (1-1620)

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Db      937 AAGTTACAGAGTGTTCCTCAAGTGCCATTCACTTATGTGACAGAGAAAATGGAATTATCT 996

Qy      25  LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
      ::
Db      997 CTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1056

Qy      45  GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
      ::
Db      1057 GAAAAATAGTGGTCTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1116

Qy      65  LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
      ::
Db      1117 TTAICTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCTGGAATCAC 1176

Qy      85  SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
      ::
Db      1177 AGTTGGGATAGCACCAATTTCTGGATCTCAAGGGCTGCATTCGTGATCACAGACCATT 1236

Qy      105  ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
      ::
Db      1237 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 1296

Qy      125  ProGlyIleAlaGlnGlnThrIleGlnSerIlyArgGluAspIleValAsnGlnMetThr 144
      ::
Db      1297 CCTGGTATAGCCACAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGAAACCAAAATGACA 1356

Qy      145  GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
      ::
Db      1357 GAAGCTCGCCTTTAACCAAGTCCTAGATGCCCTTCTGTCCAGGGACCTTGATCATGAAGAG 1416

Qy      165  AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
      ::
Db      1417 GACTATGAACCTTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 1476

Qy      185  ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
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Db      1477 ACTACTGACATCCAGAGGAGAGAATTTGCCAAGATTATAGTACAAAATTTGAAGATPAC 1536

Qy      205  LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
      ::
Db      1537 AAACAAATGGGTCTTCACGCTTACCCGGAATACTTGTGGTCTTCTAGATCACCATCTTTA 1596

Qy      225  AsnLeuLeuGlnAsnLysSerMet 232
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RESULT 6  
US-09-340-620A-3  
; Sequence 3, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-340-620A-3

Alignment Scores:  
Pred. No.: 8 39e-134 Length: 1620  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-340-620A-3 (1-1620)

QY	5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer	24
DB	937	AAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAANAATGGAATTATCT	996
QY	25	LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis	44
DB	997	CTGAACATACCTGTAAATCATGCTCCACAAAGAGGAATCATGTGATCCCTCAGCTCCAT	1056
QY	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
DB	1057	GAATAATAGTGGTTCTCCTGAAATCTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT	1116
QY	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	84
DB	1117	TTATCTAGAAAAAGCTCAAGACTGTATTATTATGAAGCTGCATCACCTGCTCTGGAAATCAC	1176
QY	85	SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	104
DB	1177	AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCCTGTGATCAAGACCATTT	1236
QY	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
DB	1237	CCATGCTCTTACGACAAATAAATCACTCTCAACTGCAGAAACTCAGAACGCTCGCAG	1296
QY	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
DB	1297	CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA	1356
QY	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleIleMetLysGlu	164
DB	1357	GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTGCCAGGGACTTGATCATGAAGAG	1416
QY	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
DB	1417	GACTATGAACCTGTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTTACTAGAC	1476
QY	185	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204



Db 1477 ACTACTGACATCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTGAAAGATAAC 1536  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224  
Db 1537 AAACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGTTCTTAGATCACCACATCTTTA 1596  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1597 AATTTACTTCAAAATAAAGCATG 1620  
RESULT 7  
US-09-865-364-3  
; Sequence 3, Application US/09865364  
; Patent No. 6613521  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/865,364  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-865-364-3  
Alignment Scores:  
Pred. No.: 8,39e-134 Length: 1620  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 4 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-865-364-3 (1-1620)  
Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24  
Db 937 AAGTTACAGAGTGTTCAGTCCCATTCACCTATGTGACAGAGAGAAATGGAATATCT 996  
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 997 CTGAACATACCTGTAATCATGTCTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1056  
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
Db 1057 GAAATAGTAGGTCTCTCCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTT 1116  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
Db 1117 TTATCTAGAAAGCTCAAGACACTGTTATTTATGAAGCTGCATCAGTCTCTGGAATATC 1176  
Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 1177 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1236  
Qy 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1237 CCATGCTCTTACGACATAATAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 1296  
Qy 125 ProGlyIleAlaGlnGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1297 CTGGTATAGCCAGCAGGTGGATCCAGACAAAGGGAAGACATTGTGAACCAATGACA 1356

Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
Db 1357 GAAGCCTGCTTAACACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1416  
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1417 GACTATGAACCTTGTGTAGTACCAGCCTCAAGGACCTCAAAAGTCAAGACATTACTAGAC 1476  
Qy 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1477 ACTACTGACATCCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTGAAAGATAAC 1536  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224  
Db 1537 AAACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGTTCTTAGATCACCACATCTTTA 1596  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1597 AATTTACTTCAAAATAAAGCATG 1620  
RESULT 8  
US-09-019-942-2  
; Sequence 2, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1931 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-019-942-2  
Alignment Scores:  
Pred. No.: 1.11e-133 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 3 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-019-942-2 (1-1931)	
QY	5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
Db	1150 AAGTTACAGAGTGTTCCTCAAGTGCCTATGTGACAGAGAAATGGAATATCT 1209
QY	25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db	1210 CTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGATCTCTCAGCTCCAT 1269
QY	45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db	1270 GAAATAGTGGTTCCTCTGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1329
QY	65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db	1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGCTCTGGAATCAG 1389
QY	85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db	1390 AGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1449
QY	105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db	1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 1509
QY	125 ProGlyIleAlaGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db	1510 CCTGGTATAGCCAGCAGTGGATCCAGCAAAAGGGAAGACATTGTGAACCAATGACA 1569
QY	145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db	1570 GAAGCTGCTTAACCCAGTCCGTAGATGCCCTTCTCTCCAGGACTTGTATCATGAAGAG 1629
QY	165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db	1630 GACTATGAATCTGTTAGTACCAAGCTCCTCAAGACCTCAAAAGTCAAGCAATTAAGAC 1689
QY	185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn 204
Db	1690 ACTACTGACATCCACAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY	205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db	1750 AAACAAATGGGTCTTCAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 1809
QY	225 AsnLeuGlnAsnLysSerMet 232
Db	1810 AATTTACTTCAAAATAAAGCATG 1833
RESULT 10	
US-09-245-281-1	
; Sequence 1, Application US/09245281	
; Patent No. 6369196	
; GENERAL INFORMATION:	
; APPLICANT: Bertin, John	
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY	
; TITLE OF INVENTION: AND USES THEREOF	
; FILE REFERENCE: 07334/118001	
; CURRENT APPLICATION NUMBER: US/09/245,281	
; CURRENT FILING DATE: 1998-02-05	
; EARLIER APPLICATION NUMBER: US 09/207,359	
; EARLIER FILING DATE: 1998-12-08	
; EARLIER APPLICATION NUMBER: US 09/099,041	

US-09-771-161A-93 (1-232) x US-09-019-942-2 (1-1931)	
QY	5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
Db	1150 AAGTTACAGAGTGTTCCTCAAGTGCCTATGTGACAGAGAAATGGAATATCT 1209
QY	25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db	1210 CTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGATCTCTCAGCTCCAT 1269
QY	45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db	1270 GAAATAGTGGTTCCTCTGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1329
QY	65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db	1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGCTCTGGAATCAG 1389
QY	85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db	1390 AGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1449
QY	105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db	1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 1509
QY	125 ProGlyIleAlaGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db	1510 CCTGGTATAGCCAGCAGTGGATCCAGCAAAAGGGAAGACATTGTGAACCAATGACA 1569
QY	145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db	1570 GAAGCTGCTTAACCCAGTCCGTAGATGCCCTTCTCTCCAGGACTTGTATCATGAAGAG 1629
QY	165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db	1630 GACTATGAATCTGTTAGTACCAAGCTCCTCAAGACCTCAAAAGTCAAGCAATTAAGAC 1689
QY	185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn 204
Db	1690 ACTACTGACATCCACAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY	205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db	1750 AAACAAATGGGTCTTCAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 1809
QY	225 AsnLeuGlnAsnLysSerMet 232
Db	1810 AATTTACTTCAAAATAAAGCATG 1833
RESULT 9	
US-09-099-041A-1	
; Sequence 1, Application US/09099041A	
; Patent No. 6340576	
; GENERAL INFORMATION:	
; APPLICANT: Bertin, John	
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED	
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF	
; FILE REFERENCE: 07334-076001	
; CURRENT APPLICATION NUMBER: US/09/099,041A	
; CURRENT FILING DATE: 1998-06-17	
; PRIOR APPLICATION NUMBER: 09/019,942	
; PRIOR FILING DATE: 1998-02-06	
; NUMBER OF SEQ ID NOS: 37	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 1	
; LENGTH: 1931	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; NAME/KEY: CDS	
; LOCATION: (214) ... (1833)	
US-09-099-041A-1	

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; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-245-281-1

Alignment Scores:
Pred. No.: 1,11e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-245-281-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCCTCAAGTCCCACTTACCTATGTGACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGTCTCAAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64
DB 1270 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTCATCTGCTCGAATATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGGATAGCACCATTCTCGAATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCGTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1510 CCTGGTATAGCCCGAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1570 GAAGCTGCTTTAACCGTTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTAAGTAG 1689
QY 185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1690 ACTACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGGTCTTCAGGCTTACCAGGAATATCTTGTGGTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuGlnAsnLysSerMet 232
DB 1810 AATTACTTCAAAATPAAAGCATG 1833

RESULT 11
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US-09-470-271-2
; Sequence 2, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-470-271-2

Alignment Scores:
Pred. No.: 1,11e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-470-271-2 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCCTCAAGTCCCACTTACCTATGTGACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGTCTCAAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64
DB 1270 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTCATCTGCTCGAATATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGGATAGCACCATTCTCGAATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1449
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QY 105 ProCysSerSerAlaIleIleLeuProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1450 CCATGCTCTTACGCAATAATAATCACTCTCAACTGCAGGAATACTCAGAAAGCTGTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1510 CTGGGTATAGCCAGCAGTGGATCCAGACCAAAAGGAGAGACATTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1570 GAAGCCTGCCTTAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1630 GACTATGAACCTGTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCCAGCAATTAAGTAC 1689
QY 185 ThrThrAspIleGlnGlyGluPheAlaLeuValIleValGlnLysLeuLysAspAsn 204
Db 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
Db 1750 AAACAAATGGTCTTCAGCCTTACCCGGAATACTTTGTGTTTCTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 12
US-09-207-359B-1
; Sequence 1, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; PRIOR FILING DATE: 1998-12-08
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)....(1833)
US-09-207-359B-1

Alignment Scores:
Pred. No.: 1,11e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 0
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-207-359B-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
Db 1150 AAGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAGAGAAATGGAATTAATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
Db 1210 CTGAACATACCTGTAATAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
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Db 1270 GAAAAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTCCAGCTCCTCAAGACAATGATTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysCysProGlyAsnHis 84
Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATAGAGCTGCATCACTCTCTCTGGAAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 1390 AGTTGGGATAGCACCAATTTCTGGATCTCAAAAGGCTGCAATTTCTGTGATCAACAAGACCATT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1450 CCATGCTCTTACGCAATAATAATCACTCTCAACTGCAGGAATACTCAGAAAGCTGTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1510 CTGGGTATAGCCAGCAGTGGATCCAGACCAAAAGGAGAGACATTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1570 GAAGCCTGCCTTAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1630 GACTATGAACCTGTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCCAGCAATTAAGTAC 1689
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
Db 1750 AAACAAATGGTCTTCAGCCTTACCCGGAATACTTTGTGTTTCTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 13
US-09-340-620A-1
; Sequence 1, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR FILING DATE: 1999-02-05
; PRIOR FILING DATE: 1998-12-08
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)....(1833)
US-09-340-620A-1

Alignment Scores:
Pred. No.: 1,11e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
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QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAAATCATGTCTCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAAAATAGTGGTTCCTCGAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyValAsnHis 84
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QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
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QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
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DB 1510 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1570 GAAGCTGCTTAAACAGTCGTAGTGCCCTTCTGTCAGGACTTGTATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACCTGTAGTACCAAGCTACAGGACCTCAAAAGCTCAGACAATTTACTAGAC 1689
QY 185 ThrTrpAspIleGlnGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1690 ACTACTGACATCAAGGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGGTCTTCAGCTTACCGGAAATCTTGTGTCTTAGATCACCATCTTTA 1809
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; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; Sequence 1, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (214) ... (1833)
US-09-865-364-1
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Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0
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QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAAATCATGTCTCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAAAATAGTGGTTCCTCGAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyValAsnHis 84
DB 1330 TTATCTAGAAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGTCTCGAAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValGlnLysLysAsp 144
DB 1510 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1570 GAAGCTGCTTAAACAGTCGTAGTGCCCTTCTGTCAGGACTTGTATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACCTGTAGTACCAAGCTACAGGACCTCAAAAGCTCAGACAATTTACTAGAC 1689
QY 185 ThrTrpAspIleGlnGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1690 ACTACTGACATCAAGGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGGTCTTCAGCTTACCGGAAATCTTGTGTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1810 AATTTACTTCAAAATAAAGCATG 1833

RESULT 15
US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
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Job time : 117 secs

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Pred. No.:	1176.00	Matches:	226
Score:	99.56%	Conservative:	1
Best Similarity:	99.12%	Mismatches:	1
Best Local Similarity:	97.51%	Indels:	0
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DB	1210	CTGACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGATCCTCTCAGCTCCAT	1269
QY	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnaspPhe	64
DB	1270	GAAATATAGTGGTTCCTCGAAATTCACAGTCCCTGCCAGCTCCTCAAGACAATGATTTT	1329
QY	65	LeuSerArgIysAlaGlnAspCysTyrPheMetIysLeuHisHisCysProGlyAsnHis	84
DB	1330	TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACGTCTCGGAAATCAC	1389
QY	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIysThrThr	104
DB	1390	AGTTGGGATAGCACCATTTCTGGAATCTCAAGAGGCTGCATTCGTGATCAAGACCATT	1449
QY	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
DB	1450	CCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAAACTCAGAACCTGTGCAG	1509
QY	125	ProGlyIleAlaGlnGlnTrpIleGlnSerIysArgGluAspIleValAsnGlnMetThr	144
DB	1510	CCTGGTATAGCCCAAGCAGTGGATCCAGACAAAAGGAGACATTTGAAACCAATGACA	1569
QY	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164
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QY	165	AspTyrGluLeuValSerThrIysProThrArgThrSerIysValArgGlnLeuLeuAsp	184
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QY	185	ThrThrAspIleGlnGlyGluPheAlaIysValIleValGlnIysLeuLysAspAsn	204
DB	1690	ACTACTGACATCCAAGGAGAGAAGATTGTGCCAAGTTATAGTACAAAAATTTGAAAGATAAC	1749
QY	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Total number of hits satisfying chosen parameters: 4930456

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	1182	98.0	2501	10	US-09-981-397A-13	Sequence 13, Appl
4	1182	98.0	2709	9	US-09-925-301-173	Sequence 173, Appl
5	1176	97.5	1620	9	US-09-728-721-3	Sequence 3, Appli
6	1176	97.5	1620	13	US-10-105-931-3	Sequence 3, Appli
7	1176	97.5	1620	13	US-10-118-984-3	Sequence 3, Appli
8	1176	97.5	1620	14	US-10-295-981-3	Sequence 3, Appli
9	1176	97.5	1931	9	US-09-748-537-2	Sequence 2, Appli
10	1176	97.5	1931	9	US-09-728-721-1	Sequence 1, Appli
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14	1176	97.5	1931	14	US-10-295-981-1	Sequence 1, Appli
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16	125	10.4	1400	9	US-09-728-721-40	Sequence 40, Appl
17	125	10.4	1400	13	US-10-118-984-40	Sequence 40, Appl
18	125	10.4	1400	14	US-10-006-883A-96	Sequence 96, Appl
19	125	10.4	1400	14	US-10-295-981-40	Sequence 40, Appl
20	125	10.4	3382	9	US-09-728-721-7	Sequence 7, Appli
21	125	10.4	3382	13	US-10-105-931-7	Sequence 7, Appli
22	125	10.4	3382	13	US-10-118-984-7	Sequence 7, Appli
23	125	10.4	3382	14	US-10-295-981-7	Sequence 2, Appli
24	125	10.4	4093	15	US-10-401-194-2	Sequence 38, Appl
25	125	10.4	4302	9	US-09-728-721-38	Sequence 38, Appl
26	125	10.4	4302	13	US-10-118-984-38	Sequence 38, Appl
27	125	10.4	4302	14	US-10-006-883A-95	Sequence 95, Appl
28	125	10.4	4302	14	US-10-295-981-38	Sequence 38, Appl
29	125	10.4	4390	14	US-10-006-883A-3	Sequence 3, Appli
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33	122.5	10.2	2859	13	US-10-105-931-9	Sequence 9, Appli
34	122.5	10.2	2859	13	US-10-118-984-9	Sequence 9, Appli
35	122.5	10.2	2859	14	US-10-295-981-9	Sequence 9, Appli
36	122.5	10.2	3789	14	US-10-013-477-10	Sequence 10, Appl
37	122.5	10.2	3893	14	US-10-106-698-2086	Sequence 2086, Ap
38	114	9.5	60	10	US-09-908-975-13799	Sequence 13799, A
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43	104.5	8.7	1470	13	US-10-118-984-27	Sequence 27, Appl
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45	104.5	8.7	3080	9	US-09-728-721-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-771-161A-2

; Sequence 2, Application US/09771161A

; Patent No. US20020110811A1

; GENERAL INFORMATION:

; APPLICANT: LEVINE, et al.

; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES

; FILE REFERENCE: 802620-2005.1

; CURRENT APPLICATION NUMBER: US/09/771,161A

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 09/724,676

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 136776

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 135619

; PRIOR FILING DATE: 2000-04-12

; NUMBER OF SEQ ID NOS: 273

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 1669

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: -

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; LOCATION: (1)..(1669)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-2

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Score: 1206.00 Matches: 232
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 21 MetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySer 40
Db 380 ATGGAAATATTCTCGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGATCC 439
QY 41 SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGln 60
Db 440 TCTCAGCTCCATGAANAATAGTGGTCTCTGAAATTCAGAGTCCCTGCCAGCTCCTCAA 499
QY 61 AspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCys 80
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; Sequence 957, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
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; Sequence 13, Application US/09981397A  
; Publication No. US20030082519A1  
; GENERAL INFORMATION:  
; APPLICANT: Axxima Pharmaceuticals AG  
; APPLICANT: Schubart, Daniel  
; APPLICANT: Habenberger, Peter  
; APPLICANT: Stein-Gerlach, Matthias  
; APPLICANT: Bevec, Dorian  
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
; TITLE OF INVENTION: Inhibition  
; FILE REFERENCE: AXM-004.1 US  
; CURRENT APPLICATION NUMBER: US/09/981,397A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/240,750  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-981-397A-13  
Alignment Scores:  
Pred. No.: 9,876-137 Length: 2501  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 98.01% Indels: 0  
DB: 10 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-981-397A-13 (1-2501)  
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
:::  
Db 1161 AAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGAATTAICT 1220  
|||  
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
|||  
Db 1221 CTGAACATACCTGTAATCATGGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1280  
|||  
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
|||  
Db 1281 GAAATAGTGGTTCCTGTAACCTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1340  
|||  
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
|||  
Db 1341 TTATCTAGAAAGCTCAAGACGTGTTATTATGAGCTGCATCCTGCTGGAATATC 1400  
|||  
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104  
|||  
Db 1401 AGTTGGATAGCACCATTTCTGTTCTCAAGGGCTGCTTCTGTGATCACAAGACCACT 1460  
|||  
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
|||  
Db 1461 CCATGCTCTTCAGCAATAATAATCCATCTCAACTGCAGGAAATCTCAAGACCTCTGCAG 1520  
|||  
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
|||  
Db 1521 CTGGTATAGCCAGCATGGATTCAGACAAAGGAAAGACATTTGTGACCAATGACA 1580  
|||  
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
|||  
Db 1581 GAAGCTGCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1640  
|||  
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
|||

Db 1641 GACTATGAACTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTACTAGAC 1700  
|||  
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspPhe 204  
|||  
Db 1701 ACTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1760  
|||  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
|||  
Db 1761 AAACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 1820  
|||  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
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Db 1821 AATTACTTCAAAATAAAAGCATG 1844  
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RESULT 4  
US-09-925-301-173  
; Sequence 173, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 173  
; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2595)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2622)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2659)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2670)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-301-173  
Alignment Scores:  
Pred. No.: 1,11e-136 Length: 2709  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 98.01% Indels: 0  
DB: 9 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-925-301-173 (1-2709)  
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
:::  
Db 1203 AAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGAATTAICT 1262  
|||  
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
|||  
Db 1263 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1322  
|||  
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
|||  
Db 1323 GAAATAGTGGTTCCTGTAACCTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1382  
|||  
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
|||

Db 1383 TTATCTAGAAAAAGCTCAAGACTGTTATTTATGTAAGCTGCATCATCTGCTCTGGAATCAC 1442

Qy 85 SerTrpAspSerThrIleSerGlnArgAlaAlaPheCysAspHisLysThrThr 104

Db 1443 AGTTGGGAYAGACCACTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACT 1502

Qy 105 ProCysSerSerAlaIleleAsnProLeuSerThrAlaGlyAsnSerGluArgGluGln 124

Db 1503 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGAACGTCGTGAG 1562

Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144

Db 1563 CCTGGTATAGCCAGCAGTGATGCCAGAACAAAGGGAAGACATTGTGAACCAATGACA 1622

Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164

Db 1623 GAAGCGCTGCTTAACCCAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 1682

Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184

Db 1683 GACTATGAACCTGTAGTACCAAGCCCTACAGGACCTCAAAAGCTCAGACAAATTACTAGAC 1742

Qy 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204

Db 1743 ACTACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1802

Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224

Db 1803 AAACAAATGGCTCTTCAGCCTTACCCGAAATCTTGTGGTTCTTAGATCACCATTCTTA 1862

Qy 225 AsnLeuLeuGlnAsnLysSerMet 232

Db 1863 AATTACTTCAAAATAAAGCATG 1886

RESULT 5

US-09-728-721-3

Sequence 3, Application US/09728721

Patent No. US20020061845A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/728,721

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: 09/340,620

PRIOR FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1620

TYPE: DNA

ORGANISM: Homo sapiens

US-09-728-721-3

Alignment Scores:

Pred. No.: 2,88e-136 Length: 1620

Score: 1176.00 Matches: 226

Percent Similarity: 99.56% Conservative: 1

Best Local Similarity: 99.12% Mismatches: 0

Query Match: 97.51% Indels: 0

DB: 9 Gaps: 9

US-09-771-161A-93 (1-232) x US-09-728-721-3 (1-1620)

Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24

Db 937 AAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAAAGAAATGGAATTAATCT 996

Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44

Db 997 CTGAACATATCTGTAAATCATGTGCCACAGAGGAATCATGTGATCCTCTCAGCTCCAT 1056

Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64

Db 1057 GAAATATAGTGGTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCTCAAGACAAATGATTTT 1116

Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84

Db 1117 TTATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGCTCTGGAATCAC 1176

Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104

Db 1177 AGTTGGGATAGACCACTTCTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAATT 1236

Qy 105 ProCysSerSerAlaIleleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124

Db 1237 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGAACGTCGTGAG 1296

Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144

Db 1297 CTTGTATAGCCAGCAGTGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 1356

Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164

Db 1357 GAAGCGCTGCTTAACCCAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 1416

Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184

Db 1417 GACTATGAACCTGTGTAGTACCAAGCCCTACAGGACCTCAAAAGCTCAGACAAATTACTAGAC 1476

Qy 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204

Db 1477 ACTACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1536

Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224

Db 1537 AAACAAATGGCTCTTCAGCCTTACCCGAAATCTTGTGGTTCTTAGATCACCATTCTTA 1596

Qy 225 AsnLeuLeuGlnAsnLysSerMet 232

Db 1597 AATTACTTCAAAATAAAGCATG 1620

RESULT 6

US-10-105-931-3

Sequence 3, Application US/10105931

Publication No. US20020150987A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-076001

CURRENT APPLICATION NUMBER: US/10/105,931

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1620

TYPE: DNA

ORGANISM: Homo sapiens

US-10-105-931-3

Alignment Scores:

Pred. No.: 2,88e-136 Length: 1620

Score: 1176.00 Matches: 226

Percent Similarity: 99.56% Conservative: 1

Best Local Similarity: 99.12% Mismatches: 1

DB: 9 Mismatches: 1

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Query Match: 97.51% Indels: 0
DB: 13 Gaps: 0
US-09-771-161A-93 (1-232) x US-10-105-931-3 (1-1620)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 937 AAGTTACAGAGTGTTCAGAGTCCCATTCACCTATGTGACAGAGAAATGGAATATATCT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
DB 997 CTGAACATACCTGTAAATCATGTCCACAGAGGAAATCATGTGGATCCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1057 GAAAAATAGTGGTTCCTCGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1117 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGCTCGGAATAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1177 AGTTGGGATAGCACCATTCTCGAATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1236
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1237 CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspLysLysLysMetLysGlu 144
DB 1297 CCTGTGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164
DB 1357 GAAGCTGCTTAAACGATGCTAGATGCTTCTGTCCAGGACTTGTATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1417 GACTATGAACCTTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAGACAATTACTAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1477 ACTACTGACATCCAAAGGAGAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1537 AAACAATGGGTCTTCAGCTTACCCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 1596
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1597 AATTTACTTCAAAATAAAAGCATG 1620
RESULT 7
US-10-118-984-3
; Sequence 3, Application US/10118984
; Publication NO. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-984-3
Alignment Scores:
Pred. No.: 2,88e-136 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 13 Gaps: 0
US-09-771-161A-93 (1-232) x US-10-118-984-3 (1-1620)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 937 AAGTTACAGAGTGTTCAGAGTCCCATTCACCTATGTGACAGAGAAATGGAATATATCT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
DB 997 CTGAACATACCTGTAAATCATGTCCACAGAGGAAATCATGTGGATCCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1057 GAAAAATAGTGGTTCCTCGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1117 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGCTCGGAATAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1177 AGTTGGGATAGCACCATTCTCGAATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1236
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1237 CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspLysLysLysMetLysGlu 144
DB 1297 CCTGTGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164
DB 1357 GAAGCTGCTTAAACGATGCTAGATGCTTCTGTCCAGGACTTGTATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1417 GACTATGAACCTTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAGACAATTACTAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1477 ACTACTGACATCCAAAGGAGAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1537 AAACAATGGGTCTTCAGCTTACCCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 1596
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1597 AATTTACTTCAAAATAAAAGCATG 1620
RESULT 8
US-10-295-981-3
; Sequence 3, Application US/10295981
; Publication NO. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
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; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3

Alignment Scores:
Pred. No.: 2,88e-136 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-295-981-3 (1-1620)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 937 AAGTTACAGAGTGTTCAGAGTCCATTACCTATGTGACAAAGAAATGGAATTATCT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44
DB 997 CTGAACATACCTGTAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1057 GAAATAGTGTTCCTCTGAAACTTCAAGTTCCTCGCAGCTCTCTCAAGCAATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
DB 1117 TTATCTAGAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCTCTCTCGAAATCAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1177 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGCTGCATTTCTGTATCAAGACCAT 1236
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1237 CCATGCTCTTCAGCAATATTAATCCACTCTCACTGCAGGAACTCAGAACGCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1297 CCTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1357 GAAGCCTGCCCTTAACCATGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1417 GACTATGAACTTGTATTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAAATTACTAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1477 ACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1537 AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTCTTAGATCACCATCTTTA 1596
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QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1597 AATTACTTCAATAATAAAGCATG 1620

RESULT 9
US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No. US20020061833A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-537-2

Alignment Scores:
Pred. No.: 3,75e-136 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-748-537-2 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCAGAGTCCATTACCTATGTGACAAAGAAATGGAATTATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAATAGTGTTCCTCTGAAACTTCAAGTTCCTCGCAGCTCTCTCAAGCAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCTCTCTCGAAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGCTGCATTTCTGTATCAAGACCAT 1449
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATATTAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1510 CCTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1570 GAAGCCTGCCCTTAACCATGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACTTGTATTAGTACCAAGCCTTACAAGGACCTCAAAAGTCAGACAAATTACTAGAC 1689
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QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnIleLysLeuLysAspAsn 204  
DB 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
DB 1750 AAACAATGGGCTTCCAGCCTTACCCGAAATACCTTGTGGTTCTAGATCACCATCTTTA 1809  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
DB 1810 AATTACTTCAAAATAAAGCATG 1833  
RESULT 10  
US-09-728-721-1  
; Sequence 1, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)....(1833)  
US-09-728-721-1  
Alignment Scores:  
Pred. No.: 3,75e-136 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 9 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-728-721-1 (1-1931)  
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
DB 1150 AGATTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAGAAATGGAATTATCT 1209  
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
DB 1210 CTGAACATACCTGTAATCATGTGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269  
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
DB 1270 GAAATAGTGGTTCCTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329  
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
DB 1330 TTATCTAGAAAAGCTCAAGACTGTATTATTATGAAGCTGCATCTCTCTGGAATATC 1389  
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
DB 1390 AGTTGGATGACCACTTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAT 1449  
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124

DB 1450 CCATGCTCTTCAGCAATAATAAATCCATCTCAACTGCAGGAAACTCAGAACGTCTGCAG 1509  
QY 125 ProGlyIleAlaGlnGlnTriPileGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
DB 1510 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGACCAATGACA 1569  
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
DB 1570 GAAGCCTGCTTAACAGCTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1629  
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
DB 1630 GACTATGAACCTTGTATTAGTACCAAGCCTCAAGGACCTCAAAAGTCAACAATTACTAGAC 1689  
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
DB 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
DB 1750 AAACAATGGGCTTCCAGCCTTACCCGAAATACCTTGTGGTTCTAGATCACCATCTTTA 1809  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
DB 1810 AATTACTTCAAAATAAAGCATG 1833  
RESULT 11  
US-10-133-780-2  
; Sequence 2, Application US/10133780  
; Publication No. US20020123115A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/133,780  
; FILING DATE: 26-Apr-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1931 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-133-780-2  
Alignment Scores:

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-105-931-1

Alignment Scores:
Pred. No.: 3,75e-136 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservatives: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-133-780-2 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaHisLeuCysAspLysLysLysMetGluLeuSer 24
Db 1150 AAGTTACAGAGTGTTCACAGTCCATTACCTATGTGACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44
Db 1210 CTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1270 GAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1330 TTATCTAGAAAGCTCAAGACTGTATTATTAAGAGCTGCATCCTCTGGAATATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db 1390 AGTTGGATAGACCACTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAAGACCA 1449
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1450 CCATGCTCTTACGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1570 GAAGCTGCCTTAACCACTAGATGCTTCTGTCCAGGACTTGTATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1630 GACTATGAACCTTGTATTAGTACCAAGCCTTACAGGACCTCAAAAGTATAGTACCAAT 1689
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysLysAspAsn 204
Db 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATA 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
Db 1750 AAACAAATGGGTCTTACCGGAAATATCTGTGGTTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 13
US-10-118-984-1
; Sequence 1, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; APPLICANT: Bertin, John
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/059,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37

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APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
FILE REFERENCE: 07334/118001  
CURRENT APPLICATION NUMBER: US/10/118,984  
CURRENT FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1931  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (214)...(1833)  
US-10-118-984-1

Alignment Scores:  
Pred. No.: 3,75e-136 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-118-984-1 (1-1931)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
DB 1150 AAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGCAAGAAGAAATGGAATATCT 1209

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44  
DB 1210 CTGAACATACCTGTAATCATGTGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64  
DB 1270 GAAATAGTGGTTCTCTGAACTTCAAGTCTCCAGCTCCTCAAGACAATGATTTT 1329

QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTCGAAATCAC 1389

QY 85 SerTirAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104  
DB 1390 AGTTGGATAGACCAATTTCTGAGTCTCAAGGGCTGCAATCTGTGATCACAGACCATT 1449

QY 105 ProCysSerSerAlaIleHisProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
DB 1450 CCATGCTCTTCAGCAATATAATATCCATCTCACTGAGGAACTCAGACGCTGTGAG 1509

QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
DB 1510 CTGTGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569

QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
DB 1570 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAGAG 1629

QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
DB 1630 GACTATGAACTTGTAGTACCAAGCTTACAGGACCTCAAAAGCTCAGACAAATTTACTAGAC 1689

QY 185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204

DB 1690 ACTACTGACATCCAAAGGAGAAGATTTCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749

QY 205 LysGlnMetGlyLeuGlnProGlyThrProGluIleValSerArgSerProSerLeu 224  
DB 1750 AAACAAATGGTCTTTCAGCCTTACCCTGGAATATCTTGTGGTTCTAGATCACCATCTTTA 1809

QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
DB 1810 AATTTACTTCAAAATATAAAGCATG 1833

RESULT 14  
US-10-295-981-1  
Sequence 1, Application US/10295981  
Publication No. US2003012005SAI  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-124001  
CURRENT APPLICATION NUMBER: US/10/295,981  
CURRENT FILING DATE: 2002-11-15  
PRIOR APPLICATION NUMBER: US/09/340,620  
PRIOR FILING DATE: 1999-06-28  
PRIOR APPLICATION NUMBER: US/09/245,281  
PRIOR FILING DATE: 1999-02-05  
PRIOR APPLICATION NUMBER: US/09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US/09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US/09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1931  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (214)...(1833)  
US-10-295-981-1

Alignment Scores:  
Pred. No.: 3,75e-136 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-295-981-1 (1-1931)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
DB 1150 AAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGCAAGAAGAAATGGAATATCT 1209

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44  
DB 1210 CTGAACATACCTGTAATCATGTGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64  
DB 1270 GAAATAGTGGTTCTCTGAACTTCAAGTCTCCAGCTCCTCAAGACAATGATTTT 1329

QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTCGAAATCAC 1389

QY 85 SerTirAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104  
DB 1390 AGTTGGATAGACCAATTTCTGAGTCTCAAGGGCTGCAATCTGTGATCACAGACCATT 1449

QY 105 ProCysSerSerAlaIleHisProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124

Db 1450 CCATGCTCTTTCAGCAATAAATCCACTCTCAACTGCAGAAACTCAGAACGCTCTGCAG 1509  
Qy 125 ProGlyLeuAlaGlnThrPheGlnSerLysArgGluAspLeuValAsnGlnMetThr 144  
Db 1510 CTTGGTATAGCCAGCAGTGGATCCAGAGAAAGGAGACAAATTGTGAACCAAAATGACA 1569  
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuLeuMetLysGlu 164  
Db 1570 GAAGCTGCTTAAACCACTCGCTAGATGCCCTTCTGTCAGGGACATTGATCATGAAAGAG 1629  
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1630 GACTATGAACCTTGTAGTACCAAGCCTACAAAGGACCTCAAAAGCTCAGACAAATTACTAGAC 1689  
Qy 185 ThrThrAspLeuGlnGlyGluPheAlaLysValLeuValGlnLysLeuLysAspAsn 204  
Db 1690 ACTACTGACATCCAGGAGAAATTTGCCAAGATTATAGTACAAAATTTGAAAGATAAC 1749  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224  
Db 1750 AACAAATGGTCTTACAGCCTTACCGGAAATACTTGTGTTCTAGATCACCATCTTTA 1809  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 15

US-09-918-995-20565  
; Sequence 20565, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20565  
; LENGTH: 491  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-20565

Alignment Scores:  
Pred. No.: 2.02e-71 Length: 491  
Score: 650.00 Matches: 120  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.17% Mismatches: 0  
Query Match: 53.90% Indels: 0  
DB: 10 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-918-995-20565 (1-491)

Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
Db 128 AAGTTACAGAGTGTTTCAAGTGCCTTCCCTTAAGTGCAGAGAAATGGAATTAATCT 187  
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 188 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 247  
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
Db 248 GAAATAATAGTGTCTCTCTGAAACCTCAAGGTCCTGCGAGCTCTCAAGACAAATGATTTT 307  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
Db 308 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCTGGAAATCAC 367

Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 368 AGTTGGATAGCACCAATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT 427  
Qy 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 428 CCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 487  
Qy 125 Pro 125  
Db 488 CCT 490

Search completed: April 1, 2004, 12:50:49  
Job time : 2517 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 09:53:45 ; Search time 2693 Seconds  
(without alignments)  
2572.605 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNSM 232

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cpn2.1/uspto.spool/US09771161/runat.29032004.124819.19503/app.query.fasta.1.391  
-DB=EST-QPMT-fastap-SUFFIX-p2n.rst -MINMATCH=0.1 -LOOPEL0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09771161 @CEN 1.1 1906 @runat.29032004.124819.19503 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estmu:  
5: em\_estov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_htc:  
9: gb\_estl:  
10: gb\_estc2:  
11: gb\_htc:  
12: gb\_est3:  
13: gb\_est4:  
14: gb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: em\_gss\_hum:  
18: em\_gss\_inv:  
19: em\_gss\_pln:  
20: em\_gss\_vrt:  
21: em\_gss\_fun:  
22: em\_gss\_mam:  
23: em\_gss\_mus:  
24: em\_gss\_pro:  
25: em\_gss\_rod:  
26: em\_gss\_phg:  
27: em\_gss\_vrl:  
28: gb\_gssl:

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	1152	95.5	1201	13	BX343071	BX343071 BX343071
C 2	1141	94.6	744	14	CD365404	CD365404 UI-H-F72-
C 3	1132	93.9	938	13	BQ670832	BQ670832 AGENCOURT
4	1105	91.6	852	12	BG57422	BG57422 602711061
C 5	1099	91.1	870	10	BE877822	BE877822 601486392
C 6	1088	90.2	683	14	CB852764	CB852764 UI-CF-FN0
C 7	1085	90.0	812	12	BI257472	BI257472 602967861
C 8	1080	89.6	1201	13	BX337147	BX337147 BX337147
C 9	1077	89.3	715	14	CB851847	CB851847 UI-CF-FN0
C 10	1067	88.5	883	12	BG393551	BG393551 602411943
C 11	1029	85.3	660	12	BM840808	BM840808 K-EST0117
C 12	1026	85.1	828	10	BE875947	BE875947 601486423
C 13	1015	84.2	672	14	CA314123	CA314123 UI-CF-FN0
C 14	1005	83.3	654	10	BE536247	BE536247 601062632
C 15	1002.5	83.1	811	12	BG170405	BG170405 60222736
C 16	988	81.9	1623	29	AY415527	AY415527 Homo sapi
C 17	987	81.8	734	12	BQ008463	BQ008463 UI-H-ED1-
C 18	980	81.3	721	13	BQ774940	BQ774940 UI-H-FH0-
C 19	975	80.8	1623	29	AY415528	AY415528 Pan trogl
C 20	973	80.7	656	12	BM973770	BM973770 UI-CF-ECL
C 21	940	77.9	592	9	AI745575	AI745575 wc34f12.x
C 22	917	76.0	647	10	AM960501	AM960501 EST372572
C 23	904	75.0	667	13	BQ773811	BQ773811 UI-H-E21-
C 24	894	74.1	636	10	BE551615	BE551615 7a42906.x
C 25	888	73.6	610	13	BUE23654	BUE23654 UI-H-FG1-
C 26	877	72.7	568	9	AA161113	AA161113 z058405.s
C 27	858	71.1	709	14	CA413941	CA413941 UI-H-E20-
C 28	839.5	69.6	1468	11	BC025611	BC025611 Mus muscu
C 29	839.5	69.6	1947	11	BC050845	BC050845 Mus muscu
C 30	838	69.5	606	9	AW085560	AW085560 wy67c04.x
C 31	827.5	68.6	2826	11	BC058088	BC058088 Mus muscu
C 32	794	65.8	1019	9	AV081633	AV081633 AV081633
C 33	789	65.4	564	12	BM796243	BM796243 K-EST0078
C 34	776	64.3	479	12	BM855477	BM855477 K-EST0138
C 35	739.5	61.3	1201	13	BX401255	BX401255 BX401255
C 36	725	60.1	505	13	BX280487	BX280487 BX280487
C 37	713	59.1	483	9	AI343247	AI343247 tb94a04.x
C 38	710.5	58.9	1599	29	AY415529	AY415529 Mus muscu
C 39	703	58.3	476	9	AA913804	AA913804 o135d11.s
C 40	697	57.8	834	12	BM014010	BM014010 603639652
C 41	692	57.4	423	9	AA574167	AA574167 nl78b01.s
C 42	692	57.4	624	14	CD368863	CD368863 UI-H-F71-
C 43	691.5	57.3	738	14	CD356485	CD356485 AGENCOURT
C 44	688	57.0	476	14	CF528565	CF528565 UI-1-BCL-
C 45	688	57.0	582	14	CB545226	CB545226 AMGNNUC:N

ALIGNMENTS

RESULT 1  
BX343071/c  
LOCUS BX343071 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
DEFINITION Homo sapiens cDNA clone CSODL009YC19 3-PRIME, mRNA sequence.  
ACCESSION BX343071  
VERSION BX343071.1 GI:30334165  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1201)



US-09-771-161A-93 (1-232) x CD365404 (1-744)

```

QY 5 GlnLeuGlnSerValSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 718 AAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATA-TCT 660

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 659 CTGAACATACCTGTAATCATGTCTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 600

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64
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Db 599 GAAATAGTGGTCTCTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 540

QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
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Db 539 TNATCTAGAAAGCTCAAGACTGTATTATTAAGCTGCATCAGCTGTCTGGAATAC 480

QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 479 AGTTGGGATAGCACCACTTCTCGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT 420

QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
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Db 419 CCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAAGACGTCTGCAG 360

QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 359 CTGTGTATAGCCAGCAGCTGGATCCAGACCAAAAGGGAAGACATTTGTGAACCAATGACA 300

QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 299 GAAGCTGCTCTTAACCCAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 240

QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 239 GACTATGAATCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGAC 180

QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 179 ACTACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 120

QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 119 AAACAAATGGTCTTCCAGCTTACCCGGAATACTTGTGTCTTAGATCACCATCTTTA 60

QY 225 AsnLeuLeuGlnAsnLysSerMet 232
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 59 AATTTACTTCAAAATAAAAGCATG 36

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## RESULT 3

```

LOCUS      BQ670832
DEFINITION BQ670832 938 bp mRNA linear EST 15-JUL-2002
           AGENCOURT_8191703 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6257019
           5', mRNA sequence.
ACCESSION  BQ670832
VERSION     BQ670832.1 GI:21781666
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 938)
           NIH-MGC http://mgi.nci.nih.gov/.
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
CONTACT    Robert Strausberg, Ph.D.
           Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ruben Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCW2410 row: k column: 04

High quality sequence stop: 659.

## FEATURES

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source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6257019"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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## ORIGIN

```

Alignment Scores:
Pred. No.:      3,648-112      Length:      938
Score:          1132.00      Matches:      222
Percent Similarity: 97.81%      Conservative:  1
Best Local Similarity: 97.37%      Mismatches:   3
Query Match:     93.86%      Indels:       2
DB:              13          Gaps:          0

US-09-771-161A-93 (1-232) x BQ670832 (1-938)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 136 AAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATATCT 195

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 196 CTGAACATACCTGTAATCATGTCTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 255

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64
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Db 256 GAAATAGTGGTCTCTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTT 315

QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 316 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCGAAATCAC 375

QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 376 AGTTGGGATAGCACCACTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT 435

QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 436 CCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAAGACGTCTGCAG 495

QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 496 CCTGTATAGCCAGCAGCTGGATCCAGACCAAAAGGGAAGACATTTGTGAACCAATGACA 555

QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 556 GAAGCTGCTTACCAAGCTGCCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 615

QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 616 GACTATGAATCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 675

QY 185 ThrThrAspIleGln-GlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAs 204
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Db 676 ACTACTGACATCCAAAGGGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 735

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Qy 204 nLysGlnMetGlyLeuGlnProTyrProGluIleLeuVal-ValSerArgSerProSerL 224
Db 736 CAACCAATGGCTTTCAGCTTACCGGAAATACTTGTGGTTTCTAGATCCCATCCT 795

Qy 224 euLenLeuGlnAsnLys 230
Db 796 TTAATTTACTTCCAAATAAA 815

RESULT 4
BG757422 852 bp mRNA linear EST 15-MAY-2001
LOCUS 602711061F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851542 5',
DEFINITION mRNA sequence.
ACCESSION BG757422
VERSION BG757422.1 GI:14068075
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 852)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-t@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCMI694 row: i column: 15
High quality sequence stop: 814.
Location/Qualifiers
1. .852
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4851542"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 2.68e-109 Length: 852
Score: 1105.00 Matches: 221
Percent Similarity: 97.40% Conservative: 4
Best Local Similarity: 95.67% Mismatches: 2
Query Match: 91.63% Indels: 4
DB: 12 Gaps: 2

US-09-771-161A-93 (1-232) x BG757422 (1-852)

Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 118 AAGTTACAGAGTGTTCAGAGTGCCATTACCTATGTGACAGAGAAATGGAATTATCT 177

Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluIleSerCysGlySerGlnLeuHis 44
Db 178 CTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 237

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Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 238 GAAATAGTAGGTCTCTCTGAAACTTCAAGGTCTCCAGCTCCTCAAGACAATGATTTT 297

Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db 298 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCACTGTCTCTGGAAATCAC 357

Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 358 AGTTGGATAGACCACTTCTGGATCTCAAGAGGCTGCATTTCTGTATCAAGACCACT 417

Qy 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 418 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 477

Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 478 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAATGACA 537

Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 538 GAAGCTTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG 597

Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 598 GACTATGAATCTGTAGTACCAAGCTTACAAAGGACCTCAAAAGCTCAGACAATTTACTAGAA 657

Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAs 204
Db 658 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 717

Qy 204 nLysGlnMetGlyLeuGlnProTyrProGluIleLeuVal-ValSerArgSerProSer- 223
Db 718 CAAACAAATGGGTCTTACGCTTACCCGGAAATACTTGTGGTTTCTAGAAATCACCATC 777

Qy 224 --LeuAsnLeuLeu---GlnAsnLysSer 231
Db 778 TTTTAATTTACTTTCAAAATAATAAAGC 806

RESULT 5
BG777822 870 bp mRNA linear EST 20-OCT-2000
LOCUS 601486392F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888815 5',
DEFINITION mRNA sequence.
ACCESSION BG777822
VERSION BG777822.1 GI:10326598
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-t@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9669 row: g column: 24
High quality sequence stop: 739.
Location/Qualifiers
1. .870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source

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/clone="IMAGE:388815"  
 /tissue\_type="large cell carcinoma, undifferentiated"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 69"  
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not I;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.1 kb. Library constructed by Life  
 Technologies."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1-25e-108 Length: 870  
 Score: 1099.00 Matches: 224  
 Percent Similarity: 97.84% Conservatives: 2  
 Best Local Similarity: 96.97% Mismatches: 1  
 Query Match: 91.13% Indels: 5  
 DB: 10 Gaps: 0

US-09-771-161A-93 (1-232) x BB877822 (1-870)

QY 5 GlnLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 24  
 :::  
 Db 44 AAGTTACAGAGTCTTCAAGTGCCATTCACTATGTGACAAAGAAAATGGAATTATCT 103  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
 :::  
 Db 104 CTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 163  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64  
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 Db 164 GAATATAGTGGTCTCTGAACTTCAAGTCTCGCCAGCTCTCTCAGACAAATGATTTT 223  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 :::  
 Db 224 TTATCTAGAAAAGCTCAAGACTGTATTATTAAGCTGCATCACTGTCTCGAAATCAC 283  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
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 Db 284 AGTTGGATAGACCACTTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAAGACCACT 343  
 QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
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 Db 344 CCATGCTCTTCCAGCAATATAATCACTCTCACTGAGGAACTCAGAAAGCTCTGAG 403  
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 :::  
 Db 404 CTGTGTATAGCCAGCAGTGGATCCAGACCAAAAGGGAAGACATTGTGAACCAATGACA 463  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
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 Db 464 GAAGCTCGCTTAAACCAAGTCGTAGATGCCCTTCTGTCCAG-GACTTGATCATGAAAGAG 522  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 :::  
 Db 523 GACTATGAACCTTTAGTACCAAGCTTACAGGACCTCAAAAGCTCAGCAATCTAGAC 582  
 QY 185 ThrThrAspIleGln-GlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAs 204  
 :::  
 Db 583 ACTACTGACATCAAGGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 642  
 QY 204 nLysGlnMetGlyLeu--GlnProTyrProGluIleLeuValValSerArgSerProSer 223  
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 Db 643 CAAACAAATGGGTCTTTTCAGGCTTACCCGGAATACTTTGTGGTTTCTAGATCACCATCT 702  
 QY 224 LeuAsn-LeuLeuGlnAsnLysSer 231  
 :::  
 Db 703 TTAATTTTACTTCAGAAATAAAGC 727

## RESULT 6

CB852764/c 683 bp mRNA linear EST 22-APR-2003  
 LOCUS  
 DEFINITION  
 UI-CF-FN0-aex-p-08-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone  
 UI-CF-FN0-aex-p-08-0-UI 3', mRNA sequence.

ACCESSION CB852764  
 VERSION CB852764.1 GI:30047800  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 683)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Genetec (www.resgen.com) or from Open Biosystems  
 (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA=Yes  
 FEATURES  
 source location/Qualifiers  
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 /clone="UI-CF-FN0-aex-p-08-0-UI"  
 /tissue\_type="Human Lung Epithelial cells"  
 /lab\_host="DH10B (Life Technologies) (Ti phage resistant)"  
 /clone\_lib="UI-CF-FN0"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-CF-FN0 is a subtracted cDNA library derived from two  
 normalized Human lung epithelial cell libraries (EN1 and  
 DU1) The library was subtracted according to according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. For additional information, contact:  
 bento-soares@uiowa.edu  
 TAG\_SEQ=None found"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1-31e-107 Length: 683  
 Score: 1088.00 Matches: 213  
 Percent Similarity: 98.61% Conservatives: 0  
 Best Local Similarity: 98.61% Mismatches: 3  
 Query Match: 90.22% Indels: 1  
 DB: 14 Gaps: 0  
 US-09-771-161A-93 (1-232) x CB852764 (1-683)  
 QY 17 AspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGlu 36  
 :::  
 Db 681 GACAAAGATGAAATGGAATA-TCTCTGAACATACCTGTAATATCATGGTCCACAAAGGAA 623  
 QY 37 SerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeu 56  
 :::  
 Db 622 TCATGTGGATCTCTCAGCTCCATGAAATAGTGGTTCTCTGAAACTTCAAGGTCCTTG 563  
 QY 57 ProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLys 76  
 :::  
 Db 562 CCAGCTCTCTCAAGCAATGATTTTTATCTAGAAAGCTCAGACTGTTATTTATGAAG 503  
 QY 77 LeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAla 96



Unpublished (2001)	185	ThrThrAspIleGlnGlyGluGluPheAlaIysValIleValGlnLysLeuLysAspAsn	204
CONTACT: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4797.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODI037AA04NP1&cluster=4797.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI037AA04NP1.	181	ACTACTGACATCCCAAGGAGAGAAATTTGCCAAGCTTTAGTACAAAATTTGAAAGATTAAC	122
FEATURES	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	224
source	212	AAACAAATGGGTCTTCAKCTTACCAGGAATATCTTGTGGTTTWTAGATCACATCTTTA	62
	225	AsnLeuLeuGlnAsnLys	230
	61	AATTTACTTCAAAWTAA	44
RESULT 9	CB851847/c		
LOCUS	CB851847.1	715 bp mRNA linear	EST 22-APR-2003
DEFINITION	UI-CF-FNO-aem-o-20-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone		
ACCESSION	CB851847	UI-CF-FNO-aem-o-20-0-UI 3', mRNA sequence.	
VERSION	CB851847.1	GI:30046667	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 715)		
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.		
TITLE	Normalization and subtraction: two approaches to facilitate gene		
JOURNAL	Genome Res. 6 (9), 791-806 (1996)		
MEDLINE	97044477		
PUBMED	8889548		
COMMENT	Contact: McCray, PB McCray Lab University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171 Email: paul-mccray@uiowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com). The following repetitive elements were found in this cDNA sequence: 1-24, >AT-rich#Low_complexity (matched compliment) Seq primer: M13 FORWARD POLYA=Yes.		
FEATURES	Location/Qualifiers		
source	1..715		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clones="UI-CF-FNO-aem-o-20-0-UI"		
	/tissue type="Human Lung Epithelial cells"		
	/lab host="DH10B (Life Technologies) (T1 phage resistant)"		
	/clone lib="UI-CF-FNO"		
	/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Score 1; Site 2: Not 1; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to EN1 and Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: Bento-soares@uiowa.edu TAG_SEQ=None found"		
ORIGIN	Alignment Scores:		
	Pred. No.: 2.23e-106	Length:	715
	Score: 1077.00	Matches:	214
	Percent Similarity: 99.08%	Conservative:	1



Best Local Similarity: 98.62% Mismatches: 2  
 Query Match: 89.30% Indels: 2  
 DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CB951847 (1-715)

QY 16 CysAspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGlu 35  
 DB 714 TGTGACAGGAAGAAATGGAATA-TCTCTGACATACCTGTAATCATGTGTCACAGAG 656  
 QY 36 GluSerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSer 55  
 DB 655 GAATCATGTGGATCTCTCAGCTCCATGAAATAGTGT-TCTCTGAAATCTCAAGGTCC 597  
 QY 56 LeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMet 75  
 DB 596 CTGCCAGCTCTCAAGCAATGATTTTATCTAGAAAAGCTCAAGACTGTTATTTATG 537  
 QY 76 LysLeuHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArg 95  
 DB 536 AAGCTGCATCAGTCTGCTGGAATACAGTTGGATAGCACCATTCTGGATCTCAAAGG 477  
 QY 96 AlaAlaPheCysAspHisLysThrProCysSerSerAlaIleLeuAsnProLeuSer 115  
 DB 476 GCTGCATTTCTGTATCAAGACACCTCCATGCTCTTTCAGCAATAATAAAATCCACTTCA 417  
 QY 116 ThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLys 135  
 DB 416 ACTGCAGAAACTCAGAACGCTGTCAGCTGTATAGCCAGCAGTGGATCCAGAGCAA 357  
 QY 136 ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeu 155  
 DB 356 AGGAAGACATTTGTAACCAAAATCACAGAACCTGCCTTAACAGTCCCTAGTAGCCCTT 297  
 QY 156 LeuSerArgAspIleMetLysGluAspTyrGluLeuValSerThrLysProThrArg 175  
 DB 296 CTGTCCAGGACTTGATCATGAAAGAGGACTATGAATCTTTAGTACCAAGCTTACAGG 237  
 QY 176 ThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLys 195  
 DB 236 ACCTCAAAAGTCAGACAAATTTACTAGACACTACTGACATCCAGGAGAAATTTGCCAA 177  
 QY 196 ValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProThrProGluIle 215  
 DB 176 GTTATAGTACAAAATTTGAAAGATAACAAACAAATGGTCTTCAGCCCTTACCCGGAATA 117  
 QY 216 LeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 232  
 DB 116 CTGTGTGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATG 66

RESULT 10  
 BG393551 883 bp mRNA linear EST 12-MAR-2001  
 LOCUS 602411943F1 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:4540787 5',  
 DEFINITION mRNA sequence.  
 ACCSSION BG393551  
 VERSION BG393551.1 GI:13286999  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 883)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM10471 row: e column: 12  
 High quality sequence stop: 767.

# FEATURES

source  
 1. .883  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4540787"  
 /tissue\_type="embryonal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 92"  
 /notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 2.5 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3 86e-105 Length: 883  
 Score: 1067.00 Matches: 204  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 88.47% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-771-161A-93 (1-232) x BG393551 (1-883)

QY 29 ValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGluAsnSerGly 48  
 DB 2 GTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATCAAAATAGTGGT 61  
 QY 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 68  
 DB 62 TCTCTGAAACTTCAAGGTCCTCCAGGCTCTTCAAGACAAATGATTTTATCTAGAAA 121  
 QY 69 AlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSer 88  
 DB 122 GCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATCACAGTTCGGATAGC 181  
 QY 89 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSer 108  
 DB 182 ACCATTTCTGGATCTCAAAAGGCTGCTGATGATCACAAGACCACTCCATGCTCTTCA 241  
 QY 109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128  
 DB 242 GCAATTAATAATCCATCTCACTGAGGAACTCAGAACTGAGCTCTGAGCTGGTATAGCC 301  
 QY 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148  
 DB 302 CACGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAAGCTGCTT 361  
 QY 149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168  
 DB 362 AACGAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAGGACTATGAAC 421  
 QY 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 188  
 DB 422 GTTAGTACCAAGCTCAGAGGACCTCAAAAGTCAGACAAATTAATAGACACTACTGACATC 481  
 QY 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208  
 DB 482 CAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGGT 541  
 QY 209 LeuGlnProThrProGluIleLeuValSerArgSerProSerLeuAsnLeuGln 228  
 DB 542 CTTACGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTAAATTTACTTCA 601  
 QY 229 AsnLysSerMet 232  
 DB 602 AATAAAGCATG 613



## RESULT 11

BM840808 660 bp mRNA linear EST 06-MAR-2002  
 K-EST0117952 S12SNU216 Homo sapiens cDNA clone S12SNU216-38-G08 5',  
 mRNA sequence.

## ACCESSION

BM840808.1 GI:19197217

## VERSION

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 660)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.

## AUTHORS

21C Frontier Korean EST Project 2001

## TITLE

Unpublished (2002)

## JOURNAL

Contact: Kim YS

## COMMENT

Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 38 row: G column: 08  
 High quality sequence stop: 660.

## FEATURES

Location/Qualifiers

1..660

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="S12SNU216-38-G08"

/sex="F"

/tissue\_type="lymph node"

/cell\_type="Epithelial"

/lab\_host="SNU-216"

/clone\_lib="S12SNU216"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;  
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dT-selected mRNA by  
 priming with dr-tailed vector. The dr-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10' by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.24e-101 Length: 660  
 Score: 1029.00 Matches: 197  
 Percent Similarity: 99.50% Conservative: 1  
 Best Local Similarity: 98.99% Mismatches: 1  
 Query Match: 85.32% Indels: 0  
 DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BM840808 (1-660)

QY 5 GlnLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24

Db 64 AAGTTACAGAGTGTTCACAGTCCATTCACATGTGCAAGAAATGAATATCT 123

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44

Db 124 CTGAACATACCTGTAAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCAT 183  
 QY 45 GlnAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 Db 184 GAAATAGTGGTCTCTCTGAAATCTCAAGGTCCTGCCAGCTCTCTCAAGACAATGATTTT 243  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
 Db 244 TTATCTAGAAAAGCTCAAGACTGTTATTTATTAAGAGCTGCATCCTCTCTGGAATCAC 303  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 Db 304 AGTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 363  
 QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 Db 364 CCATGCTCTTCAGCAATAATAATCCATCTCACTGCAGGAACCTCAGAGCTCTGCAG 423  
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 Db 424 CCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACA 483  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164  
 Db 484 GAAGCCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGAG 543  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 Db 544 GACTATGAATCTGTGTAGTACCAAGCTACAGGACTCAAAAGTCAGACAATTAAGTAC 603  
 QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsp 203  
 Db 604 ACTACTGACATCCAAAGAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGAT 660

## RESULT 12

BE875947

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE875947 828 bp mRNA linear EST 20-OCT-2000  
 601486423F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3888965 5',  
 mRNA sequence.

BE875947.1 GI:10324723

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 828)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTF/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9669 row: n column: 06

High quality sequence stop: 795.

Location/Qualifiers

1..828

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3888965"

/tissue\_type="large cell carcinoma, undifferentiated"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_69"

/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.1 kb. Library constructed by Life Technologies."

## ORIGIN

Alignment Scores:  
Pred. No.: 9,98e-101 Length: 828  
Score: 1028.00 Matches: 203  
Percent Similarity: 99.02% Conservative: 0  
Best Local Similarity: 99.02% Mismatches: 1  
Query Match: 85.07% Indels: 2  
DB: 10 Gaps: 0

US-09-771-161A-93 (1-232) x BE875947 (1-828)

Qy 29 ValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGluAsnSerGly 48  
Db 5 GTRAAATCATGGTCCACAAAGGAATCATGTGGATCTCTCAGCTCCATGAATAGTGGT 64  
Qy 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 68  
Db 65 TCTCCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTATCTAGAAA 124  
Qy 69 AlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSer 88  
Db 125 GCTCAAGACTGTATTTTGAAGCTGCATCCTCTGGAATACAGTTGGATAGC 184  
Qy 89 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSer 108  
Db 185 ACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAGACCACTCCATGCTCTTCA 244  
Qy 109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128  
Db 245 GCATAATAAATCACTCTCAACTGCAGGAACTCAGAGCTCTGCAGCCTGGTATAGCC 304  
Qy 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148  
Db 305 CAGCAGTGGATCCAGACAAAGGGAAGACATTGTGAACCAATGACAGAGGCTGCCTT 364  
Qy 149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168  
Db 365 AACCACTCGTAGATGCCCTTCTGTCCAG-GACTTGATCATGAAGAGGACTATGAATT 423  
Qy 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrAspIle 188  
Db 424 GTTAGTACCAAGCCTACAAAGACCTCAAAAGTCAGACAATTAAGTACACTGACATC 483  
Qy 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208  
Db 484 CAAGAGAAGAAATTGCAAGGTATAGTACAAAATTGAAGATAACAACAATGGGT 543  
Qy 209 LeuGlnProTyrProGluIle-LeuValValSerArgSerProSerLeuAsnLeuGlu 228  
Db 544 CTTCAAGCTTACCGGAATACTTGGTGGTTCTAGATCACCATCTTTAAATTACTTCA 603  
Qy 228 nAsnLysSerMet 232  
Db 604 AAATAAAGCATG 616

## RESULT 13

CA314123/c  
LOCUS 672 bp mRNA linear EST 04-NOV-2002  
DEFINITION UI-CF-FNO-aez-o-11-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
CA314123  
ACCESSION UI-CF-FNO-aez-o-11-0-UI 3', mRNA sequence.  
VERSION CA314123.1 GI:24532221  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 672)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL  
MEDLINE  
PUBMED

discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

## FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-FNO-aez-o-11-0-UI"  
/tissue\_type="Human Lung Epithelial cells"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-FNO"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR 1; Site 2: Not 1;  
UI-CF-FNO is a subtracted cDNA library derived from two  
normalized Human lung epithelial cell libraries (EN1 and  
DUI) The library was subtracted according to according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. For additional information, contact:  
bento-soares@uiowa.edu  
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368  
TAG LIB=UI-CF-FNO  
TAG\_SEQ=GGCTGTAGGC"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,11e-99 Length: 672  
Score: 1015.00 Matches: 203  
Percent Similarity: 97.60% Conservative: 0  
Best Local Similarity: 97.60% Mismatches: 3  
Query Match: 84.16% Indels: 3  
DB: 14 Gaps: 0  
US-09-771-161A-93 (1-232) x CA314123 (1-672)  
Qy 27 IleProValAsnHisGlyProGln-GluGluSerCysGlySerSerGlnLeuHisGluAs 46  
Db 670 ATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCATGAAA 611  
Qy 46 nSerGlySerProGluThrSerArgSerLeuProAlaPro-GlnAspAsnAspPheLeu 66  
Db 610 TAGTGGTCTCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCNAAGACAATGATTTTAT 551  
Qy 66 erArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerT 86  
Db 550 CTAGAAGACT-CAAGACTGTATTTTATTAAGAGCTGCATCCTCTCTCGAAATCACAGT 492  
Qy 86 xpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProC 106  
Db 491 GGGATAGCACCATTCTGGATCTCAAGAGGCTGCATCTGTGTATCAAGACCACTCCAT 432  
Qy 106 ysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG 126  
Db 431 GCTCTTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACTGTCAGCGCTG 372  
Qy 126 lyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 146

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Db      371  GTATAGCCAGAGTGGATCCAGACAAAGGAAGACATTTGAAACCAATGACAGAG 312
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Db      311  CCTGCCTTAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACT 252
Qy      166  yzGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrT 186
Db      251  ATGAACCTTGTAGTACCAAGCCCTACAAGGACCTCAAAAGTCAGAAATTTACTAGACACTA 192
Qy      186  hrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysG 206
Db      191  CTGACATCCAGGAGGAAGATTTGGCAAGTTATAGTACAAAATTTGAAGATAACAAC 132
Qy      206  InMetGlyLeuGlnProTyProGluIleLeuValSerArgSerProSerLeuAsnL 226
Db      131  AAATGGGCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTAAAT 72
Qy      226  euLeuGlnAsnLysSerMet 232
Db      71  TACTTCAAAATAAAGCATG 52

RESULT 14
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LOCUS   BE536247
DEFINITION BE536247 654 bp mRNA linear EST 09-AUG-2000
        601062632F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449311 5',
        mRNA sequence.
ACCESSION BE536247
VERSION   BE536247.1 GI:9764892
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 654)
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: Incyte Genomics, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM8425 row: 0 column: 08
          High quality sequence stop: 650.
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                Average insert size 1.5 kb. Library prepared by Life
                Technologies."
ORIGIN
Alignment Scores:
Pred. No.: 1.3e-98 Length: 654
Score: 1005.00 Matches: 206
Percent Similarity: 95.85% Conservative: 2
Best Local Similarity: 94.93% Mismatches: 5
Query Match: 83.33% Indels: 5
DB: 10 Gaps: 0

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US-09-771-161a-93 (1-232) x BE536247 (1-654)
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Qy      25  LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSer-GlnLeuHi 44
Db      69  CTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCANGCTCCA 128
Qy      44  sGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPh 64
Db      129  TGAATAATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCAGCTCTCTCAAGACAATGATT 188
Qy      64  eLeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisHisCysProGlyAsnHi 84
Db      189  TTTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTCTGGAATCA 248
Qy      84  sSerTrpAspSerThrIleSerGlySerGluArgAlaAlaPheCysAspHisLysThrTh 104
Db      249  CAGTTGGGATAGCACCATTTCTGGATCTCAAGAGGCTGCATTTCTGTGATCACAGACCAC 308
Qy      104  rProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGl 124
Db      309  TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAANAATCAGACGCTGCA 368
Qy      124  nProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetTh 144
Db      369  GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 428
Qy      144  rGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGl 164
Db      429  AGAAGCCTGCTT-AAACAGTCGTAGATGCCCTCTCTCCAGGGACTTGATCATGAAAGA 487
Qy      164  uAspTyrrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAs 184
Db      488  GGACTATGACTTGTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTTGCTAGA 547
Qy      184  pThrThrAspIleGlnGly-GluGluPheAlaLysValIleValGlnLys-LeuLysAsp 203
Db      548  CACTACTGACATCCAAAGGCAGAGAATTTGGCANAGTTATAGTACAAAATTTGCAAGAT 607
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Db      608  AACCACAAACAAATGGGTCTCAGCCTTACCCGGGAATACTTTGTG 650

RESULT 15
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DEFINITION BE536247 811 bp mRNA linear EST 06-FEB-2001
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        mRNA sequence.
ACCESSION BE536247
VERSION   BE536247.1 GI:12677108
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 811)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM10172 row: 9 column: 09
          High quality sequence stop: 721.

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FEATURES  
source

Location/Qualifiers  
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.47e-98 Length: 811  
Score: 1002.50 Matches: 201  
Percent Similarity: 95.81% Conservative: 5  
Best Local Similarity: 93.49% Mismatches: 8  
Query Match: 83.13% Indels: 3  
DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BG170405 (1-811)

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Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db :::  
225 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGTCCAT 284  
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64  
Db :::  
285 GAAATATAGTGTTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTT 344  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
Db :::  
345 TTATCTAGAAAGCTCAAGACTGTATTTATGAGCTGTCATCCTCTCTGGAATCAC 404  
Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db :::  
405 AGTTGGGATAGCACTTCTGGATCTCAAGGCTGCATTCTGTGATCACAAGACCCT 464  
Qy 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db :::  
465 CCATGCTCTTCAGCAATAATAATCCACTCTCACTCAGGAACTCAGAACCGTCTGCAG 524  
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db :::  
525 CTTGGTATAGCCAGCAGTGGATCCAGCAGCAAGGAGAGACATTGTGAACCAATGACA 584  
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Db :::  
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Qy 184 pThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAs 204  
Db :::  
705 CACTACTGACATCAAGAGAGAGA-TTTGCCAAGTTATACGTACAAAAAATTGACGATTA 763  
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Db :::  
764 CCAACA-ATGGGTCTTAAGCCTTACCGGAAAAATACTGTGGGTT 805

Search completed: April 1, 2004, 12:07:12  
Job time : 2717 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 02:20:16 ; Search time 6737 Seconds  
(without alignments)  
10737.646 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 1669

Sequence: 1 acctggtttataccagata.....caacgctgtgtgtataaa 1669

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vt.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

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27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

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32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rnd.\*

36: em\_htg\_man.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1333.4	79.9	2521	9	AY358814	AY358814 Homo sapi
2	1308	78.4	2501	6	AR221453	AR221453 Sequence
3	1308	78.4	2501	6	AX429236	AX429236 Sequence
4	1308	78.4	2501	9	AF027706	AF027706 Homo sapi
5	1308	78.4	2502	6	AR194318	AR194318 Sequence
6	990	59.3	116850	9	AC004003	AC004003 Homo sapi
7	879.4	52.7	320187	9	AF117829	AF117829 Homo sapi
8	879.4	52.7	320187	9	AF117829	AF117829 Homo sapi
9	876.8	52.5	2033	6	BD251808	BD251808 Phosphory
10	876.8	52.5	2033	6	BD251808	BD251808 Phosphory
11	876.8	52.5	2033	6	BD127583	BD127583 Primer fo
12	861	51.6	2098	6	AK075213	AK075213 Homo sapi
13	861	51.6	2098	6	AK075213	AK075213 Homo sapi
14	754.4	45.2	61099	2	AC139421	AC139421 Homo sapi
15	733.4	43.9	1889	9	BC004553	BC004553 Homo sapi
16	731.8	43.8	1931	6	AR183234	AR183234 Sequence
17	731.8	43.8	1931	6	AR205634	AR205634 Sequence
18	731.8	43.8	1931	6	AR216112	AR216112 Sequence
19	731.8	43.8	1931	6	AR241236	AR241236 Sequence
20	731.8	43.8	1931	6	AR256252	AR256252 Sequence
21	731.8	43.8	1931	6	AR391599	AR391599 Sequence
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26	684.8	41.0	1623	9	AF078530	AF078530 Homo sapi
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28	681.8	40.9	1620	6	AR183235	AR183235 Sequence
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36	441.6	26.5	1620	10	AF487539	AF487539 Mus muscu
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ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

AY358814  
Homo sapiens  
AY358814  
AY358814.1  
FLI\_CDNA  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2521)  
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,J., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Hsu,J., et al.

2521 bp  
mRNA  
linear  
PRI 03-OCT-2003  
mrna, complete cds.

Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seehagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I., and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
12975309  
PUBMED  
2 (bases 1 to 2521)  
REFERENCE  
AUTHORS  
TITLE  
DIRECT SUBMISSION  
JOURNAL  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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Query Match 79.9%; Score 1333.4; DB 9; Length 2521;  
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Matches 1334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2  
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ACCESSION  
VERSION AR221453.1 GI:23328503

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RESULT 4
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LOCUS AF027706 2501 bp mRNA linear PRI 10-SEP-1998
DEFINITION cds.
ACCESSION AF027706
VERSION AF027706.1 GI:3123886
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2501)
AUTHORS Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
TITLE RICK, a novel protein kinase containing a caspase recruitment
domain, interacts with CLARP and regulates CD95-mediated apoptosis
JOURNAL J. Biol. Chem. 273 (20), 12296-12300 (1998)
MEDLINE 98241596
PUBMED 9575181
REFERENCE 2 (bases 1 to 2501)
AUTHORS Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1997) Dept. Pathology, Comprehensive Cancer &
Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr., Ann Arbor,
MI 48109, USA
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LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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AC004003 116650 bp DNA linear PRI 21-DEC-1999
Homo sapiens BAC clone CTA-437L15 from 8q21, complete sequence.
AC004003
AC004003.1 GI:2722557
HTG.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ozersky, P., Holmes, A. and Broy, M.
The sequence of Homo sapiens BAC clone CTA-437L15
Unpublished
2 (bases 1 to 116650)
Waterston, R.
Direct Submission
Submitted (15-JAN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
3 (bases 1 to 116650)
Waterston, R.
Direct Submission
Submitted (27-JUN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 116650)
Waterston, R.
Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics
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Center project name: H_RG437L15
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
This chromosome 8 clone was provided by Dr. Patrick Concannon (patcon@vmc.org) at the Virginia Mason Research Institute.

SOURCE INFORMATION:  
Clone CTA-437L15 is from a release of the human BAC library CITB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).  
VECTOR: pHEBAC11  
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is CTA-237G1. The actual start of this clone is at base position 1 of CTA-437L15; actual end is at 116650 of CTA-437L15.

This clone contains STS HS275YF1 (NID: g1051703).  
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DEFINITION Homo sapiens chromosome 8 multiple clones map q21.3, complete
sequence.
ACCESSION AF117829
VERSION AF117829.2 GI:38153762
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 320187)
AUTHORS Platzer M., Varon R., Sperling K., Reis A. and Rosenthal A.
TITLE Chromosome 8 genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 320187)
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AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Platzer M. and Varon R.  
Direct Submission  
Submitted (30-DEC-1998) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
3 (bases 1 to 320187)  
Platzer M.  
Direct Submission  
Submitted (04-NOV-2003) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany  
On Nov 4, 2003 this sequence version replaced gi:4151947.  
----- Genome Center  
Center: Institute of Molecular Biotechnology  
Center code: IMB  
Web site: http://genome.imb-jena.de/  
Contact: gscj-submit@genome.imb-jena.de  
----- Project Information  
Center project name: NBSlocuSA  
Center clone name: RGP-64M4 to SCB-316M22  
----- Summary Statistics  
Sequencing vector: M13mp18; 100% of reads  
Chemistry: Dye-primer ET, Dye-terminator Big Dye;  
Consensus quality: 319496 bases at least Q40  
Consensus quality: 320184 bases at least Q30  
Consensus quality: 320187 bases at least Q20  
Quality coverage: 7.63  
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This sequence was finished as follows unless otherwise noted: all  
regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest.  
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Neighboring sequence information:  
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sequence is directed towards the centromere. The end  
(318188..320187) of this sequence overlaps with the start of  
Acc number AF049895. It covers RGP-64M4, SCB-282k6, SCB-273G1  
entirely and is overlapped by SCB-296N11, SCB-316M22.  
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Sequence Quality Assessment:  
This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than  
1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the  
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 VERSION AY358813.1 GI:37182743  
 KEYWORDS FLI CDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS  
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
 Stinson,J., Vagts,A., Vandel,R., Watanabe,C., Wieand,D., Woods,K.,  
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.

TITLE  
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 JOURNAL  
 PUBMED  
 12975309  
 REFERENCE  
 2 (bases 1 to 1886)  
 AUTHORS  
 Clark,H.F.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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BD127583 2033 bp DNA linear PAT 18-SEP-2002  
 Primer for synthesizing full-length cDNA and use thereof.  
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 BD127583.1 GI:23222528  
 JP 2002017375-A/3014  
 Homo sapiens (human)  
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REFERENCE 1 (bases 1 to 2033)  
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.  
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 JOURNAL Patent: JP 2002017375-A 3014 22-JAN-2002;  
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 PN JP 2002017375-A/3014  
 PD 22-JAN-2002  
 PF 07-JUL-2000 JP 2000253172  
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 SHINICHI KOJIMA,  
 PI TETSUJI OTSUKI,HISASHI KOGA  
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 VERSION AK075213.1  
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 ORGANISM Homo sapiens  
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 REFERENCE 1  
 AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,  
 Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,  
 Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,  
 Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,  
 Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and  
 Ninomiya,K.  
 TITLE NEDO human cDNA sequencing project  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 2033)  
 AUTHORS Isogai,T. and Otsuki,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,  
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 COMMENT NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology; cDNA library construction:  
 Institute of Medical Science, University of Tokyo, Laboratory of  
 Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass  
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 Best Local Similarity 99.8%; Pred. No. 2e-151;  
 Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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REFERENCE	1 (bases 1 to 2098)			
AUTHORS	Boldin,M. and Wallach,D.			
TITLE	MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL SURVIVAL PATHWAYS			

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----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L29371  
Center clone name: 706\_H\_15  
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\* NOTE: This record contains 67 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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AUTHORS		Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
TITLE		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
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PUBMED		12477932	
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AUTHORS		Strausberg, R.	
TITLE		Direct Submission	
JOURNAL		Submitted (14-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
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RESULT 15

BC004553

LOCUS

DEFINITION

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 00:03:50 ; Search time 661 Seconds  
(without alignments)  
10726.539 Million cell updates/sec

Title: US-09-771-161A-2  
Perfect score: 1669  
Sequence: 1 acctagttattaccagata.....caacagcctgtatgtgtaaaa 1669

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : N\_Geneseq\_29Jan04:\*
- 1: Geneseqn1980s:\*
  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001as:\*
  - 5: Geneseqn2001bs:\*
  - 6: Geneseqn2002s:\*
  - 7: Geneseqn2003as:\*
  - 8: Geneseqn2003bs:\*
  - 9: Geneseqn2003cs:\*
  - 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1332.4	79.8	2709	3 AAC77779	AAC77779 Human can
2	1308	78.4	2501	6 ABK51169	Abk51169 cDNA enco
3	1308	78.4	2501	6 AAD45172	Aad45172 Human rec
4	1308	78.4	2502	3 AAZ48762	Aaz48762 Human RIC
5	879.4	52.7	2024	3 AAZ46143	Aaz46143 cDNA sequ
6	876.8	52.5	2033	4 AAQ94554	Aaq94554 Human ful
7	861	51.6	2098	2 AAX02558	Aax02558 Human B1
8	786.2	47.1	1959	9 ADC99131	Adc99131 Human KPP
9	731.8	43.8	1931	2 AAZ09246	Aaz09246 Human CAR
10	731.8	43.8	1931	4 AAF30001	Aaf30001 Human CAR
11	731.8	43.8	1931	6 ABK89280	Abk89280 Human cDN
12	731.8	43.8	1931	6 AAL40752	Aal40752 cDNA of h
13	731.8	43.8	1931	7 ABX75869	Abx75869 Human cDN
14	731.8	43.8	1931	9 ADB81363	Adb81363 Human cas
15	681.8	40.9	1620	7 ABX75870	Abx75870 Human cas
16	669.8	40.1	1619	6 AAL40753	Aal40753 DNA of hu
17	447.6	26.8	575	4 AAK93010	Aak93010 Human cDN
18	363.4	21.8	491	8 ACH33353	Ach33353 Human end
19	283	17.0	762	7 ACD96414	Acd96414 Human col
20	271	16.2	299	6 ABK55074	Abk55074 Human col
21	102	6.1	108	2 AAT19776	Aat19776 Human gen
22	69	4.1	8056	7 ABZ10246	Abz10246 Haematopo
23	69	4.1	8056	7 ABZ10100	Abz10100 Haematopo

c	24	60.6	3.6	8056	7	ABZ10246	Abz10246 Haematopo
	25	60	3.6	60	6	ABN58531	Abn58531 Human spl
	26	60	3.6	60	6	ABN58793	Abn58793 Human spl
	27	60	3.6	60	6	ABN41051	Abn41051 Human spl
	28	59	3.5	19576	6	ABL70575	Abi70575 Chemical
	29	59	3.5	19576	6	AAS61258	Aas61258 Human gen
	30	58.2	3.5	23683	6	ABL34623	Abi34623 Human met
	31	58.2	3.5	23683	6	ABL70482	Abi70482 Chemical
	32	57.4	3.4	6286	4	AAS46591	Aas46591 Tumour su
	33	57.4	3.4	8711	4	AAS46700	Aas46700 Tumour su
	34	57.4	3.4	46951	9	ADE13891	Adel13891 Human bpe
c	35	57.2	3.4	883	4	AAL15210	Aal15210 Human opt
	36	57.2	3.4	6816	4	AAS46688	Aas46688 Tumour su
	37	56.8	3.4	12142	6	ABL33673	Abi33673 Human imm
	38	56.6	3.4	7814	4	AAS46530	Aas46530 Tumour su
	39	56.6	3.4	17848	4	AAS45323	Aas45323 Chemical
	40	56.6	3.4	17848	6	ABK39976	Abk39976 Human che
	41	56.6	3.4	17848	6	ABK28164	Abk28164 DNA trans
	42	56.2	3.4	5945	6	ABL32085	Abi32085 Human imm
c	43	56.2	3.4	6880	6	ABK31322	Abk31322 Signal tr
	44	56.2	3.4	6880	6	ABL70293	Abi70293 Chemical
c	45	56.2	3.4	6880	6	AAS61223	Aas61223 Human gen

ALIGNMENTS

RESULT 1  
AAC77779  
ID AAC77779 standard; cDNA; 2709 BP.  
XX  
AC AAC77779;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated gene sequence SEQ ID NO:173.  
XX

Human; cancer associated gene; cancer antigen; detection; cancer;  
diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;  
antidiabetic; antiaesthetic; antirheumatic; antithrombotic; antiviral;  
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;  
dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;  
immune disorder; haematopoietic cell disorder; autoimmune disorder;  
allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening; ss.  
XX Homo sapiens.  
OS  
XX WO200055350-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005882.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
XX WPI; 2000-587533/55.  
DR P-PSDB; AAB43570.  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
useful for treating or diagnosing e.g. cancer.  
XX  
PS Claim 1; Page 751-752; 2352pp; English.  
XX  
CC AAC77607 to AAC78448 encode the human cancer associated proteins given in  
AACB3398 to AAB44239. The proteins can have activities based on the  
tissues and cells the genes are expressed in. Example of activities

CC include: cytostatic; proliferative; vulnery; immunomodulator;  
 CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological diseases and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC7849 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 0 U; 10 Other;

Query Match 79.8%; Score 1332.4; DB 3; Length 2709;  
 Best Local Similarity 99.6%; Pred. No. 2.4e-259;  
 Matches 1330; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCTTCAAGTCCATTACCTATGTGACAGAGAAATGGAATTATC 390  
 DB 1202 AAGTTACAGAGTGTTCAGTGCCTTCAAGTCCATTACCTATGTGACAGAGAAATGGAATTATC 1261  
 QY 391 TCTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCCTCTCAGTCCCA 450  
 DB 1262 TCTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCCTCTCAGTCCCA 1321  
 QY 451 TGAATATAGTGTCTCTCTGAACCTTCAAGTCCCTGCCAGCTCCCTCAAGACATGATTT 510  
 DB 1322 TGAATATAGTGTCTCTCTGAACCTTCAAGTCCCTGCCAGCTCCCTCAAGACATGATTT 1381  
 QY 511 TTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGGAATCA 570  
 DB 1382 TTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGGAATCA 1441  
 QY 571 CAGTGGGATPAGCACCAATTTCTGGATCTMAAGGGCTGCATTTCTGTGATCACAAGACCAC 630  
 DB 1442 CAGTGGGATPAGCACCAATTTCTGGATCTMAAGGGCTGCATTTCTGTGATCACAAGACCAC 1501  
 QY 631 TCCATGCTCTTCCAGCAATAAATCCACTCACTCAAGTCCAGGAACTCAGAACGTCTGCA 1561  
 DB 1502 TCCATGCTCTTCCAGCAATAAATCCACTCACTCAAGTCCAGGAACTCAGAACGTCTGCA 1561  
 QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
 DB 1562 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1621  
 QY 751 AGAAGCCTGCTTAAACAGTGGTATAGTGCCTTCTGTCCAGGACTGTGATCATGAAGA 810  
 DB 1622 AGAAGCCTGCTTAAACAGTGGTATAGTGCCTTCTGTCCAGGACTGTGATCATGAAGA 1681  
 QY 811 GGACTATGAAGTGTGTAGTACAGCCTCAAGACCTCAAAAGTCAAGCAATTTACTAGA 870  
 DB 1682 GGACTATGAAGTGTGTAGTACAGCCTCAAGACCTCAAAAGTCAAGCAATTTACTAGA 1741  
 QY 871 CACTACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930  
 DB 1742 CACTACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 1801  
 QY 931 CAAACAAATGGTCTTCCAGCCTTACCCGGAAATCTTGTGGTTCTAGATCACCATCTTT 990  
 DB 1802 CAAACAAATGGTCTTCCAGCCTTACCCGGAAATCTTGTGGTTCTAGATCACCATCTTT 1861  
 QY 991 AAATTTACTTCAAAATAAAGCATGTAAAGTACGTGTTTTTCAAGAGAAATGTGTTTCAT 1050  
 DB 1862 AAATTTACTTCAAAATAAAGCATGTAAAGTACGTGTTTTTCAAGAGAAATGTGTTTCAT 1921

QY 1051 AAAAGGATATTTATATCTCTGTGCTTTGACCTTTTATATAAAAATCCGTGAGTATTAA 1110  
 DB 1922 AAAAGGATATTTATATCTCTGTGCTTTGACCTTTTATATAAAAATCCGTGAGTATTAA 1981  
 QY 1111 AGCTTTATGAAGTGTCTTTGGGTAATAATATAGTCTCCCTCCATGACACTGACAGTATTTT 1170  
 DB 1982 AGCTTTATGAAGTGTCTTTGGGTAATAATATAGTCTCCCTCCATGACACTGACAGTATTTT 2041  
 QY 1171 TTTTAAATTAACAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1230  
 DB 2042 TTTTAAATTAACAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2101  
 QY 1231 TTTTAAATTAACAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1290  
 DB 2102 TTTTAAATTAACAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2161  
 QY 1291 AGTATGATGATTTCTGTGATGGAAGCATTTCACATCATGCTTCTCATGAGTATTTTG 1350  
 DB 2162 AGTATGATGATTTCTGTGATGGAAGCATTTCACATCATGCTTCTCATGAGTATTTTG 2221  
 QY 1351 TTACTTGTCTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1410  
 DB 2222 TTACTTGTCTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2281  
 QY 1411 GTACAGATCCCTGCCCTAAATCCAGGCTTAAATGGCCCTACAAAGGGTAAATTAATTTA 1470  
 DB 2282 GTACAGATCCCTGCCCTAAATCCAGGCTTAAATGGCCCTACAAAGGGTAAATTAATTTA 2341  
 QY 1471 AAACCTCATATAGGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1530  
 DB 2342 AAACCTCATATAGGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2401  
 QY 1531 ATTTCAAGGCTAAACAAATACAAATATAAGAAAAATAATATAATATAATATAATATAATATAATATAATATA 1590  
 DB 2402 ATTTCAAGGCTAAACAAATACAAATATAAGAAAAATAATATAATATAATATAATATAATATAATATAATATA 2461  
 QY 1591 TGTCCCAATTTTAACTCAGGCTTCCCTTCTGTCTACCAACCAACCAACCAACCAACCAACCAACCAACCA 1650  
 DB 2462 TGTCCCAATTTTAACTCAGGCTTCCCTTCTGTCTACCAACCAACCAACCAACCAACCAACCAACCAACCA 2521  
 QY 1651 AACAGCCTGATGTGA 1666  
 DB 2522 AACAGCCTGATGTGA 2537

RESULT 2  
 ABK51169  
 ID ABK51169 standard; cDNA; 2501 BP.

XX ABK51169;  
 AC AC  
 XX XX  
 DT 30-JUL-2002 (first entry)  
 XX cDNA encoding human cellular kinase RICK protein.  
 DE Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;  
 XX RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene; ss.  
 KW Homo sapiens.  
 OS Homo sapiens.

Key Location/Qualifiers  
 CDS 225..1847  
 FT /\*tag= a  
 FT /product= "Human cellular kinase RICK"

XX EP1201765-A2.  
 XX 02-MAY-2002.  
 XX 15-OCT-2001; 2001EP-00124604.  
 XX 16-OCT-2000; 2000US-0240750P.



PA	(AXXI-) AXXIMA PHARM AG.	
XX	PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;	
XX	DR WPI; 2002-373930/41.	
XX	DR P-PSDB; AAU08369.	
XX	Identifying agents for treatment or prevention of cytomegalovirus	
PT	infection, comprises contacting test compound with cellular kinase and	
PT	detecting change in cellular kinase activity.	
PS	Disclosure; Page 20-23; 49pp; English.	
XX		
CC	The present invention relates to a new method for identifying compounds	
CC	for treating and/or preventing cytomegalovirus (CMV) infection and/or	
CC	related diseases. The method of the invention comprises contacting a test	
CC	compound with at least one of the cellular kinases RICK, RIP, Nck-	
CC	interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase	
CC	activity. The method of the invention can be used to treat and/or prevent	
CC	CMV infections and related diseases. Oligonucleotides that can detect the	
CC	specified kinases can also be used for diagnosis of infection. The	
CC	present nucleic acid sequence encodes the human cellular kinase RICK	
CC	protein of the invention, as described above	
XX		
SQ	Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;	
	Query Match 78.4%; Score 1308; DB 6; Length 2501;	
	Best Local Similarity 99.0%; Pred. No. 2e-254;	
	Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;	
QY	331 ACAGTTACAGAGTGTTCGAAGTGCATTCACCTATGTGACAGAGAGAAATGGAATTATC 390	
Db	1160 AAAAGTTACAGAGTGTTCGAAGTGCATTCACCTATGTGACAGAGAGAAATGGAATTATC 1219	
QY	391 TCTGAACATACCTGTAAATCATGTGCTCCACAGAGGAATCATGTGGATCCTCTCAGTCCA 450	
Db	1220 TCTGAACATACCTGTAAATCATGTGCTCCACAGAGGAATCATGTGGATCCTCTCAGTCCA 1279	
QY	451 TGAATAATAGTGTGTTCTCTGAAACTTCAAGTGCCCTGCCAGCTCCTCAAGACAATGATTT 510	
Db	1280 TGAATAATAGTGTGTTCTCTGAAACTTCAAGTGCCCTGCCAGCTCCTCAAGACAATGATTT 1339	
QY	511 TTTATCTAGAAAGCTCAAGACGTGTTATTTATGAAGCTGATCATCTGTCCTGGAATCA 570	
Db	1340 TTTATCTAGAAAGCTCAAGACGTGTTATTTATGAAGCTGATCATCTGTCCTGGAATCA 1399	
QY	571 CAGTTGGGATGACCATTTCTGGATCTCAAGGGCTGATTCGTGATCACAAGACCAC 630	
Db	1400 CAGTTGGGATGACCATTTCTGGTCTCAAGGGGCTGATTCGTGATCACAAGACCAC 1459	
QY	631 TCCATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAAACTCAGAAGCTCTGCA 690	
Db	1460 TCCATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAAACTCAGAAGCTCTGCA 1519	
QY	691 GCCTGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750	
Db	1520 GCCTGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1579	
QY	751 AGAAGCTGCCCTTAACCACTGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGA 810	
Db	1580 AGAAGCTGCCCTTAACCACTGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGA 1639	
QY	811 GGACTATGAATCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 870	
Db	1640 GGACTATGAATCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 1699	
QY	871 CACTACTGATCCTCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 930	
Db	1700 CACTACTGATCCTCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 1759	
QY	931 CAAACAAATGGGTCTTCAGCCTTACCCGGAATATCTTGTGGTTCTAGATCACCATCTTT 990	
Db	1760 CAAACAAATGGGTCTTCAGCCTTACCCGGAATATCTTGTGGTTCTAGATCACCATCTTT 1819	

QY	991 AAATTTACTTCAAATAAAAGCATGTAAAGTGAAGTCTGTTTTTCAAGAAGAAATGTGTTTCAT 1050	
Db	1820 AAATTTACTTCAAATAAAAGCATGTAAAGTGAAGTCTGTTTTTCAAGAAGAAATGTGTTTCAT 1879	
QY	1051 AAAAGGATATTATATCTCTGCTGCTTTGACCTTTTTTATATATAAAATCCGTGAGTATTAA 1110	
Db	1880 AAAAGGATATTATATCTCTGCTGCTTTGACCTTTTTTATATATAAAATCCGTGAGTATTAA 1939	
QY	1111 AGCTTTATTTGAAGTTCCTTTGGGTAATAATTAGTCTCCCTCCATGACACTGCAGTATTTT 1170	
Db	1940 AGCTTTATTTGAAGTTCCTTTGGGTAATAATTAGTCTCCCTCCATGACACTGCAGTATTTT 1999	
QY	1171 TTTTAATTTAATCAAGTAAAAAGTT-----TGAATTTTGTCTACATAGTTCAATTTT 1222	
Db	2000 TTTTAATTTAATCAAGTAAAAAGTTGAATTTGGTTGAATTTTGTCTACATAGTTCAATTTT 2059	
QY	1223 ATGCTCTCTTTTGTAAACAGAACCACTTTTAAAGGATAGTAAATTTCTTGTGTTATAACA 1282	
Db	2060 ATGCTCTCTTTTGTAAACAGAACCACTTTTAAAGGATAGTAAATTTCTTGTGTTATAACA 2119	
QY	1283 GTGCCTTAAAGGTATGATGATTTCTGATGGAAGCCATTTTACATTCATGTTCTTTCATGG 1342	
Db	2120 GTGCCTTAAAGGTATGATGATTTCTGATGGAAGCCATTTTACATTCATGTTCTTTCATGG 2179	
QY	1343 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATATACCTTTTACCCAC 1402	
Db	2180 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATATACCTTTTACCCAC 2239	
QY	1403 CAGAGACAGTACAGNAATCCCTGCCCTAAATCCAGGCTTAATTCGCCCTACAGAGGGTTA 1462	
Db	2240 CAGAGACAGTACAGNAATCCCTGCCCTAAATCCAGGCTTAATTCGCCCTACAGAGGGTTA 2299	
QY	1463 TTAATTTAAACTCCATTTATTAGGATTAACATTTTAAAGTTTATTATGAAATCCCTTTA 1522	
Db	2300 TTAATTTAAACTCCATTTATTAGGATTAACATTTTAAAGTTTATTATGAAATCCCTTTA 2359	
QY	1523 AAAATGATATTTCAAAGGTAAAAACAATAATATAAAGAAAAAAATAAATATATTATATAC 1582	
Db	2360 AAAATGATATTTCAAAGGTAAAAACAATAATATAAAGAAAAAAATAAATATATTATATAC 2419	
QY	1583 CGGCTTCTGTCGCCCATTTTAACTCAGCCTCCCTACTGTCACCAACAACAGCTTAA 1642	
Db	2420 CGGCTTCTGTCGCCCATTTTAACTCAGCCTCCCTACTGTCACCAACAACAGCTTAA 2479	
QY	1643 ATAAAGTCAACAGCCTGATGTG 1664	
Db	2480 ATAAAGTCAACAGCCTGATGTG 2501	

RESULT 3  
AAD45172 standard; DNA; 2501 BP.  
XX AAD45172;  
AC AAD45172;  
XX 27-DEC-2002 (first entry)  
DT  
XX Human receptor interacting protein (RIP)2 DNA.  
DE Human; receptor interacting protein; RIP2; antisense; gene therapy; gene;  
XX ds.  
KW Homo sapiens.  
XX OS  
XX FH Key Location/Qualifiers  
XX FT CDS 225..1847  
XX FT /\*tag= a  
XX FT /product= "Human RIP2 protein"  
XX PN US6426221-B1.  
XX PD 30-JUL-2002.

XX 01-AUG-2001; 2001US-00920663.  
XX 01-AUG-2001; 2001US-00920663.  
XX (ISIS-) ISIS PHARM INC.  
XX Ward DT, Cowser LM;  
XX WPI; 2002-673017/72.  
XX P-PSDB; AAE27882.  
XX New antisense oligonucleotide that targets regions of a nucleic acid  
XX encoding human receptor interacting protein (RIP)2, for treating diseases  
XX associated with RIP2 expression.  
XX Claim 1; Col 49-54; 35pp; English.  
XX The invention relates to antisense compounds targetted to a nucleic acid  
XX encoding human receptor interacting protein (RIP)2 to inhibit its  
XX expression. Antisense compounds are used for treating diseases associated  
XX with RIP2 expression. They are also useful in antisense gene therapy. The  
XX present sequence is human RIP2 DNA  
XX  
SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
Query Match 78.4%; Score 1308; DB 6; Length 2501;  
Best Local Similarity 99.0%; Pred. No. 2e-254;  
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;  
QY 331 ACAGTTACAGAGTGTTCACAGTCCATTCACCTATGTGACAAAGAAATGAATATC 390  
DB 1160 AAGTTACAGAGTGTTCACAGTCCATTCACCTATGTGACAAAGAAATGAATATC 1219  
QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCCCTCAGCTCCA 450  
DB 1220 TCTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCCCTCAGCTCCA 1279  
QY 451 TGAAGATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTT 510  
DB 1280 TGAAGATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTT 1339  
QY 511 TTATCTAGAAAAGCTCAAGACTGTATTTATGAAGTCGATCATGTCTCGAAATCA 570  
DB 1340 TTATCTAGAAAAGCTCAAGACTGTATTTATGAAGTCGATCATGTCTCGAAATCA 1399  
QY 571 CAGTTGGATAGACCAATTTCTGATCTCAAGGGTGCATTTCTGTGATCACAAGACCAC 630  
DB 1400 CAGTTGGATAGACCAATTTCTGATCTCAAGGGTGCATTTCTGTGATCACAAGACCAC 1459  
QY 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCA 690  
DB 1460 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCA 1519  
QY 691 GCCTGGTATACCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGAAACCAATGAC 750  
DB 1520 GCCTGGTATACCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGAAACCAATGAC 1579  
QY 751 AGAGCCTGCTTAAACAGTCGTAGATGCCCTCTGCTCAGGGACTTGATCATGAAGA 810  
DB 1580 AGAGCCTGCTTAAACAGTCGTAGATGCCCTCTGCTCAGGGACTTGATCATGAAGA 1639  
QY 811 GGACTATGAATCTTGTAGTACCAAGCTCACAAGGACCTCAAAAGTCAGACAAATTTACTAGA 870  
DB 1640 GGACTATGAATCTTGTAGTACCAAGCTCACAAGGACCTCAAAAGTCAGACAAATTTACTAGA 1699  
QY 871 CACTACTGACATCCAAAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 930  
DB 1700 CACTACTGACATCCAAAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 1759  
QY 931 CAAACAAATGGCTCTTACAGCTTACCCGGAAATTTGCTGTCTAGATCACCATCTTT 990  
DB 1760 CAAACAAATGGCTCTTACAGCTTACCCGGAAATTTGCTGTCTAGATCACCATCTTT 1819

QY 991 AAATTTACTTTCAAAATAAAAGCATGTAACTGACTGTTTTCAGGAAGAAATGTGTTTCAT 1050  
DB 1820 AAATTTACTTTCAAAATAAAAGCATGTAACTGACTGTTTTCAGGAAGAAATGTGTTTCAT 1879  
QY 1051 AAAAGGATATTTATATCTCTGTTGCTTTCATCTTTTATATATAAAATCCGTGAGTATTA 1110  
DB 1880 AAAAGGATATTTATATCTCTGTTGCTTTCATCTTTTATATATAAAATCCGTGAGTATTA 1939  
QY 1111 AGCTTTATTTGAAGGTTCTTTGGTAAATATAGTCTCCCTCCATGACACATGCGAGTATTTT 1170  
DB 1940 AGCTTTATTTGAAGGTTCTTTGGTAAATATAGTCTCCCTCCATGACACATGCGAGTATTTT 1999  
QY 1171 TTTTAATTAATACAGTAATAAAAGTT-----TGAATTTTGTCTACATAGTTTCAATTTTT 1222  
DB 2000 TTTTAATTAATACAGTAATAAAAGTTTGAATTTGCTGTAATTTTCAATTTTT 2059  
QY 1223 ATGCTCTCTTTGTTTAAACAGAAACCACTTTAAAGGATAGTAATTTCTGTTTATAACA 1282  
DB 2060 ATGCTCTCTTTGTTTAAACAGAAACCACTTTAAAGGATAGTAATTTCTGTTTATAACA 2119  
QY 1283 GTGCTTAAAGGTATGATGATTTCTGATGGAAGCCATTTTCAATTCATGTTCTTCATGG 1342  
DB 2120 GTGCTTAAAGGTATGATGATTTCTGATGGAAGCCATTTTCAATTCATGTTCTTCATGG 2179  
QY 1343 ATTATTTGTTACTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 1402  
DB 2180 ATTATTTGTTACTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 2239  
QY 1403 CAGAGACATGACAGAAATCCCTGCCCTTAAATCCAGGCTTAATTTGCCCTTACAAAGGTTA 1462  
DB 2240 CAGAGACATGACAGAAATCCCTGCCCTTAAATCCAGGCTTAATTTGCCCTTACAAAGGTTA 2299  
QY 1463 TTAATTTAAACTTCCATTTATAGGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTA 1522  
DB 2300 TTAATTTAAACTTCCATTTATAGGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTA 2359  
QY 1523 AAAATGATATTTCAAAGGTAAACCAATATATAAAGAAAAAATAATAATTAATATAC 1582  
DB 2360 AAAATGATATTTCAAAGGTAAACCAATATATAAAGAAAAAATAATAATTAATATAC 2419  
QY 1583 CGGCTTCTGTCCTCCCATTTTAACTCAGCTTCCCTACTGTCCACCAACCAAGCTAA 1642  
DB 2420 CGGCTTCTGTCCTCCCATTTTAACTCAGCTTCCCTACTGTCCACCAACCAAGCTAA 2479  
QY 1643 ATAAAGTCAACAGCTGATGTG 1664  
DB 2480 ATAAAGTCAACAGCTGATGTG 2501

RESULT 4  
AAZ48762  
ID AAZ48762 standard; cDNA; 2502 BP.  
XX AAZ48762;  
AC XX  
DT 21-MAR-2000 (first entry)  
XX Human RICK coding sequence.  
DE RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
XX aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.  
OS Homo sapiens.  
XX WO9955134-A2.  
XX 04-NOV-1999.  
XX 27-APR-1999; 99WO-US009183.

XX 27-APR-1998; 98US-00069023.  
XX (UNMI ) UNIV MICHIGAN.  
XX Nunez G, Inohara N, Koseki T;  
XX WPI; 2000-072163/06.  
XX P-PSDB; AAY59404.  
XX Compositions for identifying apoptosis signaling pathway inhibitors  
XX useful for treating diseases.  
XX Claim 8; Fig 7b; 93pp; English.  
XX This sequence encodes the human RICK (RIP-like interacting CLARP kinase)  
XX protein of the invention. The RICK protein acts as a positive regulator  
XX of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
XX during CD95 signalling. The invention provides methods for identifying  
XX apoptosis signalling pathway inhibitors and activators, and methods and  
XX compositions for screening compounds which will modulate the interactions  
XX of the various compositions identified: ARC, RICK, and the CIDE family of  
XX activators (CIDE-A, CIDE-B and DRBP-1). RICK is useful in screening  
XX assays for agents, useful in the diagnosis, prognosis or treatment of  
XX disease associated with excess cell growth and dysregulation of  
XX apoptosis. Complexes containing RICK and CLARP can be used in drug  
XX screening assays to identify inhibitor molecules blocking CD95-mediated  
XX apoptosis. Overexpression of ARC in an in vitro cell system can be used  
XX to identify inhibitors of the enzymatic activity of caspase-8.  
XX Identification of ARC-like inhibitory compounds may be useful for gene  
XX therapy treatment of disease with increased cell death in muscle tissue  
XX and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
XX treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
XX ischaemic injury, and toxin-induced liver disease. Anti-RICK antibodies  
XX can be used as reagents for the preparation or affinity chromatography  
XX media, and for diagnostically measuring RICK levels. A specific inhibitor  
XX of an essential step in the biochemistry of apoptosis is needed. RICK  
XX interaction with intracellular factors such as CLARP and FADD appears to  
XX be essential for apoptosis, inhibitors of RICK binding to intracellular  
XX apoptosis factors are potential drug candidates  
XX  
XX Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other;

Query Match 78.4%; Score 1308; DB 3; Length 2502;  
Best Local Similarity 99.0%; Pred. No. 2e-254;  
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

QY 331 ACAGTTACAGAGCTTTTCAAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 390  
DB 1161 AAAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 1220  
QY 391 TCTGAACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
DB 1221 TCTGAACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1280  
QY 451 TGAATAATAGTGGTCTCTGAAACTTCAAGGTCCTGCCAGCTCTCTCAAGACAATGATTT 510  
DB 1281 TGAATAATAGTGGTCTCTGAAACTTCAAGGTCCTGCCAGCTCTCTCAAGACAATGATTT 1340  
QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTCTCGGAATCA 570  
DB 1341 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTCTCGGAATCA 1400  
QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAACCA 630  
DB 1401 CAGTTGGGATAGCACCATTCTGGTCTCAAGGGCTGCATCTGTGATCAAGAACCA 1460  
QY 631 TCCATGCTCTTACAGCAATAATAATCACTCTCAACTGCAGGAAATCTCAGAACGCTGCA 690  
DB 1461 TCCATGCTCTTACAGCAATAATAATCACTCTCAACTGCAGGAAATCTCAGAACGCTGCA 1520  
QY 691 GCTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGAC 750

DB 1521 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGAC 1580  
QY 751 AGAAGCCTGCCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGGACTTGATCATCAAGA 810  
DB 1581 AGAAGCCTGCCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGA 1640  
QY 811 GGACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAATTA 870  
DB 1641 GGACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAATTA 1700  
QY 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGCTTATAGTACAAAATTCAGAAATTA 930  
DB 1701 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGCTTATAGTACAAAATTCAGAAATTA 1760  
QY 931 CAAACAAATGGTCTTCCAGCCTTACCCGAAATACCTGTGGTTCTAGATCACCAATCTTT 990  
DB 1761 CAAACAAATGGTCTTCCAGCCTTACCCGAAATACCTGTGGTTCTAGATCACCAATCTTT 1820  
QY 991 AAATTTACTTCAAAATAAAGCATGTAGTGCATGTTTTTCAAGAGAAATGCTGTTTCAT 1050  
DB 1821 AAATTTACTTCAAAATAAAGCATGTAGTGCATGTTTTTCAAGAGAAATGCTGTTTCAT 1880  
QY 1051 AAAGGATATTTATATCTCTGTGCTTGTGACCTTTTATATAAAATCCGTGAGTATTAA 1110  
DB 1881 AAAGGATATTTATATCTCTGTGCTTGTGACCTTTTATATAAAATCCGTGAGTATTAA 1940  
QY 1111 AGCTTTATTTGAAGTCTTCTGGGTAATATTAAGTCTCCCTCCATGACACTGAGTATTTT 1170  
DB 1941 AGCTTTATTTGAAGTCTTCTGGGTAATATTAAGTCTCCCTCCATGACACTGAGTATTTT 2000  
QY 1171 TTTTAATTAATCAAGTAAAAAGTT-----TGAATTTGCTACATAGTTCAATTTTT 1222  
DB 2001 TTTTAATTAATCAAGTAAAAAGTTGAAATTTGGTTGAAATTTGCTACATAGTTCAATTTTT 2060  
QY 1223 ATGTCTCTTTTGTAAAGAACCACTTTTAAAGGATAGTAAATTTCTTGTGTTTATAACA 1282  
DB 2061 ATGTCTCTTTTGTAAAGAACCACTTTTAAAGGATAGTAAATTTCTTGTGTTTATAACA 2120  
QY 1283 GTGCCTTAAAGGTATGATGTTTCTGTGATGGAGCCATTTTCACTTTCATGCTTCTCATGG 1342  
DB 2121 GTGCCTTAAAGGTATGATGTTTCTGTGATGGAGCCATTTTCACTTTCATGCTTCTCATGG 2180  
QY 1343 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTTACCCAC 1402  
DB 2181 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTTACCCAC 2240  
QY 1403 CAGAGACAGTACAGAAATCCCTGCCCTTAAATCCCAAGGCTTAATTTGCCCTACAAAGGGTTA 1462  
DB 2241 CAGAGACAGTACAGAAATCCCTGCCCTTAAATCCCAAGGCTTAATTTGCCCTACAAAGGGTTA 2300  
QY 1463 TTAATTTAAACTCCATTTATAGGATTAATTTTAAAGTTTTTATTAATTTCCCTTTA 1522  
DB 2301 TTAATTTAAACTCCATTTATAGGATTAATTTTAAAGTTTTTATTAATTTCCCTTTA 2360  
QY 1523 AAAATGATATTTCAAAGGTAAAAACAATATATAAGAAAAAATAATATAATATAATAC 1582  
DB 2361 AAAATGATATTTCAAAGGTAAAAACAATATATAAGAAAAAATAATATAATATAATAC 2420  
QY 1583 CGGCTTCTGTCCCATTTTAAACCTTCAGCCTTCCCTACTGTCCACCAACCAAGCTAA 1642  
DB 2421 CGGCTTCTGTCCCATTTTAAACCTTCAGCCTTCCCTACTGTCCACCAACCAAGCTAA 2480  
QY 1643 ATAAAGTCAACAGCCTGATGTG 1664  
DB 2481 ATAAAGTCAACAGCCTGATGTG 2502

RESULT 5  
AAZ46143  
ID AAZ46143 standard; cDNA; 2024 BP.  
XX  
AC AAZ46143;  
XX

DT	16-MAY-2000	(first entry)	
XX			
DE	cDNA sequence encoding a human phosphorylation effector PHSP-6.		
XX			
KW	Human; phosphorylation effector; PHSP; proliferative disorder;		
XX	immune disorder; neuronal disorder; ss.		
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	203..1825	
FT		/*tag= a	
FT		/product= "phosphorylation effector"	
XX			
PN	WO200006728-A2.		
XX			
PD	10-FEB-2000.		
XX			
XX	28-JUL-1999;	99WO-US017132.	
XX			
PR	28-JUL-1998;	98US-0155213P.	
PR	14-SEP-1998;	98US-0155196P.	
PR	14-OCT-1998;	98US-0155239P.	
PR	03-NOV-1998;	98US-0106889P.	
PR	19-NOV-1998;	98US-0109093P.	
PR	22-DEC-1998;	98US-0113796P.	
PR	12-JAN-1999;	99US-0155233P.	
XX			
PA	(INCY-) INCYTE PHARM INC.		
XX			
PI	Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;		
PI	Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;		
PI	Reddy R, Lu DAM, Shih L;		
XX			
DR	WPI; 2000-183125/16.		
DR	P-PSDB; AAY68774.		
XX			
PT	New human phosphorylation effectors useful for the diagnosis, treatment		
PT	and prevention of proliferative, immune and neuronal disorders.		
XX			
PS	Claim 9; Page 121-122; 142pp; English.		
XX			
CC	AZ46138-Z46168 encode human phosphorylation effectors (PHSP), designated		
CC	PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the		
CC	specification). The sequences were isolated from cDNA libraries prepared		
CC	from various human tissues. The PHSP proteins are useful for the		
CC	diagnosis, treatment and prevention of proliferative disorders, immune		
CC	disorders and neuronal disorders. The PHSP proteins form pharmaceutical		
CC	compositions which useful for treating or preventing disorders associated		
CC	with decreased PHSP expression/activity. PHSP antagonists are useful for		
CC	treating or preventing disorders associated with increased PHSP		
CC	expression/activity		
XX			
SQ	Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 U; 0 Other;		
	Query Match 52.7%; Score 879.4; DB 3; Length 2024;		
	Best Local Similarity 99.9%; Pred. No. 6.2e-168;		
	Matches 880; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	331 ACAGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAGAGAAATGGAATATC 390		
DB	1138 AAAGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAGAGAAATGGAATATC 1197		
QY	391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCCTCAGCTCCA 450		
DB	1198 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCCTCAGCTCCA 1257		
QY	451 TGAATAATAGTGGTTCCTCGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAATGATT 510		
DB	1258 TGAATAATAGTGGTTCCTCGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAATGATT 1317		
QY	511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTGGAATCA 570		
DB	1318 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTGGAATCA 1377		
QY	571 CAGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATCTGTGATCACAAGACCAC 630		
DB	1378 CAGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATCTGTGATCACAAGACCAC 1437		
QY	631 TCCATGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGGAAATCTCAGAGCTGCA 690		
DB	1438 TCCATGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGGAAATCTCAGAGCTGCA 1497		
QY	691 GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGAC 750		
DB	1498 GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGAC 1557		
QY	751 AGAAGCCTGCTTTAACCCAGTCCGTAGATGCCCTTCTGTCCAGGACTTCATCATGAAGA 810		
DB	1558 AGAAGCCTGCTTTAACCCAGTCCGTAGATGCCCTTCTGTCCAGGACTTCATCATGAAGA 1617		
QY	811 GGACTATGAACCTTGTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTTACTAGA 870		
DB	1618 GGACTATGAACCTTGTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTTACTAGA 1677		
QY	871 CACTACTGACATCCAAAGGAGAAATTTGCCAAAAGTTATAGTACAAAAATTTGAAGATAA 930		
DB	1678 CACTACTGACATCCAAAGGAGAAATTTGCCAAAAGTTATAGTACAAAAATTTGAAGATAA 1737		
QY	931 CAAACAAATGGGTCTTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT 990		
DB	1738 CAAACAAATGGGTCTTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT 1797		
QY	991 AAATTTACTTCAAAATATAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTTTTCAT 1050		
DB	1798 AAATTTACTTCAAAATATAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTTTTCAT 1857		
QY	1051 AAAAGGATATTATATCTCTGTGCTTTCAGCTTTTTTATATAAATCCGTGAGTATTAA 1110		
DB	1858 AAAAGGATATTATATCTCTGTGCTTTCAGCTTTTTTATATAAATCCGTGAGTATTAA 1917		
QY	1111 AGCTTTATTGAAGTCTTTTGGTAAATATAGTCTCCCTCCATGACACTGCAGTATTTT 1170		
DB	1918 AGCTTTATTGAAGTCTTTTGGTAAATATAGTCTCCCTCCATGACACTGCAGTATTTT 1977		
QY	1171 TTTTAATTAATACAGTAAATAAGTTTGAATTTTGTACATA 1211		
DB	1978 TTTTAATTAATACAGTAAATAAGTTTGAATTTTGTACATA 2018		
XX	RESULT 6		
XX	AAK94554		
XX	ID AAK94554 standard; cDNA; 2033 BP.		
XX	AC AAK94554;		
XX	DT 06-NOV-2001 (first entry)		
XX	Human full-length cDNA, SEQ ID NO: 3453.		
XX	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.		
XX	Homo sapiens.		
XX	EP1130094-A2.		
XX	05-SEP-2001.		
XX	07-JUL-2000; 2000EP-00114089.		
XX	08-JUL-1999; 99JP-00194486.		
XX	11-JAN-2000; 2000JP-00118774.		
XX	02-MAY-2000; 2000JP-00183765.		
XX	(HELI-) HELIX RES INST.		

PI Ota T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.  
DR P-PSDB; AAW93621.  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
PT  
XX  
XX Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.  
XX  
XX The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a full length human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in CD-ROM format directly  
CC from EPO  
XX  
XX Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;  
SQ

Query Match 52.5%; Score 876.8; DB 4; Length 2033;  
Best Local Similarity 99.8%; Pred. No. 2.1e-167;  
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATTATC 390  
DB 1154 AAAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATTATC 1213

QY 391 TCTGAACATACCTGTAATCTGTCACAGAGGAAATCATGTGATCTCTCAGCTCA 450  
DB 1214 TCTGAACATACCTGTAATCTGTCACAGAGGAAATCATGTGATCTCTCAGCTCA 1273

QY 451 TGAATAATAGTGTTCCTGAAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATT 510  
DB 1274 TGAATAATAGTGTTCCTGAAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATT 1333

QY 511 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTCTCGGAATCA 570  
DB 1334 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTCTCGGAATCA 1393

QY 571 CAGTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATCTGTGATCAGACACAC 630  
DB 1394 CAGTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATCTGTGATCAGACACAC 1453

QY 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGACGCTCTGCA 690  
DB 1454 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGACGCTCTGCA 1513

QY 691 GCCTGTATAGCCCGACAGTGGATCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 750  
DB 1514 GCCTGTATAGCCCGACAGTGGATCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 1573

QY 751 AGAAGCTGCTTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGCATGAAAGA 810  
DB 1574 AGAAGCTGCTTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGCATGAAAGA 1633

QY 811 GGACTATGAATGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCCAGACAATTTACTAGA 870  
DB 1634 GGACTATGAATGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCCAGACAATTTACTAGA 1693

QY 871 CACTACTGACATCAAGGGAAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAA 930  
DB 1694 CACTACTGACATCAAGGGAAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAA 1753

QY 931 CAAACAAATGGGTCTTCAGCTTACCCGGAATAATCTGTGGTTCTTAGATCACCATCTTT 990  
DB 1754 CAAACAAATGGGTCTTCAGCTTACCCGGAATAATCTGTGGTTCTTAGATCACCATCTTT 1813

QY 991 AAATTTACTTCAAAATAAAAGCATCTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAAT 1050  
DB 1814 AAATTTACTTCAAAATAAAAGCATCTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAAT 1873

QY 1051 AAAGGATATTTATATCTCTGTTGCTTTTACCTTTTATATATAAAATCCGTGAGTATTA 1110  
DB 1874 AAAGGATATTTATATCTCTGTTGCTTTTATATATAAAATCCGTGAGTATTA 1933

QY 1111 AGCTTTATTTGAAGTGTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1170  
DB 1934 AGCTTTATTTGAAGTGTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1993

QY 1171 TTTTAATTAATCAAGTAAAGTTTGAATTTTGTCTACAT 1210  
DB 1994 TTTTAATTAATCAAGTAAAGTTTGAATTTTGTCTACAT 2033

RESULT 7  
AA02558  
ID AAX02558 standard; cDNA; 2098 BP.  
XX  
XX AAX02558;  
XX  
XX 07-MAY-1999 (first entry)  
XX Human B1 cDNA.  
XX B1 protein; intracellular mediator; modulator; inflammation; cell death;  
XX cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.  
XX Homo sapiens.  
XX WO9855507-A2.  
XX 10-DEC-1998.  
XX 01-JUN-1998; 98WO-IL000255.  
XX 05-JUN-1997; 97IL-00121011.  
XX 30-JUN-1997; 97IL-00121199.  
XX 11-SEP-1997; 97IL-00121746.  
XX (YEDA ) YEDA RES & DEV CO LTD.  
XX Wallach D, Boldin M, Malinin N;  
XX WPI; 1999-070258/06.  
XX P-PSDB; AAW92795.  
XX  
XX New B1 protein regulates cell death and cell survival pathways -  
XX derivatives, DNA and antibodies, also regulate intracellular inflammation  
XX ; for treating AIDS, cancer.  
XX  
XX Claim 4; Fig 3B; 90pp; English.  
XX  
XX This invention describes the isolation of a novel human B1 protein which  
XX can interact with intracellular mediators or modulators of inflammation,  
XX cell death and/or cell survival pathways; directly or indirectly. Cells  
XX can be modulated or mediated in inflammation, cell death or cell survival  
XX pathways or another intracellular signalling activity using B1.  
XX Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
XX oligonucleotides and ribozymes can also be used to regulate the above  
XX pathways  
XX  
XX Sequence 2098 BP; 649 A; 452 C; 449 G; 539 T; 0 U; 9 Other;  
SQ

Query Match 51.6%; Score 861; DB 2; Length 2098;  
Best Local Similarity 98.5%; Pred. No. 3.2e-164;  
Matches 858; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATTATC 390  
DB 1154 AAAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATTATC 1213







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QY 571 CAGTTGGGATAGCACCATTCTCTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAC 630
DB 1389 CAGTTGGGATAGCACCATTCTCTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAC 1448
QY 631 TCCATGCTCTTCAGCAATAATAATCACTCTCACTGACGAGAACTCAGAACTGTGCA 690
DB 1449 TCCATGCTCTTCAGCAATAATAATCACTCTCACTGACGAGAACTCAGAACTGTGCA 1508
QY 691 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGAGACATTTGACCAATGAC 750
DB 1509 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGAGACATTTGACCAATGAC 1568
QY 751 AGAAGCTGCTTAAACAGTCGTAGATGCCCTCTCTGTCAGGACTTGTATCATGAAAGA 810
DB 1569 AGAAGCTGCTTAAACAGTCGTAGATGCCCTCTCTGTCAGGACTTGTATCATGAAAGA 1628
QY 811 GGAATATGAATCTGTTAGTACCAAGCTTCAAGGACTCAAAAGTCAGACAATTTACTAGA 870
DB 1629 GGAATATGAATCTGTTAGTACCAAGCTTCAAGGACTCAAAAGTCAGACAATTTACTAGA 1688
QY 871 CACTACTGACATCCAGGAGAAATTTGCCAAGTATATAGTACAAAATTTGAAGATAA 930
DB 1689 CACTACTGACATCCAGGAGAAATTTGCCAAGTATATAGTACAAAATTTGAAGATAA 1748
QY 931 CAAACAAATGGGTCTTCAGCCTTACCGGAAATACTTGTGTTCTAGATCACCATCTTT 990
DB 1749 CAAACAAATGGGTCTTCAGCCTTACCGGAAATACTTGTGTTCTAGATCACCATCTTT 1808
QY 991 AAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1050
DB 1809 AAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1868
QY 1051 AAAAGGATATTATA 1065
DB 1869 AAAAGGATATTATA 1883

RESULT 10
AAF30001
ID AAF30001 standard; cDNA; 1931 BP.
XX AC AAF30001;
XX AC
XX AC
DT 23-APR-2001 (first entry)
XX DE Human CARD-3 cDNA.
XX KW CARD-3; caspase recruitment domain; human; cancer; infection;
XX KW autoimmune disease; neurological disease; haematological disease;
XX KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;
XX KW antiinflammatory; apoptosis; diagnosis; gene therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CD 214..1826
FT FT /*tag= a
FT FT /note= "the open reading frame is also specifically
FT FT claimed in Claim 1(a)"
XX PN WO200100826-A2.
XX PD 04-JAN-2001.
XX PF 28-JUN-2000; 2000WO-US017691.
XX PR 28-JUN-1999; 99US-00340620.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Bertin J;
XX XX
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DR WPI; 2001-061973/07.
XX P-PSDB; AAB20079.
PT Isolated intracellular proteins predicted to be involved in regulating
PT caspase activation are used for diagnosis and treatment of e.g. cancer,
PT viral infections, autoimmune diseases, neurological diseases and
PT hematological disorders.
XX Claim 1(a); Fig 1; 208pp; English..
XX The present sequence is that of cDNA encoding human caspase recruitment
CC domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a
CC database search using known CARD sequences. Plasmid pXel17A containing
CC CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular
CC protein predicted to be involved in regulating caspase activation. It is
CC useful as a modulating agent in regulating cellular processes include
CC cell growth and cell death. Methods of diagnosing and treating patients
CC suffering from a disorder associated with an abnormal level or rate of
CC apoptotic cell death, abnormal activity of the Fas/APO-1 receptor
CC complex, abnormal activity of the tumour necrosis factor receptor complex
CC or abnormal activity of a caspase involve administering a compound that
CC modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6
CC e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide.
CC Such disorders include cancer, viral infection, autoimmune disorders,
CC neurological diseases, haematological disorders, inflammatory disorders,
CC and immune disorders. CARD nucleic acids can be used to express CARD
CC proteins in a host cell e.g. for gene therapy applications, to detect a
CC genetic lesion and to modulate CARD activity
XX SQ Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;

Query Match 43.8%; Score 731.8; DB 4; Length 1931;
Best Local Similarity 99.7%; Pred. No. 3.8e-138;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 390
DB 1149 AAAAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 1208
QY 391 TCTGACATACCTGTAAATCATGTCACCAAGAGGAATCATGTGGATCTCTCAGCTCCA 450
DB 1209 TCTGACATACCTGTAAATCATGTCACCAAGAGGAATCATGTGGATCTCTCAGCTCCA 1268
QY 451 TGAATAATAGTGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCTCTCAAGACAATGATT 510
DB 1269 TGAATAATAGTGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCTCTCAAGACAATGATT 1328
QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTTGGAAATCA 570
DB 1329 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTTGGAAATCA 1388
QY 571 CAGTTGGGATAGCACCATTCTCTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAC 630
DB 1389 CAGTTGGGATAGCACCATTCTCTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAC 1448
QY 631 TCCATGCTCTTCAGCAATAATAATCACTCTCACTGACGAGAACTCAGAACTGTGCA 690
DB 1449 TCCATGCTCTTCAGCAATAATAATCACTCTCACTGACGAGAACTCAGAACTGTGCA 1508
QY 691 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGAGACATTTGACCAATGAC 750
DB 1509 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGAGACATTTGACCAATGAC 1568
QY 751 AGAAGCTGCTTAAACAGTCGTAGATGCCCTCTCTGTCAGGACTTGTATCATGAAAGA 810
DB 1569 AGAAGCTGCTTAAACAGTCGTAGATGCCCTCTCTGTCAGGACTTGTATCATGAAAGA 1628
QY 811 GGAATATGAATCTGTTAGTACCAAGCTTCAAGGACTCAAAAGTCAGACAATTTACTAGA 870
DB 1629 GGAATATGAATCTGTTAGTACCAAGCTTCAAGGACTCAAAAGTCAGACAATTTACTAGA 1688
QY 871 CACTACTGACATCCAGGAGAAATTTGCCAAGTATATAGTACAAAATTTGAAGATAA 930
```



Db 1689 CACTACTGACATCCAGGAGAGAAATTTGCCAAAGTATATAGTACAAAATTTGAAAGATAA 1748

Qy 931 CAAACAAATGGTCTTACGCTTACCGGAATACTTGTGGTTCTTAGATCACCATCTTT 990

Db 1749 CAAACAAATGGTCTTACGCTTACCGGAATACTTGTGGTTCTTAGATCACCATCTTT 1808

Qy 991 AAATTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAATGTTTCAT 1050

Db 1809 AAATTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAATGTTTCAT 1868

Qy 1051 AAAAGGATATTATA 1065

Db 1869 AAAGGATATTATA 1883

RESULT 11

ABK89280

ID ABK89280 standard; cDNA; 1931 BP.

XX AC ABK89280;

XX DT 21-OCT-2002 (first entry)

XX DE Human cDNA encoding caspase recruitment domain protein CARD-3.

XX KW Human; ss; gene; caspase recruitment domain; CARD-3; CARD-4; LRR;

XX KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;

XX KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;

XX KW systemic lupus erythematosus; immune-mediated glomerulonephritis;

XX KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;

XX KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;

XX KW gastrointestinal allergy; insulin-dependent diabetes;

XX KW bacterial infection; tuberculosis; lepromatous leprosy;

XX KW cell signalling disorder; tissue disorder.

XX OS Homo sapiens.

XX FH Key

FT CDS

FT Location/Qualifiers

FT 214..1836

FT /\*tag= a

FT /\*product= "CARD-3"

XX PN WO200253765-A1.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-US049798.

XX PR 29-DEC-2000; 2000US-0258724P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Bertin J, Philpott D, Sansonetti P, Girardin S;

XX WPI; 2002-583627/62.

DR P-PSDB; ABG31075.

XX Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.

XX Example 2; Fig 1; 139pp; English.

XX The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a

cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as asthma, allergy, psoriasis, contact dermatitis, atopic conditions such as allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence is the human cDNA encoding CARD-3

XX Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Qy 331 ACAGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAATGGAATTATC 390

Db 1149 AAAGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAATGGAATTATC 1208

Qy 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGTCCA 450

Db 1209 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGTCCA 1268

Qy 451 TGAATAATAGTGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510

Db 1269 TGAATAATAGTGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1328

Qy 511 TTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCATCTGCTCGGAAATCA 570

Db 1329 TTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCATCTGCTCGGAAATCA 1388

Qy 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCAAC 630

Db 1389 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCAAC 1448

Qy 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTGCA 690

Db 1449 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTGCA 1508

Qy 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 750

Db 1509 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 1568

Qy 751 AGAGCCCTGCTTACACAGTGCCTAGATGCCCTCTGTCAGGGACTTGATCATGAAGA 810

Db 1569 AGAGCCCTGCTTACACAGTGCCTAGATGCCCTCTGTCAGGGACTTGATCATGAAGA 1628

Qy 811 GGACTATGAATCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTACTAGA 870

Db 1629 GGACTATGAATCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTACTAGA 1688

Qy 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGTATATAGTACAAAATTTGAAAGATAA 930

Db 1689 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGTATATAGTACAAAATTTGAAAGATAA 1748

Qy 931 CAAACAAATGGTCTTACGCTTACCGGAATACTTGTGGTTCTTAGATCACCATCTTT 990

Db 1749 CAAACAAATGGTCTTACGCTTACCGGAATACTTGTGGTTCTTAGATCACCATCTTT 1808

Qy 991 AAATTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAATGTTTCAT 1050

Db 1809 AAATTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAATGTTTCAT 1868

Qy 1051 AAAGGATATTATA 1065

Db	1869	AAAAAGGATATTATA	1883		391	TCCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA	450
Db	1209	TCCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA	1268		1209	TCCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA	1268
Qy	451	TGAAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCCTGCAGCTCTCTCAAGACAATGATTT	510		451	TGAAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCCTGCAGCTCTCTCAAGACAATGATTT	510
Db	1269	TGAAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCCTGCAGCTCTCTCAAGACAATGATTT	1328		1269	TGAAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCCTGCAGCTCTCTCAAGACAATGATTT	1328
Qy	511	TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTCTCTCTGGAATCA	570		511	TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTCTCTCTGGAATCA	570
Db	1329	TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTCTCTCTGGAATCA	1388		1329	TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTCTCTCTGGAATCA	1388
Qy	571	CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCACTCTCTCTGATCAACAAGCAC	630		571	CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCACTCTCTCTGATCAACAAGCAC	630
Db	1389	CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCACTCTCTCTGATCAACAAGCAC	1448		1389	CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCACTCTCTCTGATCAACAAGCAC	1448
Qy	631	TCCATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCCTGCA	690		631	TCCATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCCTGCA	690
Db	1449	TCCATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCCTGCA	1508		1449	TCCATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCCTGCA	1508
Qy	691	GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC	750		691	GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC	750
Db	1509	GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC	1568		1509	GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC	1568
Qy	751	AGAAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA	810		751	AGAAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA	810
Db	1569	AGAAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA	1628		1569	AGAAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA	1628
Qy	811	GGACTATGAACTTGTAGTACCAAGCTACAGGACCTCAAAAGTCAGACATTTACTAGA	870		811	GGACTATGAACTTGTAGTACCAAGCTACAGGACCTCAAAAGTCAGACATTTACTAGA	870
Db	1629	GGACTATGAACTTGTAGTACCAAGCTACAGGACCTCAAAAGTCAGACATTTACTAGA	1688		1629	GGACTATGAACTTGTAGTACCAAGCTACAGGACCTCAAAAGTCAGACATTTACTAGA	1688
Qy	871	CACACTGACATCCCAAGGAGAAGAAATTTGCCAAAAGTTATAGTACAAAATTCGAAAGATAA	930		871	CACACTGACATCCCAAGGAGAAGAAATTTGCCAAAAGTTATAGTACAAAATTCGAAAGATAA	930
Db	1689	CACACTGACATCCCAAGGAGAAGAAATTTGCCAAAAGTTATAGTACAAAATTCGAAAGATAA	1748		1689	CACACTGACATCCCAAGGAGAAGAAATTTGCCAAAAGTTATAGTACAAAATTCGAAAGATAA	1748
Qy	931	CAACAAATGGGTCTTACCGGAAATACCTTGTGGTTCTTAGATCCACCATCTTT	990		931	CAACAAATGGGTCTTACCGGAAATACCTTGTGGTTCTTAGATCCACCATCTTT	990
Db	1749	CAACAAATGGGTCTTACCGGAAATACCTTGTGGTTCTTAGATCCACCATCTTT	1808		1749	CAACAAATGGGTCTTACCGGAAATACCTTGTGGTTCTTAGATCCACCATCTTT	1808
Qy	991	AAATTTACTTCAAAATAAAGCATGTAGTACTGTTTTCAGAGGAATATGTTTCAT	1050		991	AAATTTACTTCAAAATAAAGCATGTAGTACTGTTTTCAGAGGAATATGTTTCAT	1050
Db	1809	AAATTTACTTCAAAATAAAGCATGTAGTACTGTTTTCAGAGGAATATGTTTCAT	1868		1809	AAATTTACTTCAAAATAAAGCATGTAGTACTGTTTTCAGAGGAATATGTTTCAT	1868
Qy	1051	AAAAGGATATTATA	1065		1051	AAAAGGATATTATA	1065
Db	1869	AAAAGGATATTATA	1883		1869	AAAAGGATATTATA	1883
RESULT 13							
ABX75869							
ID	ABX75869	standard; cdna; 1931 BP.					
XX	ABX75869;						
AC	ABX75869;						
XX	30-APR-2003 (first entry)						
DT	Human cDNA encoding Caspase recruitment domain protein, CARD-3.						
XX	Human; ss; gene; caspase recruitment domain; CARD; CARD-3; CARD-4;						
XX	CARD-4L; CARD-4S; CARD-4Y; apoptosis; cancer; AIDS;						
XX	autoimmune disorder; systemic lupus erythematosus; viral infection;						
XX	immune related glomerulonephritis; acquired immunodeficiency syndrome;						
XX	neurological disease; Alzheimer's disease; Parkinson's disease;						
XX	anyotrophic lateral sclerosis; retinitis pigmentosa;						
XX	spinal muscular atrophy; cerebellar degeneration; haematological disease;						
XX	anaemia; neutropenia; myelodysplastic syndrome; myocardial infarction;						
XX	stroke; chromosome 7.						
OS	Homo sapiens.						
XX	US6469140-B1.						
PN							

XX PD 22-OCT-2002.  
XX PF 08-DEC-1998; 98US-00207359.  
XX PR 06-FEB-1998; 98US-00019942.  
XX PR 17-JUN-1998; 98US-00099041.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Bertin J;  
XX DR WPI; 2003-147109/14.  
XX DR P-PSDB; ABUS6269.  
XX PT Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z  
XX PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,  
XX PT detection assays, predictive medicine, and in therapeutic applications.  
XX PS Example 2; Fig 1; 99pp; English.  
XX CC The invention relates to an isolated polypeptide, comprising at least 25  
CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,  
CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)  
CC polypeptide. Also included is an isolated fusion protein, comprising the  
CC CARD polypeptide covalently linked by a peptide bond to a heterologous  
CC polypeptide. The CARD polypeptide is useful in screening assays,  
CC detection assays (e.g. chromosomal mapping, tissue typing and forensic  
CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,  
CC monitoring clinical trials and pharmacogenomics), and in therapeutic and  
CC prophylactic treatments (in diseases associated with apoptotic cell death  
CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and  
CC immune related glomerulonephritis), viral infections, AIDS (acquired  
CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's  
CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),  
CC haematological diseases (e.g. anaemia, neutropenia and myelodysplastic  
CC syndromes), myocardial infarction and stroke). The CARD polypeptide is  
CC useful as bait protein in a two-hybrid assay or three hybrid assay to  
CC identify other proteins, which bind to or interact with other CARD  
CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
CC human CARD-4 is located on chromosome 7. The present sequence is a human  
CC CARD cDNA  
XX SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;  
Query Match 43.8%; Score 731.8; DB 7; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 3.8e-138;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 331 ACAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAGAAATGGAATTATC 390  
DB 1149 AAAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAGAAATGGAATTATC 1208  
QY 391 TGTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGTCCA 450  
DB 1209 TGTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGTCCA 1268  
QY 451 TGAATAATAGTGTTCCTCTGAACTTCAAGTCCCTGAGGTCCTCTCAGAGCAATGATT 510  
DB 1269 TGAATAATAGTGTTCCTCTGAACTTCAAGTCCCTGAGGTCCTCTCAGAGCAATGATT 1328  
QY 511 TTATCTAGAAAGCTCAAGACTGTGTATTTATGAAGCTGCATCACTGCTCGGAATCA 570  
DB 1329 TTATCTAGAAAGCTCAAGACTGTGTATTTATGAAGCTGCATCACTGCTCGGAATCA 1388  
QY 571 CAGTTGGGATAGACCATTTCTGGATCTCAAGGGGTGCAATCTGTGATCAAGACCAAC 630  
DB 1389 CAGTTGGGATAGACCATTTCTGGATCTCAAGGGGTGCAATCTGTGATCAAGACCAAC 1448  
QY 631 TCCATGCTCTCAGCAATAATAAATCACTCTCACTGAGGAACTCAGACGCTGCA 690  
DB 1449 TCCATGCTCTCAGCAATAATAAATCACTCTCACTGAGGAACTCAGACGCTGCA 1508

QY 691 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
DB 1509 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1568  
QY 751 AGAGCCCTGCTTACACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 810  
DB 1569 AGAGCCCTGCTTACACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1628  
QY 811 GGACTATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAAGCAATTTACTAGA 870  
DB 1629 GGACTATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAAGCAATTTACTAGA 1688  
QY 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGTATATAGTACAAAATTTGAAAGATAA 930  
DB 1689 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGTATATAGTACAAAATTTGAAAGATAA 1748  
QY 931 CAAACAATGGTCTTACAGCCTTACCGGAAATCTGTGGTTCTAGATCACCATCTTT 990  
DB 1749 CAAACAATGGTCTTACAGCCTTACCGGAAATCTGTGGTTCTAGATCACCATCTTT 1808  
QY 991 AAATTTACTTCAAAATAAAAGCATGTAAAGTGAAGTCTTTTCAAGAGAAATGTGTTTCAT 1050  
DB 1809 AAATTTACTTCAAAATAAAAGCATGTAAAGTGAAGTCTTTTCAAGAGAAATGTGTTTCAT 1868  
QY 1051 AAAAGGATATTATA 1065  
DB 1869 AAAAGGATATTATA 1883  
RESULT 14  
ADB81363  
ID ADB81363 standard; cDNA; 1931 BP.  
XX AC ADB81363;  
XX DT 04-DEC-2003 (first entry)  
XX DE Human caspase recruitment domain 3 (CARD-3) cDNA.  
XX KW human; ss; Gene; CARD-3; CARD-4; caspase recruitment domain; apoptosis;  
KW p75; tumour necrosis factor; TNF; neurotrophin receptor; cancer;  
KW autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;  
KW viral infection; neurological; retinitis pigmentosa; haematologic;  
KW chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 214..1836  
FT FT /\*tag= a  
FT FT /product= "CARD-3 protein"  
XX PN US2002061833-A1.  
XX PD 23-MAY-2002.  
XX PF 26-DEC-2000; 2000US-00748537.  
XX PR 06-FEB-1998; 98US-00019942.  
XX PR 17-JUN-1998; 98US-00099041.  
XX PA (BERT/) BERTIN J.  
XX PA (CHAO/) CHAO M V.  
XX PI Bertin J, Chao MV;  
XX DR WPI; 2003-657125/62.  
XX DR P-PSDB; ADB81362.  
XX PT Detecting compounds which alter binding of the caspase recruitment domain  
XX PT (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful  
XX PT to provide compounds for treating CARD-3 mediated disorders.



CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
CC human CARD-4 is located on chromosome 7. The present sequence is a human  
CC CARD cDNA

XX Sequence 1620 BP; 517 A; 360 C; 320 G; 423 T; 0 U; 0 Other;

Query Match	40.9%;	Score 681.8;	DB 7;	Length 1620;
Best Local Similarity	99.7%;	Pred. No. 4.5e-128;		
Matches 683;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

  

QY	331	ACAGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAAAGAGAAAATGGAATTATC	390
DB	936	AAAGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAAAGAGAAAATGGAATTATC	995
QY	391	TTGAAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA	450
DB	996	TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA	1055
QY	451	TGAAATAGTGGTCTCCTGAACTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT	510
DB	1056	TGAAATAGTGGTCTCCTGAACTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT	1115
QY	511	TTTATCTAGAAAGCTCAAGAGCTGTATTTATTAAGCTGCATCACTGTCTGGAAATCA	570
DB	1116	TTTATCTAGAAAGCTCAAGAGCTGTATTTATTAAGCTGCATCACTGTCTGGAAATCA	1175
QY	571	CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCAC	630
DB	1176	CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCAC	1235
QY	631	TCATGCTCTTCAGCAATTAATAATCCACTCTCACTGCAGGAATCTCAGAAGCTCTGCA	690
DB	1236	TCATGCTCTTCAGCAATTAATAATCCACTCTCACTGCAGGAATCTCAGAAGCTCTGCA	1295
QY	691	GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC	750
DB	1296	GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC	1355
QY	751	AGAAGCCTGCCTTAAACCACTCGCTAGATGCCCTTCTGTCCAGGACTTGTATGAAAGA	810
DB	1356	AGAAGCCTGCCTTAAACCACTCGCTAGATGCCCTTCTGTCCAGGACTTGTATGAAAGA	1415
QY	811	GGACTATGAATTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACAATTACTAGA	870
DB	1416	GGACTATGAATTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACAATTACTAGA	1475
QY	871	CACCTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA	930
DB	1476	CACCTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA	1535
QY	931	CAAAACAATGGGTCTTCAGCCTTTACCCGGAAATACCTTGTGGTTCTAGATCACCATCTTT	990
DB	1536	CAAAACAATGGGTCTTCAGCCTTTACCCGGAAATACCTTGTGGTTCTAGATCACCATCTTT	1595
QY	991	AAATTACTTCAAAATAAAGCATG	1015
DB	1596	AAATTACTTCAAAATAAAGCATG	1620

Search completed: April 1, 2004, 03:06:47  
Job time : 670 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 02:38:40 ; Search time 156 Seconds  
(without alignments)  
5937.263 Million cell updates/sec

Title: US-09-771-161A-2

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308	78.4	2501	4	US-09-920-663-3
2	1308	78.4	2502	4	US-09-069-023-2
3	731.8	43.8	1931	3	US-09-019-942-2
4	731.8	43.8	1931	4	US-09-099-041A-1
5	731.8	43.8	1931	4	US-09-245-281-1
6	731.8	43.8	1931	4	US-09-470-271-2
7	731.8	43.8	1931	4	US-09-207-359B-1
8	731.8	43.8	1931	4	US-09-340-620A-1
9	731.8	43.8	1931	4	US-09-865-364-1
10	731.8	43.8	1931	4	US-09-748-537-2
11	695.4	41.7	1060	4	US-09-023-655-684
12	681.8	40.9	1620	4	US-09-099-041A-3
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14	681.8	40.9	1620	4	US-09-207-359B-3
15	681.8	40.9	1620	4	US-09-340-620A-3
16	681.8	40.9	1620	4	US-09-865-364-3
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18	52.8	3.2	20674	4	US-09-641-638-651
19	50.4	3.0	832	4	US-09-621-976-2813
20	48	2.9	6152	3	US-08-973-462-1
21	48	2.9	6156	4	US-10-204-708-60
22	47.8	2.9	6583	4	US-10-204-708-25
23	47.6	2.9	396	4	US-09-640-173-53
24	47.6	2.9	396	4	US-09-713-550-53
25	47.6	2.9	834	3	US-08-998-416-305
26	47.6	2.9	10144	4	US-10-204-708-93
27	47.4	2.8	5610	4	US-10-204-708-54

c	28	47.4	2.8	5852	1	US-07-867-106-2	Sequence 2, Appli
	29	47.4	2.8	640681	4	US-09-790-988-1	Sequence 1, Appli
	30	47	2.8	640681	4	US-09-790-988-1	Sequence 1, Appli
	31	46.2	2.8	474	4	US-09-621-976-18033	Sequence 18033, A
	32	46	2.8	5562	4	US-10-204-708-63	Sequence 63, Appl
	33	45.8	2.7	701	3	US-08-998-416-701	Sequence 701, Appl
c	34	45.8	2.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
	35	45.8	2.7	6669	4	US-10-204-708-6	Sequence 6, Appli
	36	45.8	2.7	8920	2	US-08-446-855A-1	Sequence 1, Appli
	37	45.8	2.7	8920	3	US-09-150-741-1	Sequence 1, Appli
	38	45.6	2.7	9347	4	US-10-204-708-35	Sequence 35, Appl
	39	45.6	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
c	40	45.2	2.7	711	3	US-08-998-416-786	Sequence 786, App
	41	44.8	2.7	6317	4	US-10-204-708-11	Sequence 11, Appli
	42	44.2	2.6	636	3	US-08-998-416-1137	Sequence 1137, Ap
c	43	44.2	2.6	3095	6	5231168-1	Patent No. 5231168
	44	44.2	2.6	5455	4	US-10-204-708-33	Sequence 33, Appl
	45	44.2	2.6	6182	4	US-10-204-708-88	Sequence 88, Appl

RESULT 1  
US-09-920-663-3  
; Sequence 3, Application US/09920663  
; Patent No. 6426221  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Lex M. Cowert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION  
; FILE REFERENCE: RTS-0233  
; CURRENT APPLICATION NUMBER: US/09/920,663  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 3  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (225)...(1847)  
US-09-920-663-3

Query Match 78.4%; Score 1308; DB 4; Length 2501;  
Best Local Similarity 99.0%; Pred. No. 2.3e-293;  
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

Qy	331	ACAGTTACAGAGTGTTC	CAAGTGC	CAATTCAC	TATGTG	CAAGAGAAATGGAATTC	390
Db	1160	AAAGTTACAGAGTGTTC	CAAGTGC	CAATTCAC	TATGTG	CAAGAGAAATGGAATTC	1219
Qy	391	TCTGAACATACCTGT	TAATCATG	GTCC	CAAGAGGAAT	CTGTGGATCCTCTCAGCTCA	450
Db	1220	TCTGAACATACCTGT	TAATCATG	GTCC	CAAGAGGAAT	CTGTGGATCCTCTCAGCTCA	1279
Qy	451	TGAAATAGTGGTTC	CTCTG	AAACTT	CAAGTCC	CTGCGAGCTCTCAAGCAATGATTT	510
Db	1280	TGAAATAGTGGTTC	CTCTG	AAACTT	CAAGTCC	CTGCGAGCTCTCAAGCAATGATTT	1339
Qy	511	TTTATCTAGAAAGCT	CAAGCTG	TATTTAT	TATGAAGCTG	ATCACTGCTCTCGGAAATCA	570
Db	1340	TTTATCTAGAAAGCT	CAAGCTG	TATTTAT	TATGAAGCTG	ATCACTGCTCTCGGAAATCA	1399
Qy	571	CAGTTGGGATAGC	CACTTTCT	GGATCT	CAAGGCTC	ATTCTGTGATCAAGACCAAC	630
Db	1400	CAGTTGGGATAGC	CACTTTCT	GGATCT	CAAGGCTC	ATTCTGTGATCAAGACCAAC	1459
Qy	631	TCCATGCTCTT	CAGCAATA	ATAATCA	CTCTCA	ACTCAGGAAACTCAGACGCTGCA	690
Db	1460	TCCATGCTCTT	CAGCAATA	ATAATCA	CTCTCA	ACTCAGGAAACTCAGACGCTGCA	1519
Qy	691	GCCTGGTATAG	CCCCAG	AGCTGG	ATCC	AGAGAAAGGGAAGACATTTGTTGAACCAATGAC	750

ALIGNMENTS

Db 1520 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1579  
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Db 1580 AGAAGCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 1639  
QY 811 GGACTATGAATCTGTAGTACCAAGCTACAGGACTCAAGGACTCAAAAGTATAGTACAAATTTACTAGA 870  
Db 1640 GGACTATGAATCTGTAGTACCAAGCTACAGGACTCAAGGACTCAAAAGTATAGTACAAATTTACTAGA 1699  
QY 871 CACTACTGACATCAAGGGAAGAATTTGCCAAAGTTATAGTACAAATTTGAAGATAA 930  
Db 1700 CACTACTGACATCAAGGGAAGAATTTGCCAAAGTTATAGTACAAATTTGAAGATAA 1759  
QY 931 CAAACAAATGGGCTTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 990  
Db 1760 CAAACAAATGGGCTTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 1819  
QY 991 AAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1050  
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Db 1940 AGCTTTATGAAGGTTCTTGGGTAATATAGTCTCCCTCCATGACACTGCAATTTT 1999  
QY 1171 TTTTAAATTAACAAGTAAAGTT-----TGAATTTGTACATAGTTCAATTTT 1222  
Db 2000 TTTTAAATTAACAAGTAAAGTTTGAATTTGGTTGATTTGCTACATAGTTCAATTTT 2059  
QY 1223 ATGTCCTTTTGTAAACAGAAACACTTTTAAAGGATAGTAAATTTCTGTTTATAAACA 1282  
Db 2060 ATGTCCTTTTGTAAACAGAAACACTTTTAAAGGATAGTAAATTTCTGTTTATAAACA 2119  
QY 1283 GTGCTTAAAGTATGATGATTTCTGATGAAGCCATTTTCAATTCATGTTCTTCATGG 1342  
Db 2120 GTGCTTAAAGTATGATGATTTCTGATGAAGCCATTTTCAATTCATGTTCTTCATGG 2179  
QY 1343 ATATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 1402  
Db 2180 ATATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 2239  
QY 1403 CAGAGACAGTACAGAAATCCCTGCCCCATAAATCCAGGCTTAATTTGCCCTACAAAGGTTA 1462  
Db 2240 CAGAGACAGTACAGAAATCCCTGCCCCATAAATCCAGGCTTAATTTGCCCTACAAAGGTTA 2299  
QY 1463 TTAATTTAAACCTCCATTTAGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTA 1522  
Db 2300 TTAATTTAAACCTCCATTTAGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTA 2359  
QY 1523 AAATATGATTTTCAAGGTAATAACAATATATATAAAGAAATAAATAATATATATAC 1582  
Db 2360 AAATATGATTTTCAAGGTAATAACAATATATATAAAGAAATAAATAATATATATAC 2419  
QY 1583 CGGCTTCCGTCCCATTTTAACTCAGCTTCCCTTCTGTCACCAACCAACAGCTAA 1642  
Db 2420 CGGCTTCCGTCCCATTTTAACTCAGCTTCCCTTCTGTCACCAACCAACAGCTAA 2479  
QY 1643 ATAAAGTCAACAGCTCATGTG 1664  
Db 2480 ATAAAGTCAACAGCTCATGTG 2501

RESULT 2  
US-09-069-023-2  
; Sequence 2, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Nachiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2502  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-069-023-2  
  
Query Match 78.4%; Score 1308; DB 4; Length 2502;  
Best Local Similarity 99.0%; Pred. No. 2.3e-293;  
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;  
  
QY 331 ACAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGTGACAAAGAAATGGAATATC 390  
Db 1161 AAAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGTGACAAAGAAATGGAATATC 1220  
QY 391 TCTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
Db 1221 TCTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1280  
QY 451 TGAATAATAGTGTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGCAATGATTT 510  
Db 1281 TGAATAATAGTGTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGCAATGATTT 1340  
QY 511 TTTATCTGAAAGCTCAAGACTGTATTTATGAAGTGCATCACTGTCTCTGGAATCA 570  
Db 1341 TTTATCTGAAAGCTCAAGACTGTATTTATGAAGTGCATCACTGTCTCTGGAATCA 1400  
QY 571 CAGTTGGGATAGCACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACAC 630  
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QY 631 TCCATGCTCTTCAGCAATAATAAATCCACTCTCACTCAGGAACTCAGAACCTCTGCA 690  
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QY 691 GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
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QY 811 GGACTATGAATCTGTAGTACCAAGCTACAGGACTCAAAAGTATAGTACAAATTTACTAGA 870  
Db 1641 GGACTATGAATCTGTAGTACCAAGCTACAGGACTCAAAAGTATAGTACAAATTTACTAGA 1700  
QY 871 CACTACTGACATCCAGGGAAGAATTTGCCAAAGTTATAGTACAAATTTGAAGATAA 930  
Db 1701 CACTACTGACATCCAGGGAAGAATTTGCCAAAGTTATAGTACAAATTTGAAGATAA 1760  
QY 931 CAAACAAATGGGCTTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 990  
Db 1761 CAAACAAATGGGCTTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 1820  
QY 991 AAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1050  
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QY 1051 AAAGGATATTTATATCTCTGTGCTTGTGCTTTTATATATAAATCCGTGAGTATTA 1110  
Db 1881 AAAGGATATTTATATCTCTGTGCTTGTGCTTTTATATATAAATCCGTGAGTATTA 1940  
QY 1111 AGCTTTATGAAGGTTCTTGGGTAATATAGTCTCCCTCCATGACACTGCAATTTT 1170



Db 1941 ACCTTTATGAAGTTCTTTGGTAAATATAGTCTCCCTCATGACACGAGTATTTT 2000  
Qy 1171 TTTTAATTAATCAAGTAAAAAGTT-----TGAATTTGCTACATAGTTCAATTTT 1222  
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Qy 1223 ATGCTCTTTTGTAAACAGAAACCACTTTAAAGGATAGTAATTTCTGTTTATAACA 1282  
Db 2061 ATGCTCTTTTGTAAACAGAAACCACTTTAAAGGATAGTAATTTCTGTTTATAACA 2120  
Qy 1283 GTGCTTAAAGGTATGATGATTTCTGATGGAAGCCATTTTCACATTCATGTTCTTCATGG 1342  
Db 2121 GTGCTTAAAGGTATGATGATTTCTGATGGAAGCCATTTTCACATTCATGTTCTTCATGG 2180  
Qy 1343 ATTATTGTTTACTTCTTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 1402  
Db 2181 ATTATTGTTTACTTCTTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 2240  
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Qy 1463 TTAATTTAAACCTCCAATTATAGGATTAATTTTAAAGTTTATTTATGAATTCCTTTA 1522  
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Qy 1583 CGCTTCCCTGCTCCCACTTTTAACTCAGCTTCCCTACTGTCAACAACCAAGCTAA 1642  
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Db 2481 ATAAAGTCAACAGCCTGATGTG 2502

RESULT 3

US-09-019-942-2  
; Sequence 2, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1931 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-09-019-942-2

Query Match 43.8%; Score 731.8; DB 3; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 331 ACAGTTACAGAGTGTTCACAGTGCACATTCACCTATGTGACAGAAATGGAATATTC 390  
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Qy 571 CAGTTGGATAGCACTATTCAGATCTCAAGGCTGCATTCGTGTGATCAAGACCAAC 630  
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Qy 991 AAATTTACTTCAAAATAAAGCATGATGATGCTGTTTTTCAAGAGAAATGTGTTTAT 1050  
Db 1809 AAATTTACTTCAAAATAAAGCATGATGATGCTGTTTTTCAAGAGAAATGTGTTTAT 1868  
Qy 1051 AAAAGGATATTATA 1065  
Db 1869 AAAAGGATATTATA 1883

RESULT 4

US-09-099-041A-1  
; Sequence 1, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:

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; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-099-041A-1

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Query Match      43.8%; Score 731.8; DB 4; Length 1931;
Best Local Similarity 99.7%; Pred. No. 4.1e-160;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy	331	ACAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAAGAGAAAATGGAATTATC	390
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Qy	391	TCCTGAACATACCTCGTAAATCATGCTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA	450
Db	1209	TCCTGAACATACCTCGTAAATCATGCTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA	1268
Qy	451	TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTT	510
Db	1269	TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTT	1328
Qy	511	TTTTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCAGTCTCTGGAAATCA	570
Db	1329	TTTTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCAGTCTCTGGAAATCA	1388
Qy	571	CAGTTGGGATAGACACCATTTCTGGATCTCAAAAGGGCTGCATTCCTGTCATCAACAAGACCAC	630
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Db	1809	AAATTTTACTTCAAAATAAAGCATGTAAAGTCATGTTTCTTTTCAAGAGAAATGTGTTTCAT	1868
Qy	1051	AAAAGGATATTTTATA	1065

Db 1689 CACTACTGACATCCAAAGGAGAAATTTCCCAAAGTTATATAGTACAAAAATTTGAAAGATAA 1748

QY 931 CAAACAAATGGGTCTTTCAGCCTTACCCGGAATACTTTGTGGTTTCTAGATCACCATCTTT 990

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QY 991 AAATTACTTCAAATAAAGCATGTAACTGTTTTCAGGAAGAAATGTGTTTCAAT 1050

Db 1809 AAATTACTTCAAATAAAGCATGTAACTGTTTTCAGGAAGAAATGTGTTTCAAT 1868

QY 1051 AAAAGGATATTATA 1065

Db 1869 AAAGGATATTATA 1883

RESULT 6

US-09-470-271-2

; Sequence 2, Application US/09470271

; Patent No. 6410689

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/470,271

; FILING DATE:

; PRIOR APPLICATION NUMBER: 09/019,942

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Meiklejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 07334/068001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1931 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-470-271-2

Query Match 43.8%; Score 731.8; DB 4; Length 1931;

Best Local Similarity 99.7%; Pred. No. 4.1e-160;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTTACAGAGTGTTCAGTGCCATTCCACCTATGTGCAAGAGAAATGGAATTATC 390

Db 1149 AAGTTTACAGAGTGTTCAGTGCCATTCCACCTATGTGCAAGAGAAATGGAATTATC 1208

QY 391 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCA 450

Db 1209 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCA 1268

QY 451 TGAATAATAGTGGTCTCTCTGAAACTTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTT 510

Db 1269 TGAATAATAGTGGTCTCTCTGAAACTTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTT 1328

QY 511 TTTATCTAGAAAAGCTCAAGACTGTGTTATTTTATGAAGCTGCACTCACTGTCTCTGGAATCA 570

Db 1329 TTTATCTAGAAAAGCTCAAGACTGTGTTATTTTATGAAGCTGCACTCACTGTCTCTGGAATCA 1388

QY 571 CAGTTGGGATAGCACCATTCTTGGATCTCAAGGGCTGATCTCTGTGATCAACAAGCCAC 630

Db 1389 CAGTTGGGATAGCACCATTCTTGGATCTCAAGGGCTGATCTCTGTGATCAACAAGCCAC 1448

QY 631 TCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTTCTGCA 690

Db 1449 TCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTTCTGCA 1508

QY 691 GCCTGTATAGCCCAAGCAGTGGATCCAGAGCAAAAAGGGAAGACATTTGTGAACCAAAATGAC 750

Db 1509 GCCTGTATAGCCCAAGCAGTGGATCCAGAGCAAAAAGGGAAGACATTTGTGAACCAAAATGAC 1568

QY 751 AGAGCCTGCTTAAACAGTGGTAGATGCCCTTCTGTCCAGGAGCTTGTGATCATGAAAGA 810

Db 1569 AGAGCCTGCTTAAACAGTGGTAGATGCCCTTCTGTCCAGGAGCTTGTGATCATGAAAGA 1628

QY 811 GGACTATGAATCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 870

Db 1629 GGACTATGAATCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 1688

QY 871 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 930

Db 1689 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 1748

QY 931 CAAACAAATGGGTCTTTCAGCCTTACCCGGAATACTTTGTGGTTTCTAGATCACCATCTTT 990

Db 1749 CAAACAAATGGGTCTTTCAGCCTTACCCGGAATACTTTGTGGTTTCTAGATCACCATCTTT 1808

QY 991 AAATTACTTCAAATAAAGCATGTAACTGTTTTCAGGAAGAAATGTGTTTCAAT 1050

Db 1809 AAATTACTTCAAATAAAGCATGTAACTGTTTTCAGGAAGAAATGTGTTTCAAT 1868

QY 1051 AAAAGGATATTATA 1065

Db 1869 AAAGGATATTATA 1883

RESULT 7

US-09-207-359B-1

; Sequence 1, Application US/09207359B

; Patent No. 6469140

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; FILE REFERENCE: 07334-112001

; CURRENT APPLICATION NUMBER: US/09/207,359B

; CURRENT FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1931

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (214)...(1833)

US-09-207-359B-1

Query Match 43.8%; Score 731.8; DB 4; Length 1931;

Best Local Similarity 99.7%; Pred. No. 4.1e-160;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 331 ACAGTTACAGAGTGTCTTCAAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATC 390
Db 1149 AAAGTTACAGAGTGTCTTCAAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATC 1208
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCA 1268
QY 451 TGAAGATAGTGTCTCTGAAATCTCAAGTGCCTCCAGCTCCCTCAAGACATGATTT 510
Db 1269 TGAAGATAGTGTCTCTGAAATCTCAAGTGCCTCCAGCTCCCTCAAGACATGATTT 1328
QY 511 TTTATCTAGAAAAGCTCAAGACCTGTATTTTATGAAGCTGCATCAGTCTCTGGAATCA 570
Db 1329 TTTATCTAGAAAAGCTCAAGACCTGTATTTTATGAAGCTGCATCAGTCTCTGGAATCA 1388
QY 571 CAGTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCC 630
Db 1389 CAGTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCC 1448
QY 631 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCTGCA 690
Db 1449 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCTGCA 1508
QY 691 GCCTGGTATAGCCCGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750
Db 1509 GCCTGGTATAGCCCGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1568
QY 751 AGAAGCCTGCTTAAACAGTCGCTAGATGCTTCTGTGAGGACCTTGTGATCAAGAA 810
Db 1569 AGAAGCCTGCTTAAACAGTCGCTAGATGCTTCTGTGAGGACCTTGTGATCAAGAA 1628
QY 811 GGACTATGAATTTGTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGAAATTTACTAGA 870
Db 1629 GGACTATGAATTTGTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGAAATTTACTAGA 1688
QY 871 CACTACTGACATCCAAAGGAGAAGATTTGCCAAAGTTATAGTACAAAAATTTGAAGATA 930
Db 1689 CACTACTGACATCCAAAGGAGAAGATTTGCCAAAGTTATAGTACAAAAATTTGAAGATA 1748
QY 931 CAAACAAATGGCTTTCAGCTTACCCGGAATACCTTGTGGTCTTAGATCACCATCTTT 990
Db 1749 CAAACAAATGGCTTTCAGCTTACCCGGAATACCTTGTGGTCTTAGATCACCATCTTT 1808
QY 991 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1868
QY 1051 AAAAGGATATTTATA 1065
Db 1869 AAAAGGATATTTATA 1883

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RESULT 8

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US-09-340-620A-1
; Sequence 1, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-340-620A-1

Query Match      43.8%; Score 731.8; DB 4; Length 1931;
Best Local Similarity 99.7%; Pred. No. 4.1e-160;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTCTTCAAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATC 390
Db 1149 AAAGTTACAGAGTGTCTTCAAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATC 1208
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCA 1268
QY 451 TGAAGATAGTGTCTCTGAAATCTCAAGTGCCTCCAGCTCCCTCAAGACATGATTT 510
Db 1269 TGAAGATAGTGTCTCTGAAATCTCAAGTGCCTCCAGCTCCCTCAAGACATGATTT 1328
QY 511 TTTATCTAGAAAAGCTCAAGACCTGTATTTTATGAAGCTGCATCAGTCTCTGGAATCA 570
Db 1329 TTTATCTAGAAAAGCTCAAGACCTGTATTTTATGAAGCTGCATCAGTCTCTGGAATCA 1388
QY 571 CAGTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCC 630
Db 1389 CAGTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCC 1448
QY 631 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCTGCA 690
Db 1449 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCTGCA 1508
QY 691 GCCTGGTATAGCCCGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750
Db 1509 GCCTGGTATAGCCCGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1568
QY 751 AGAAGCCTGCTTAAACAGTCGCTAGATGCTTCTGTGAGGACCTTGTGATCAAGAA 810
Db 1569 AGAAGCCTGCTTAAACAGTCGCTAGATGCTTCTGTGAGGACCTTGTGATCAAGAA 1628
QY 811 GGACTATGAATTTGTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGAAATTTACTAGA 870
Db 1629 GGACTATGAATTTGTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGAAATTTACTAGA 1688
QY 871 CACTACTGACATCCAAAGGAGAAGATTTGCCAAAGTTATAGTACAAAAATTTGAAGATA 930
Db 1689 CACTACTGACATCCAAAGGAGAAGATTTGCCAAAGTTATAGTACAAAAATTTGAAGATA 1748
QY 931 CAAACAAATGGCTTTCAGCTTACCCGGAATACCTTGTGGTCTTAGATCACCATCTTT 990
Db 1749 CAAACAAATGGCTTTCAGCTTACCCGGAATACCTTGTGGTCTTAGATCACCATCTTT 1808
QY 991 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1868
QY 1051 AAAAGGATATTTATA 1065
Db 1869 AAAAGGATATTTATA 1883

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RESULT 9

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US-09-865-364-1
; Sequence 1, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

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;; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
;; FILE REFERENCE: 07334-112001  
;; CURRENT APPLICATION NUMBER: US/09/865,364  
;; CURRENT FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 09/207,359  
;; PRIOR FILING DATE: 1998-12-08  
;; PRIOR APPLICATION NUMBER: US 09/099,041  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: US 09/019,942  
;; PRIOR FILING DATE: 1998-02-06  
;; NUMBER OF SEQ ID NOS: 47  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 1931  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (214)...(1833)  
US-09-865-364-1

Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 390  
Db |||||||  
QY 391 TCTGACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
Db |||||||  
QY 1209 TCTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268  
QY 451 TGAATAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGTCTCTCAAGACAAATGATTT 510  
Db |||||||  
QY 1269 TGAATAATAGTGGTCTCTCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAAATGATTT 1328  
QY 511 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTCGGAAATCA 570  
Db |||||||  
QY 1329 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTCGGAAATCA 1388  
QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAGCCAC 630  
Db |||||||  
QY 1389 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAGCCAT 1448  
QY 631 TCCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCA 690  
Db |||||||  
QY 1449 TCCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCA 1508  
QY 691 GCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
Db |||||||  
QY 1509 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1568  
QY 751 AGAAGCTGCTTAAACAGTGCATAGCCCTTCTGTCCAGGACTTGCATCATGAAGA 810  
Db |||||||  
QY 1569 AGAAGCTGCTTAAACAGTGCATAGCCCTTCTGTCCAGGACTTGCATCATGAAGA 1628  
QY 811 GGACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCTGATCAATTAAGTAC 870  
Db |||||||  
QY 1629 GGACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCTGATCAATTAAGTAC 1688  
QY 871 CACTACTGACATCCAGGGAAGAAATTTGCAAGTTATAGTACAAAAATGGAAGATAA 930  
Db |||||||  
QY 1689 CACTACTGACATCCAGGGAAGAAATTTGCAAGTTATAGTACAAAAATGGAAGATAA 1748  
QY 931 CAAACAAATGGGTCTTACCGGAAATCTGTGGTTCTTAGATCACCATCTTT 990  
Db |||||||  
QY 1749 CAAACAAATGGGTCTTACCGGAAATCTGTGGTTCTTAGATCACCATCTTT 1808  
QY 991 AATTTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTTCAAGAGAAATGTTTTTCAAT 1050  
Db |||||||  
QY 1809 AATTTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTTCAAGAGAAATGTTTTTCAAT 1868  
Db |||||||

QY 1051 AAAAGGATATTATA 1065  
Db |||||||  
QY 1869 AAAAGGATATTATA 1883  
Db |||||||

RESULT 10  
US-09-748-537-2  
;; Sequence 2, Application US/09748537  
;; Patent No. 6680167  
;; GENERAL INFORMATION:  
;; APPLICANT: Chao, Moses V.  
;; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
;; FILE REFERENCE: 07334-316001  
;; CURRENT APPLICATION NUMBER: US/09/748,537  
;; CURRENT FILING DATE: 2000-12-26  
;; PRIOR APPLICATION NUMBER: US 09/099,041  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: US 09/019,942  
;; PRIOR FILING DATE: 1998-02-06  
;; NUMBER OF SEQ ID NOS: 14  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 1931  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-748-537-2

Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 390  
Db |||||||  
QY 391 TCTGACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
Db |||||||  
QY 1209 TCTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268  
QY 451 TGAATAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGTCTCTCAAGACAAATGATTT 510  
Db |||||||  
QY 1269 TGAATAATAGTGGTCTCTCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAAATGATTT 1328  
QY 511 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTCGGAAATCA 570  
Db |||||||  
QY 1329 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTCGGAAATCA 1388  
QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAGCCAC 630  
Db |||||||  
QY 1389 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAGCCAT 1448  
QY 631 TCCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCA 690  
Db |||||||  
QY 1449 TCCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCA 1508  
QY 691 GCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
Db |||||||  
QY 1509 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1568  
QY 751 AGAAGCTGCTTAAACAGTGCATAGCCCTTCTGTCCAGGACTTGCATCATGAAGA 810  
Db |||||||  
QY 1569 AGAAGCTGCTTAAACAGTGCATAGCCCTTCTGTCCAGGACTTGCATCATGAAGA 1628  
QY 811 GGACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCTGATCAATTAAGTAC 870  
Db |||||||  
QY 1629 GGACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCTGATCAATTAAGTAC 1688  
QY 871 CACTACTGACATCCAGGGAAGAAATTTGCAAGTTATAGTACAAAAATGGAAGATAA 930  
Db |||||||  
QY 1689 CACTACTGACATCCAGGGAAGAAATTTGCAAGTTATAGTACAAAAATGGAAGATAA 1748  
QY 931 CAAACAAATGGGTCTTACCGGAAATCTGTGGTTCTTAGATCACCATCTTT 990  
Db |||||||

Db 1749 CAACAAATGGTCTTCAGCCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTT 1808  
Qy 991 AAATTTACTTCARAAATAAAGCATGTAAGTGACCTGTTTTCAGAGAAATGTTTCAT 1050  
Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTGACCTGTTTTCAGAGAAATGTTTCAT 1868  
Qy 1051 AAAAGGATATTATA 1065  
Db 1869 AAAAGGATATTATA 1883

RESULT 11  
US-09-023-655-684  
; Sequence 684, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 684:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1060 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: MPHGNOT03  
; CLONE: 445186  
US-09-023-655-684

Query Match 41.7%; Score 695.4; DB 4; Length 1060;  
Best Local Similarity 99.7%; Pred. No. 8.8e-152;  
Matches 707; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
Qy 331 ACAGTTACAGAGTGTTCAGTGCCATTCCACCTATGTGACAGAGAAATGGAATATC 390  
Db 352 AAAGTTACAGAGTGTTCAGTGCCATTCCACCTATGTGACAGAGAAATGGAATATC 411  
Qy 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 450  
Db 412 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 471

Qy 451 TGAAATA-GTGGTTCTCTGAAATCTCAAGGTCCCTGCAGCTCCTCAAGACAATGATT 509  
Db 472 TGAATAATAGTGTCTCTCTGAAATCTCAAGGTCCCTGCAGCTCCTCAAGACAATGATT 531  
Qy 510 TTTTATCTAGAAAAGCTCAAGACTGTATTATTATGAAGCTGCATCATCTGTCTTGGAAATC 569  
Db 532 TTTTATCTAGAAAAGCTCAAGACTGTATTATTATGAAGCTGCATCATCTGTCTTGGAAATC 591  
Qy 570 ACAGTTGGGATAGCACCATTTCTGGATCTCAAAAGGCTGCATTCTCTGTATCACAAGACCA 629  
Db 592 ACAGTTGGGATAGCACCATTTCTGGATCTCAAAAGGCTGCATTCTCTGTATCACAAGACCA 651  
Qy 630 CTCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTGC 689  
Db 652 CTCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTGC 711  
Qy 690 AGCTGTGTATAGCCCGAGCAGTGATCCAGAGCAAAAGGGAAGACATGTGAACCAATGA 749  
Db 712 AGCTGTGTATAGCCCGAGCAGTGATCCAGAGCAAAAGGGAAGACATGTGAACCAATGA 771  
Qy 750 CAGAAGCTGCTTAAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAG 809  
Db 772 CAGAAGCTGCTTAAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAG 831  
Qy 810 AGGACTATGAACCTTGTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTAG 869  
Db 832 AGGACTATGAACCTTGTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTAG 891  
Qy 870 ACAGTACTGACATCCAGGAGGAAGATTTGCCAAGTTTATAGTACAAAATTTGAAAGATA 929  
Db 892 ACAGTACTGACATCCAGGAGGAAGATTTGCCAAGTTTATAGTACAAAATTTGAAAGATA 951  
Qy 930 ACAACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTT 989  
Db 952 ACAACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTT 1011  
Qy 990 TAAATTTACTTCAAAATAAAAGCATGTAAGTGACTCTTTTCAAGAAGA 1038  
Db 1012 TAAATTTACTTCAAAATAAAAGCATGTAAGTGACTCTTTTCAAGAAGA 1060

RESULT 12  
US-09-099-041A-3  
; Sequence 3, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-099-041A-3

Query Match 40.9%; Score 681.8; DB 4; Length 1620;  
Best Local Similarity 99.7%; Pred. No. 1.4e-148;  
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 331 ACAGTTACAGAGTGTTCAGTGCCATTCCACCTATGTGACAGAGAAATGGAATATC 390  
Db 936 AAAGTTACAGAGTGTTCAGTGCCATTCCACCTATGTGACAGAGAAATGGAATATC 995  
Qy 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 450  
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 ; Sequence 3, Application US/09245281  
 ; Patent No. 6369196  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; FILE REFERENCE: 07334/118001  
 ; CURRENT APPLICATION NUMBER: US/09/245,281  
 ; EARLIER FILING DATE: 1999-02-05  
 ; EARLIER APPLICATION NUMBER: US 09/207,359  
 ; EARLIER FILING DATE: 1998-12-08  
 ; EARLIER APPLICATION NUMBER: US 09/099,041  
 ; EARLIER FILING DATE: 1998-06-17  
 ; EARLIER APPLICATION NUMBER: US 09/019,942  
 ; EARLIER FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-245-281-3  
 Query Match 40.9%; Score 681.8; DB 4; Length 1620;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-148;  
 Matches 663; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 ; Patent No. 6469140  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/207,359B  
 ; CURRENT FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 47  
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 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-207-359B-3

Query Match 40.9%; Score 681.8; DB 4; Length 1620;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-148;  
 Matches 663; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



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QY 331 ACAGTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAGAGAGAAATGGAATTATC 390
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; Sequence 3, Application US/09340620A
; Patent No. 6482933
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; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
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; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-340-620A-3

Query Match 40.9%; Score 681.8; DB 4; Length 1620;
Best Local Similarity 99.7%; Pred. No. 1.4e-148;
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAGAGAGAAATGGAATTATC 390
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	1332.4	78.8	2709	US-09-925-301-173	Sequence 173, Appl
3	1308	78.4	2501	US-09-981-397A-13	Sequence 13, Appl
4	731.8	43.8	1931	US-09-748-537-2	Sequence 2, Appli
5	731.8	43.8	1931	US-09-728-721-1	Sequence 1, Appli
6	731.8	43.8	1931	US-10-133-780-2	Sequence 2, Appli
7	731.8	43.8	1931	US-10-105-931-1	Sequence 1, Appli
8	731.8	43.8	1931	US-10-118-984-1	Sequence 1, Appli
9	731.8	43.8	1931	US-10-295-981-1	Sequence 3, Appli
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14	363.4	21.8	491	US-09-918-995-20565	Sequence 20565, A
15	271	16.2	299	US-09-919-580-544	Sequence 544, App

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18	60	3.6	60	10	US-09-908-975-13799	Sequence 13799, A
19	60	3.6	60	10	US-09-908-975-31279	Sequence 31279, A
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27	57.4	3.4	8711	12	US-10-221-714A-424	Sequence 424, Appl
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35	56.6	3.4	17848	14	US-10-239-676-28	Sequence 28, Appl
36	56.6	3.4	17848	14	US-10-240-453-38	Sequence 38, Appl
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ALIGNMENTS

RESULT 1

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; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771.161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1669  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: (1)..(1669)  
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'  
US-09-771-161A-2

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 Db 1021 GACTGTTTTTCAAGAAAGATGTTTTCAAAAAGGATATTTATCTCTGTGCTTTGA 1080  
 Qy 1081 CTTTTTTTATATAAAATCCGTGAGTATTAAGCTTTTATTAAGGTTCTTTGGGTAAATAT 1140  
 Db 1081 CTTTTTTTATATAAAATCCGTGAGTATTAAGCTTTTATTAAGGTTCTTTGGGTAAATAT 1140  
 Qy 1141 TAGTCTCCCTCCATGACACTGCAGTATTTTATTAATTAATACAGTAAAAAGTTGAAT 1200  
 Db 1141 TAGTCTCCCTCCATGACACTGCAGTATTTTATTAATTAATACAGTAAAAAGTTGAAT 1200

Qy 1201 TTTTGCTACATAGTTCAATTTTATGTTCTTTTGTAAACAGAAACACATTTTAAAGGATA 1260  
 Db 1201 TTTTGCTACATAGTTCAATTTTATGTTCTTTTGTAAACAGAAACACATTTTAAAGGATA 1260  
 Qy 1261 GTAATTTATTTCTTTTATAACAGTGCCTTTAAGGTATGATGTTTCTGATGAAGCCATT 1320  
 Db 1261 GTAATTTATTTCTTTTATAACAGTGCCTTTAAGGTATGATGTTTCTGATGAAGCCATT 1320  
 Qy 1321 TTCACATTCATGTTCTTCTCATGGAATTTATTTGTTACTTGTCTAAGATGCAATTTGATTTAT 1380  
 Db 1321 TTCACATTCATGTTCTTCTCATGGAATTTATTTGTTACTTGTCTAAGATGCAATTTGATTTAT 1380  
 Qy 1381 GAAGTATATATACCTTTTACCCACAGACAGTACAGAAATCCCTGCCCTAAAAATCCAGGC 1440  
 Db 1381 GAAGTATATATACCTTTTACCCACAGACAGTACAGAAATCCCTGCCCTAAAAATCCAGGC 1440  
 Qy 1441 TTAATTTGCCCTACAAAGGGTTATTAATTTAAATCCCATTTATAGGATTTACATTTTAAAG 1500  
 Db 1441 TTAATTTGCCCTACAAAGGGTTATTAATTTAAATCCCATTTATAGGATTTACATTTTAAAG 1500  
 Qy 1501 TTTTATTTATGAAATCCCTTTTAAATGATATTTTCAAGGTAAACAAATACAAATATAAAG 1560  
 Db 1501 TTTTATTTATGAAATCCCTTTTAAATGATATTTTCAAGGTAAACAAATACAAATATAAAG 1560  
 Qy 1561 AAAAAAATAAATATATTAATATACCGGCTTCTCTGCCCATTTTAACTCAGCCTTCCCTA 1620  
 Db 1561 AAAAAAATAAATATATTAATATACCGGCTTCTCTGCCCATTTTAACTCAGCCTTCCCTA 1620  
 Qy 1621 CTGTCCCAACCAACCAAGCTAAATAAAGTCAACAGCTGATGTGTAAAA 1669  
 Db 1621 CTGTCCCAACCAACCAAGCTAAATAAAGTCAACAGCTGATGTGTAAAA 1669

RESULT 2

US-09-925-301-173  
 ; Sequence 173, Application US/09925301  
 ; Patent No. US20020052308A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA106  
 ; CURRENT APPLICATION NUMBER: US/09/925,301  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 1694  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 173  
 ; LENGTH: 2709  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (2595)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (2622)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (2659)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (2670)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; US-09-925-301-173

Query Match 79.8%; Score 1332.4; DB 9; Length 2709;  
 Best Local Similarity 99.6%; Pred. No. 1.8e-272;  
 Matches 1330; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAGAGAAATGGAAATATC 390  
DB |||||  
1202 AAAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAGAGAAATGGAAATATC 1261  
QY |||||  
391 TCTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
DB |||||  
1262 TCTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1321  
QY |||||  
451 TGAATAATAGTGTCTCTGAAATCTCAAGTTCCTGAGTCCCTGAGTCTCTCAAGCAATGATTT 510  
DB |||||  
1322 TGAATAATAGTGTCTCTGAAATCTCAAGTTCCTGAGTCCCTGAGTCTCTCAAGCAATGATTT 1381  
QY |||||  
511 TTATCTAGAAAGCTCAAGACTGTATTTATGAGCTGCATCACTCTCTGGAATCA 570  
DB |||||  
1382 TTATCTAGAAAGCTCAAGACTGTATTTATGAGCTGCATCACTCTCTGGAATCA 1441  
QY |||||  
571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCCTGATCAAGACCAAC 630  
DB |||||  
1442 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCCTGATCAAGACCAAC 1501  
QY |||||  
631 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTCCA 690  
DB |||||  
1502 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTCCA 1561  
QY |||||  
691 GCCTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 750  
DB |||||  
1562 GCCTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 1621  
QY |||||  
751 AGAAGCTGCTTAAACAGTCCAGTCCAGTCCCTCTGTCAGGGACTTGCATCAAGAA 810  
DB |||||  
1622 AGAAGCTGCTTAAACAGTCCAGTCCAGTCCCTCTGTCAGGGACTTGCATCAAGAA 1681  
QY |||||  
811 GGACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAAGTA 870  
DB |||||  
1682 GGACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAAGTA 1741  
QY |||||  
871 CACTACTGACATCCAGAGGAAGAAATTTGCCAAAGTTATAGTACAAAATGGAAGATAA 930  
DB |||||  
1742 CACTACTGACATCCAGAGGAAGAAATTTGCCAAAGTTATAGTACAAAATGGAAGATAA 1801  
QY |||||  
931 CAAACAAATGGGCTTTCAGCCTTACCGGAATCTTGTGGTTCTAGATCACCATCTTT 990  
DB |||||  
1802 CAAACAAATGGGCTTTCAGCCTTACCGGAATCTTGTGGTTCTAGATCACCATCTTT 1861  
QY |||||  
991 AAATTTACTTCAAAATAAAGCATGTAGTACTGTGTTTCAAGAGAAATGTGTTTCT 1050  
DB |||||  
1862 AAATTTACTTCAAAATAAAGCATGTAGTACTGTGTTTCAAGAGAAATGTGTTTCT 1921  
QY |||||  
1051 AAAGGATATTTATATCTCTGTTGTTGACTTTTATATAAATCCGTGAGTATTA 1110  
DB |||||  
1922 AAAGGATATTTATATCTCTGTTGTTGACTTTTATATAAATCCGTGAGTATTA 1981  
QY |||||  
1111 AGCTTTATGAGGTTCTTTGGGTAATATAGTCTCCCTCCATCAGACTGAGTATTT 1170  
DB |||||  
1982 AGCTTTATGAGGTTCTTTGGGTAATATAGTCTCCCTCCATCAGACTGAGTATTT 2041  
QY |||||  
1171 TTTTAAATTAACAAGTAAAGTTGAAATTTGCTACATAGTTCAAATTTTATGCTCT 1230  
DB |||||  
2042 TTTTAAATTAACAAGTAAAGTTGAAATTTGCTACATAGTTCAAATTTTATGCTCT 2101  
QY |||||  
1231 TTTGTTAACAAGAACCCACTTTTAAAGGATAGTAAATTTCTGTTTATAAAGTGCCTTA 1290  
DB |||||  
2102 TTTGTTAACAAGAACCCACTTTTAAAGGATAGTAAATTTCTGTTTATAAAGTGCCTTA 2161  
QY |||||  
1291 AGGTATGATGATTTCTGATGAGGCAATTTTCAATTCATGTTCTTCAAGATTTT 1350  
DB |||||  
2162 AGGTATGATGATTTCTGATGAGGCAATTTTCAATTCATGTTCTTCAAGATTTT 2221  
QY |||||  
1351 TTACTTGTCTAAGATCAATTTGATTTTATGAGTATATACCTTTTACCACAGAGACA 1410  
DB |||||  
2222 TTACTTGTCTAAGATCAATTTGATTTTATGAGTATATACCTTTTACCACAGAGACA 2281  
QY |||||  
1411 GTACAGAAATCCCTGCCCTAAAAATCCAGGCTTAAATTTGCCCTTCAAAAGGGTTTAAATTTA 1470

DB 2282 GTACAGAAATCCCTGCCCTAAATCCAGGCTTAAATTTGCCCTCAAAAGGGTTTAAATTTA 2341  
QY |||||  
1471 AAACCTCCATTTATTAGGATTCATTTTAAAGTTTATTATGAATTCCTTTAAAAAATGAT 1530  
DB |||||  
2342 AAACCTCCATTTATTAGGATTCATTTTAAAGTTTATTATGAATTCCTTTAAAAAATGAT 2401  
QY |||||  
1531 ATTTCAAAGGTTAAACATACATATAAAGAAATAAATAATATATTAATACCGGCTTCC 1590  
DB |||||  
2402 ATTTCAAAGGTTAAACATACATATAAAGAAATAAATAATATATTAATACCGGCTTCC 2461  
QY |||||  
1591 TGTCCCAATTTTAACTCAGCTTCCCTACTGTCCACCAACCAAGCTAAATAAAGTC 1650  
DB |||||  
2462 TGTCCCAATTTTAACTCAGCTTCCCTACTGTCCACCAACCAAGCTAAATAAAGTC 2521  
QY |||||  
1651 AACAGCCTGATGTGTA 1666  
DB |||||  
2522 AACAGCCTGATGTGTA 2537

RESULT 3  
US-09-981-397A-13  
; Sequence 13, Application US/09981397A  
; Publication No. US20030082519A1  
; GENERAL INFORMATION:  
; APPLICANT: Axxima Pharmaceuticals AG  
; APPLICANT: Schubart, Daniel  
; APPLICANT: Habenberger, Peter  
; APPLICANT: Stein-Gerlach, Matthias  
; APPLICANT: Bevec, Dorian  
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
; FILE REFERENCE: AXM-004.1 US  
; CURRENT APPLICATION NUMBER: US/09/981.397A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/240,750  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-981-397A-13

Query Match 78.4%; Score 1308; DB 10; Length 2501;  
Best Local Similarity 99.0%; Pred. No. 2.6e-267;  
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

QY 331 ACAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAGAGAAATGGAAATATC 390  
DB |||||  
1160 AAAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAGAGAAATGGAAATATC 1219  
QY 391 TCTGNACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
DB |||||  
1220 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1279  
QY 451 TGAATAATAGTGTCTCTGAAACTTCAAGGTCCTGCCAGCTCTCAAGACAAATGATTT 510  
DB |||||  
1280 TGAATAATAGTGTCTCTGAAACTTCAAGGTCCTGCCAGCTCTCAAGACAAATGATTT 1339  
QY 511 TTTATCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCGGAAATCA 570  
DB |||||  
1340 TTTATCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCGGAAATCA 1399  
QY 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCCTGATCAAGACCAAC 630  
DB |||||  
1400 CAGTTGGGATAGCACCATTTCTGGTTCTCAAGGGCTGCATTCCTGATCAAGACCAAC 1459  
QY 631 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCA 690  
DB |||||  
1460 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCA 1519

```
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGAC 750
Db 1520 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGAC 1579
QY 751 AGAAGCCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCAGGACCTTGATCATGAAGA 810
Db 1580 AGAAGCCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCAGGACCTTGATCATGAAGA 1639
QY 811 GGAATATGAATTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGACAAATTTACTAGA 870
Db 1640 GGAATATGAATTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGACAAATTTACTAGA 1699
QY 871 CACTACTGACATCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930
Db 1700 CACTACTGACATCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 1759
QY 931 CAAACAAATGGGCTTCAGGCTTACCCGGAATATCTTGCTGTTCTAGATCACAATCTTT 990
Db 1760 CAAACAAATGGGCTTCAGGCTTACCCGGAATATCTTGCTGTTCTAGATCACAATCTTT 1819
QY 991 AAAATTTACTTCAAAATAAAAGCATGTAAGTACCTTACCCGGAATATCTTGCTGTTCT 1050
Db 1820 AAAATTTACTTCAAAATAAAAGCATGTAAGTACCTTACCCGGAATATCTTGCTGTTCT 1879
QY 1051 AAAAGGATATTTATCTCTGTTGCTTTGACTTTTTTTTATATAAAATCCGCTGATATTA 1110
Db 1880 AAAAGGATATTTATCTCTGTTGCTTTGACTTTTTTTTATATAAAATCCGCTGATATTA 1939
QY 1111 AGCTTTATGAAGTCTTCTGGGTAAATATAGTCTCCCTCCATGACACTGCAATGATTTT 1170
Db 1940 AGCTTTATGAAGTCTTCTGGGTAAATATAGTCTCCCTCCATGACACTGCAATGATTTT 1999
QY 1171 TTTTAAATTAACAAGTAAAGTT-----TGAATTTTGTACATAGTTCAATTTTTT 1222
Db 2000 TTTTAAATTAACAAGTAAAGTTGAAATTTGGTTGAAATTTGTCTACATAGTTCAATTTTT 2059
QY 1223 ATGTCTCTTTTGTAAACAGAAACACCTTTTAAAGGATAGTAATATTTCTTTTATAACA 1282
Db 2060 ATGTCTCTTTTGTAAACAGAAACACCTTTTAAAGGATAGTAATATTTCTTTTATAACA 2119
QY 1283 GTGCTTAAAGTATGATGATTTCTGATGGAAGCATTTCACATTCATGTTCTTCATGG 1342
Db 2120 GTGCTTAAAGTATGATGATTTCTGATGGAAGCATTTCACATTCATGTTCTTCATGG 2179
QY 1343 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 1402
Db 2180 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 2239
QY 1403 CAGAGACAGTACAGAATCCCTGCCCTTAAATCCAGGCTTAAATGCGCCTACAAAGGTTA 1462
Db 2240 CAGAGACAGTACAGAATCCCTGCCCTTAAATCCAGGCTTAAATGCGCCTACAAAGGTTA 2299
QY 1463 TTAATTTAAACTCCATTATAGATTAATTTTAAAGTTTATTTATGAATTCCTTTTA 1522
Db 2300 TTAATTTAAACTCCATTATAGATTAATTTTAAAGTTTATTTATGAATTCCTTTTA 2359
QY 1523 AAAATGATATTTCAAAGGTAACAATACATAATAAAGAAAATAAATAATATTAATAC 1582
Db 2360 AAAATGATATTTCAAAGGTAACAATACATAATAAAGAAAATAAATAATATTAATAC 2419
QY 1583 CGGCTTCTGCTCCCAATTTTAACTCAGCCTTCCCTACTGTGTCACCAACCAACCAAGCTAA 1642
Db 2420 CGGCTTCTGCTCCCAATTTTAACTCAGCCTTCCCTACTGTGTCACCAACCAACCAAGCTAA 2479
QY 1643 ATAAAGTCAACAGCCTGATGTG 1664
Db 2480 ATAAAGTCAACAGCCTGATGTG 2501
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RESULT 4

US-09-748-537-2

; Sequence 2, Application US/09748537

; Patent No. US20020061833A1

```
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-748-537-2
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Query Match 43.8%; Score 731.8; DB 9; Length 1931;
Best Local Similarity 99.7%; Pred. No. 4.5e-145;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGAGTCCCATTCACCTATGTGACAAAGAGAAATGGAATATC 390
Db 1149 AAAGTTACAGAGTGTTCAGAGTCCCATTCACCTATGTGACAAAGAGAAATGGAATATC 1208
QY 391 TCTGAACATACCTGTAATCATGGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAATCATGGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268
QY 451 TGAATAATAGTGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATT 510
Db 1269 TGAATAATAGTGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATT 1328
QY 511 TTTATCTAGAAAGCTCAAGACATGTTTATTTATGAAGCTGCATCACTGTCTGGAATCA 570
Db 1329 TTTATCTAGAAAGCTCAAGACATGTTTATTTATGAAGCTGCATCACTGTCTGGAATCA 1388
QY 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAGAGACCAC 630
Db 1389 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAGAGACCAC 1448
QY 631 TCCATCTCTTCAAGCAATAATAATCACTCACTCACTGAGGAAACTCAGAACCTCTGCA 690
Db 1449 TCCATCTCTTCAAGCAATAATAATCACTCACTCACTGAGGAAACTCAGAACCTCTGCA 1508
QY 691 GCTGTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750
Db 1509 GCTGTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1568
QY 751 AGNAGCTCGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTCATCATGAAGA 810
Db 1569 AGNAGCTCGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTCATCATGAAGA 1628
QY 811 GGAATATGAATTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGACAAATTTACTAGA 870
Db 1629 GGAATATGAATTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGACAAATTTACTAGA 1688
QY 871 CACTACTGATCCCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930
Db 1689 CACTACTGATCCCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 1748
QY 931 CAAACAAATGGGCTTCAGCCTTACCCGGAATATCTTGCTGTTCTAGATCACCATCTTT 990
Db 1749 CAAACAAATGGGCTTCAGCCTTACCCGGAATATCTTGCTGTTCTAGATCACCATCTTT 1808
QY 991 AAAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1050
Db 1809 AAAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1868
QY 1051 AAAAGGATATTTATA 1065
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Db 1869 AAAAGGATATTATA 1883

RESULT 5

US-09-728-721-1

Sequence 1, Application US/09728721

Patent No. US20020061845A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/728,721

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: 09/340,620

PRIOR FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1931

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (214)....(1833)

US-09-728-721-1

Query Match 43.8%; Score 731.8; DB 9; Length 1931;

Best Local Similarity 99.7%; Pred. No. 4.5e-145;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 390

Db 1149 AAAAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 1208

QY 391 TCTGAACATACCTGTAATCATGCTGCCAAGAGGAATCATGTGGATCCTCTCAGTCCA 450

Db 1209 TCTGAACATACCTGTAATCATGCTGCCAAGAGGAATCATGTGGATCCTCTCAGTCCA 1268

QY 451 TGAATAATAGTGTTCCTGAACTTTCAAGTCCCTGCCAGTCCCTCAAGACAAATGATTT 510

Db 1269 TGAATAATAGTGTTCCTGAACTTTCAAGTCCCTGCCAGTCCCTCAAGACAAATGATTT 1328

QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAATCA 570

Db 1329 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAATCA 1388

QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAACAC 630

Db 1389 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAACAC 1448

QY 631 TCCATCTCTTTCAGCAATAAATCACTCTCACTGCAGGAACTCAGAACGCTGCA 690

Db 1449 TCCATCTCTTTCAGCAATAAATCACTCTCACTGCAGGAACTCAGAACGCTGCA 1508

QY 691 GCTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGCAATTTGTAACCAATGAC 750

Db 1509 GCTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGCAATTTGTAACCAATGAC 1568

QY 751 AGAAGCCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGAGCTTCATCATGAAGA 810

Db 1569 AGAAGCCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGAGCTTCATCATGAAGA 1628

QY 811 GGACTATGAATCTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAAGCAATTTACTAGA 870

Db 1629 GGACTATGAATCTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAAGCAATTTACTAGA 1688

QY 871 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAA 930

Db 1689 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTCGAAGATAA 1748

QY 931 CAACAAAATGGTCTTTCAGCCCTTACCCGGAATACTGTGGTTTCTAGATCACCATCTTT 990

Db 1749 CAACAAAATGGTCTTTCAGCCCTTACCCGGAATACTGTGGTTTCTAGATCACCATCTTT 1808

QY 991 AAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAATGTTTCAT 1050

Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAATGTTTCAT 1868

QY 1051 AAAAGCATATTATA 1065

Db 1869 AAAAGCATATTATA 1883

RESULT 6

US-10-133-780-2

Sequence 2, Application US/10133780

Publication No. US20020123115A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT

DOMAIN POLYPEPTIDES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/133,780

FILING DATE: 26-Apr-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/019,942

FILING DATE: 06-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1931 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-133-780-2

Query Match 43.8%; Score 731.8; DB 13; Length 1931;

Best Local Similarity 99.7%; Pred. No. 4.5e-145;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 390

Db 1149 AAAAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 1208

QY 391 TCTGAACATACCTGTAATCATGCTGCCAAGAGGAATCATGTGGATCCTCTCAGTCCA 450

Db 1209 TCTGAACATACCTGTAATCATGCTGCCAAGAGGAATCATGTGGATCCTCTCAGTCCA 1268

QY 451 TGAATAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTCCAGCTCTCTCAAGACAATGATTT 510  
 DB 1269 TGAATAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTCCAGCTCTCTCAAGACAATGATTT 1328  
 QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGATCAGTCTCTGGAATCA 570  
 DB 1329 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGATCAGTCTCTGGAATCA 1388  
 QY 571 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCAATCTTGATCACAAGACCAC 630  
 DB 1389 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCAATCTTGATCACAAGACCAC 1448  
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 DB 1449 TCCATGCTCTCTCAAGCAATAAATCACTCTCAACTGCAAGAACTCAGAACTCTGCA 1508  
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 DB 1509 GCCTGGATAGCCAGAGTGGATCCAGAGAAAGGGAAGACATTTGTGAACCAATGAC 1568  
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 DB 1569 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGA 1628  
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 DB 1809 AAATTTACTTCAAAATAAAAGCATGTAGTACTGTTTTTCAAGAGAATGTGTTTCAT 1868  
 QY 1051 AAAAGGATATTATA 1065  
 DB 1869 AAAAGGATATTATA 1883

RESULT 7

US-10-105-931-1  
 ; Sequence 1, Application US/10105931  
 ; Publication No. US20020150987A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-076001  
 ; CURRENT APPLICATION NUMBER: US/10/105,931  
 ; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (214)...(1833)  
 US-10-105-931-1  
 Query Match 43.8%; Score 731.8; DB 13; Length 1931;  
 Best Local Similarity 99.7%; Pred. No. 4.5e-145;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 331 ACAGTTACAGAGTGGTTCCTCAAGTCCCTCAAGTCCCTCCAGCTCTCTCAAGACAATGATTT 390  
 DB 1149 AAAGTTACAGAGTGGTTCCTCAAGTCCCTCAAGTCCCTCCAGCTCTCTCAAGACAATGATTT 1208  
 QY 391 TCTGAACATACCTGTAATCATGTCCTCAAGAGGAATCATGTGGATCTCTCAGCTCCA 450  
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 QY 451 TGAATAATAGTGGTTCCTGGAATCTCAAGGTCCCTCCAGCTCTCTCAAGACAATGATTT 510  
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 QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGATCAGTCTCTGGAATCA 570  
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 QY 571 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCAATCTTGATCACAAGACCAC 630  
 DB 1389 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCAATCTTGATCACAAGACCAC 1448  
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 DB 1509 GCCTGGATAGCCAGAGTGGATCCAGAGAAAGGGAAGACATTTGTGAACCAATGAC 1568  
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 DB 1569 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGA 1628  
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 QY 871 CACTACTGACATCAAGGAGAAGATTTGGCAAGTTATAGTACAAAATTTGAAGATAA 930  
 DB 1689 CACTACTGACATCAAGGAGAAGATTTGGCAAGTTATAGTACAAAATTTGAAGATAA 1748  
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 QY 991 AAATTTACTTCAAAATAAAAGCATGTAGTACTGTTTTTCAAGAGAATGTGTTTCAT 1050  
 DB 1809 AAATTTACTTCAAAATAAAAGCATGTAGTACTGTTTTTCAAGAGAATGTGTTTCAT 1868  
 QY 1051 AAAAGGATATTATA 1065  
 DB 1869 AAAAGGATATTATA 1883

RESULT 8

US-10-118-984-1  
 ; Sequence 1, Application US/10118984  
 ; Publication No. US20020197693A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: 07334/118001  
 ; CURRENT APPLICATION NUMBER: US/10/118,984  
 ; CURRENT FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942

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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
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; NUMBER OF SEQ ID NOS: 44
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; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1
;
; LENGTH: 1931
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; TYPE: DNA
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; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: (214)...(1833)
;
; US-10-118-984-1

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Query Match	43.9%	Score	731.8	DB	13	Length	1931
Best Local Similarity	99.7%	Pred. No.	4.5e-145				
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DB	1149	AAAGTTACAGAGTGTTC	CAAGTGCCATT	CACCTATGTG	CAAGAAGAAAAATGGAATATTC	1208	
QY	391	TCTGAACATACCTGT	AAATCATGGT	CCACAAGAGGAATCAT	TGGATCTCTCAGCTCCA	450	
DB	1209	TCTGAACATACCTGT	AAATCATGGT	CCACAAGAGGAATCAT	TGGATCTCTCAGCTCCA	1268	
QY	451	TGAAAAATAGTGGTCT	CCTGAACTT	CAAGGTCCTGCCAGCTCCT	CAAGACATGATTT	510	
DB	1269	TGAAAAATAGTGGTCT	CCTGAACTT	CAAGGTCCTGCCAGCTCCT	CAAGACATGATTT	1328	
QY	511	TTTTATCTAGAAAAAGCT	CAAGACTGTT	ATTTTATGAAGCTGCAT	CACCTGTCTCTGGAATCA	570	
DB	1329	TTTTATCTAGAAAAAGCT	CAAGCTGTT	ATTTTATGAAGCTGCAT	CACCTGTCTCTGGAATCA	1388	
QY	571	CAGTTGGGATPAGCA	CCATTTCTGGATCT	CAAAAGGCTGCA	TTCTGTGATCACAAAGCCAC	630	
DB	1389	CAGTTGGGATPAGCA	CCATTTCTGGATCT	CAAAAGGCTGCA	TTCTGTGATCACAAAGCCAT	1448	
QY	631	TCCATGCTCTTCAGCA	TAATAATCACTCT	CAACTGCAGGAACTC	CAGAACTGTCTGCA	690	
DB	1449	TCCATGCTCTTCAGCA	TAATAATCACTCT	CAACTGCAGGAACTC	CAGAACTGTCTGCA	1508	
QY	691	GCCTGTGTATAGCC	CAGCTGGATCC	CAGAGCAAAAGGGAAGACAT	TGTGAACCAAAATGCAC	750	
DB	1509	GCCTGTGTATAGCC	CAGCTGGATCC	CAGAGCAAAAGGGAAGACAT	TGTGAACCAAAATGCAC	1568	
QY	751	AGAAGCCTGCCTTAA	CCAGTCGCTAGAT	GGCCTTCTGTCCAGGAC	TTGATCATGAAAGA	810	
DB	1569	AGAAGCCTGCCTTAA	CCAGTCGCTAGAT	GGCCTTCTGTCCAGGAC	TTGATCATGAAAGA	1628	
QY	811	GGACTATGAAC	TGTTAGTACCAAGCCT	CACAAAGACCTCAAA	AGCTCAGACAAATTTACTAGA	870	
DB	1629	GGACTATGAAC	TGTTAGTACCAAGCCT	CACAAAGACCTCAAA	AGCTCAGACAAATTTACTAGA	1688	
QY	871	CACCTACTGACAT	CCAAGGAGAAGAA	TTTGCCAAAGTTATAGT	ACAAAAATTTGAAAGATAA	930	
DB	1689	CACCTACTGACAT	CCAAGGAGAAGAA	TTTGCCAAAGTTATAGT	ACAAAAATTTGAAAGATAA	1748	
QY	931	CAAAACAAATGGGCT	CTCAGCCTTAC	CCGGAATAC	TTGTGGTTCTATAGATCACCACATCTTT	990	
DB	1749	CAAAACAAATGGGCT	CTCAGCCTTAC	CCGGAATAC	TTGTGGTTCTATAGATCACCACATCTTT	1808	
QY	991	AAATTTACTTT	CAAAATAAAAGCAT	GTAAAGTGACT	TGTTTTTCAAGAGAAATGTGTTTCAT	1050	
DB	1809	AAATTTACTTT	CAAAATAAAAGCAT	GTAAAGTGACT	TGTTTTTCAAGAGAAATGTGTTTCAT	1868	
QY	1051	AAAAGGATATTTATA	1065				
DB	1869	AAAAGGATATTTATA	1883				

## RESULT 9

US-10-295-981-1

US-10-293-381-1  
: Sequence 1. Application US/10295981

Sequence 1, Application 03/102391  
Publication No. US20030120055A1

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1  / GENERAL INFORMATION:
2  / APPLICANT: Bertin, John
3  / TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
4  / FILE REFERENCE: 07334-124001
5  / CURRENT APPLICATION NUMBER: US/10/295,981
6  / CURRENT FILING DATE: 2002-11-15
7  / PRIOR APPLICATION NUMBER: US/09/340,620
8  / PRIOR FILING DATE: 1999-06-28
9  / PRIOR APPLICATION NUMBER: US 09/245,281
10 / PRIOR FILING DATE: 1999-02-05
11 / PRIOR APPLICATION NUMBER: US 09/207,359
12 / PRIOR FILING DATE: 1998-12-08
13 / PRIOR APPLICATION NUMBER: US 09/099,041
14 / PRIOR FILING DATE: 1998-06-17
15 / PRIOR APPLICATION NUMBER: US 09/019,942
16 / PRIOR FILING DATE: 1998-02-06
17 / NUMBER OF SEQ ID NOS: 71
18 / SOFTWARE: FastSeq for Windows Version 4.0
19 / SEQ ID NO 1
20 / LENGTH: 1931
21 / TYPE: DNA
22 / ORGANISM: Homo sapiens
23 / FEATURE:
24 / NAME/KEY: CDS
25 / LOCATION: (214) ... (1833)
26 / US-10-295-981-1

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Query Match	43.8%;	Score 731.8;	DB 14;	Length 1931;
Best Local Similarity	99.7%;	Pred. No. 4.5e-145;		
Matches 733;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	331	ACAGTTACAGAGTGTTTCAAGTGCACATTCACCTATCTGACAGAAGAAAATGGAATTTATC	390	
DB	1149	AAAGTTACAGAGTGTTTCAAGTGCACATTCACCTATCTGACAGAAGAAAATGGAATTTATC	1208	
QY	391	TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCTCAGCTCCA	450	
DB	1209	TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCTCAGCTCCA	1268	
QY	451	TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTT	510	
DB	1269	TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTT	1328	
QY	511	TTTATCTGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCATCTGTCCTCGAATCA	570	
DB	1329	TTTATCTGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCATCTGTCCTCGAATCA	1388	
QY	571	CAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCGTGATCACAAGACCCAC	630	
DB	1389	CAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCGTGATCACAAGACCCAT	1448	
QY	631	TCCATGCTCTTAGCAATTAATAATCCATCTCAACTGCAGGAAATCTCAGAAAGTCTGCA	690	
DB	1449	TCCATGCTCTTAGCAATTAATAATCCATCTCAACTGCAGGAAATCTCAGAAAGTCTGCA	1508	
QY	691	GCTCGTATAGCCACGAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGAC	750	
DB	1509	GCTCGTATAGCCACGAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGAC	1568	
QY	751	AGAAGCTCGCTTAAACAGTCGCTAGATGCCCTTCTCTCCAGGACTTGATCATGAAAGA	810	
DB	1569	AGAAGCTCGCTTAAACAGTCGCTAGATGCCCTTCTCTCCAGGACTTGATCATGAAAGA	1628	
QY	811	GGACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGA	870	
DB	1629	GGACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGA	1688	
QY	871	CACCTACTGATCCAAAGGAGAAGAAATTTGCAAGTTATAGTACAAAATTTGAAAGATAA	930	
DB	1689	CACCTACTGATCCAAAGGAGAAGAAATTTGCAAGTTATAGTACAAAATTTGAAAGATAA	1748	
QY	931	CAAAACAAATGGGTCTTTCAGCTTTACCCGGAAATCTTGTGGTTTCTTAGATCACCATCTTT	990	



Db 1749 CAAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 1808  
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 Db 1809 AATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTTCAAGAAATGTTTCAT 1868  
 QY 1051 AAAAGGATATTATA 1065  
 Db 1869 AAAAGGATATTATA 1883  
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 US-09-728-721-3  
 ; Sequence 3, Application US/09728721  
 ; Patent No. US20020061845A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/728,721  
 ; CURRENT FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 09/340,620  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-728-721-3  
 Query Match 40.9%; Score 681.8; DB 9; Length 1620;  
 Best Local Similarity 99.7%; Pred. No. 1.7e-134;  
 Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 331 ACAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 390  
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 QY 391 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
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 QY 451 TGAATAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 510  
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 US-10-105-931-3  
 ; Sequence 3, Application US/10105931  
 ; Publication No. US20020150987A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE REFERENCE: 07334-076001  
 ; CURRENT APPLICATION NUMBER: US/10/105,931  
 ; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-105-931-3  
 Query Match 40.9%; Score 681.8; DB 13; Length 1620;  
 Best Local Similarity 99.7%; Pred. No. 1.7e-134;  
 Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 331 ACAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 390  
 Db 936 AAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 995  
 QY 391 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
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 QY 451 TGAATAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 510  
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; Sequence 3, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-984-3
Query Match 40.9%; Score 681.8; DB 13; Length 1620;
Best Local Similarity 99.7%; Pred. No. 1.7e-134;
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAGAGGAATATGGAATTATC 390
Db 936 AAAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAGAGGAATATGGAATTATC 995
QY 391 TCTGAACATACCTGTAAATCATGTGTCACCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
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QY 571 CAGTTGGGATAGCACCATTCTCGATCTCAAAGGGTGCATTCGTGATCAAGAACAC 630
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QY 631 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAAGCTCTGCA 690
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QY 931 CAAAACAATGGGTCTTCAGCCTTACCGGAATATCTTGTGGTTCTAGATCACCATCTTT 990
Db 1536 CAAAACAATGGGTCTTCAGCCTTACCGGAATATCTTGTGGTTCTAGATCACCATCTTT 1595
QY 991 AAATTTACTTCAAAATAAAAGCATG 1015
Db 1596 AAATTTACTTCAAAATAAAAGCATG 1620
RESULT 13
US-10-295-981-3
; Sequence 3, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3
Query Match 40.9%; Score 681.8; DB 14; Length 1620;
Best Local Similarity 99.7%; Pred. No. 1.7e-134;
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAGAGGAATATGGAATTATC 390
Db 936 AAAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAGAGGAATATGGAATTATC 995
QY 391 TCTGAACATACCTGTAAATCATGTGTCACCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
Db 996 TCTGAACATACCTGTAAATCATGTGTCACCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1055
QY 451 TGAATAATAGTGTTCTCCTGAAACTTCAAGTGCCCTGCCAGTCTCTCAAGACAATGATTT 510
Db 1056 TGAATAATAGTGTTCTCCTGAAACTTCAAGTGCCCTGCCAGTCTCTCAAGACAATGATTT 1115
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCAGTCTCGGAATCA 570
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Db 1116 TTTATCTAGAAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCA 1175  
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Db 1176 CAGTTGGATAGACACCAATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCAC 1235  
Qy 631 TCCATGCTCTTACGCAATAAATCCACTCTCAACTGCGAGGAACTCAGAACGTCGTGCA 690  
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Qy 691 GCCTGATATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGAC 750  
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Qy 811 GGACTATGAATCTTTAGTAGTACCAAGCCTACAAGGACCTCAAAAGTTCAGACAATTTACTAGA 870  
Db 1416 GGACTATGAATCTTTAGTAGTACCAAGCCTACAAGGACCTCAAAAGTTCAGACAATTTACTAGA 1475  
Qy 871 CACTACTGACATCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAGATA 930  
Db 1476 CACTACTGACATCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAGATA 1535  
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Qy 991 AAATTTACTTCAAAATTAAGCATG 1015  
Db 1596 AAATTTACTTCAAAATTAAGCATG 1620

## RESULT 14

US-09-918-995-20565  
; Sequence 20565, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20565  
; LENGTH: 491  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-20565

Query Match 21.8%; Score 363.4; DB 10; Length 491;  
Best Local Similarity 99.7%; Pred. No. 3.4e-67;  
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 331 ACAGTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAAGAGAAATTTGAATATC 390  
Db 127 AAAGTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAAGAGAAATTTGAATATC 186  
Qy 391 TCTGAACATACCTGTAATCATGTGCCACAGAGGAATCATGTGATCCCTCTCAGCTCCA 450  
Db 187 TCTGAACATACCTGTAATCATGTGCCACAGAGGAATCATGTGATCCCTCTCAGCTCCA 246  
Qy 451 TGAATATAGTGGTTCCTCTGAAATTTCAAGGTCCTGCCAGCTCCTCAAGACATGATTT 510  
Db 247 TGAATATAGTGGTTCCTCTGAAATTTCAAGGTCCTGCCAGCTCCTCAAGACATGATTT 306  
Qy 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCA 570

Db 307 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCA 366  
Qy 571 CAGTTGGATAGACACCAATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCAC 630  
Db 367 CAGTTGGATAGACACCAATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCAC 426  
Qy 631 TCCATGCTCTTACGCAATAAATCCACTCTCAACTGCGAGGAACTCAGAACGTCGTGCA 690  
Db 427 TCCATGCTCTTACGCAATAAATCCACTCTCAACTGCGAGGAACTCAGAACGTCGTGCA 486  
Qy 691 GCCTG 695  
Db 487 GCCTG 491

## RESULT 15

US-09-919-580-544/c  
; Sequence 544, Application US/09919580  
; Patent No. US20020110832A1  
; GENERAL INFORMATION:  
; APPLICANT: Pyle, Ruth  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER  
; FILE REFERENCE: 210121-552  
; CURRENT APPLICATION NUMBER: US/09/919,580  
; CURRENT FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 544  
; LENGTH: 299  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 243  
; OTHER INFORMATION: n = A,T,C or G  
US-09-919-580-544

Query Match 16.2%; Score 271; DB 9; Length 299;  
Best Local Similarity 97.9%; Pred. No. 1.1e-47;  
Matches 274; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1390 ACCCTTTACCCACGAGACAGTACAGAAATCCCTGCCCTAAAATCCAGGCTTTAATGCC 1449  
Db 293 ACCCTTTACCCACGAGACAGTACAGAAATCCCTGCCCTAAAATCCAGGCTTTAATGCC 234  
Qy 1450 CTACAAAGGGTTATTAAATTTAAACTCCATTATTAGGATTACATTTTAAAGTTTATTTA 1509  
Db 233 CTACAAAGGGTTATTAAATTTAAACTCCATTATTAGGATTACATTTTAAAGTTTATTTA 174  
Qy 1510 TGAATCCCTTTAAAAATGATATTTCAAAGGTTAAAAACAATATATAAGAAAAAATA 1569  
Db 173 TGAATTCCTTTAAAAATGATATTTCAAAGGTTAAAAACAATATATAAGAAAAAATA 114  
Qy 1570 AATATATTATACCGGCTTCCTGTCCTCCCATTTTTTAACCTCAGCTTCCCTACTGTACCA 1629  
Db 113 AATATATTATACCGGCTTCCTGTCCTCCCATTTTTTAACCTCAGCTTCCCTACTGTACCA 54  
Qy 1630 ACAACCAAGCTTAATAAAGTCAACAGCTGATGTGTAATA 1669  
Db 53 ACAACCAAGCTTAATAAAGTCAACAGCTGAAAAAATA 14

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Job time : 673 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 02:23:55 ; Search time 4639 Seconds  
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Scoring table: IDENTITY NUC  
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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: em\_esthum:\*
- 3: em\_estmu:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hcc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_nam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gsl:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	783	46.9	834	12	EM014010	EM014010 603639652
C 3	732.8	43.9	738	9	AI824070	AI824070 wj35907.x
C 4	721	43.2	738	10	AW978568	AW978568 EST390677

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C 6	695.8	41.7	1201	13	BX343071	BX343071 BX343071
C 7	692.8	41.5	744	14	CD365404	CD365404 UI-H-F72-
C 8	692	41.5	709	14	CA413941	CA413941 UI-H-E20-
C 9	691.4	41.4	1201	13	BX337147	BX337147 BX337147
C 10	689	41.3	734	12	BQ008463	BQ008463 UI-H-ED1-
C 11	676.4	40.5	715	14	CB851847	CB851847 UI-CF-FN0
C 12	673	40.3	721	13	BQ774940	BQ774940 UI-H-FH0-
C 13	660	39.5	812	12	B1257472	B1257472 602967861
C 14	657.2	39.4	828	10	BE875947	BE875947 601486423
C 15	656.6	39.3	683	14	CB852764	CB852764 UI-CF-FN0
C 16	651.4	39.0	938	13	BQ670832	BQ670832 AGENCOURT
C 17	642.4	38.5	870	10	BE877822	BE877822 601486392
C 18	637	38.2	667	13	BQ773811	BQ773811 UI-H-EZ1-
C 19	636	38.1	1081	12	BM557041	BM557041 AGENCOURT
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C 21	624.2	37.4	672	14	CA314123	CA314123 UI-CF-FN0
C 22	624	37.4	656	12	BM973770	BM973770 UI-CF-EC1
C 23	621.8	37.3	636	10	BE551615	BE551615 742906.x
C 24	619.8	37.1	641	10	AW150819	AW150819 xg39f08.x
C 25	607.4	36.4	624	14	CD368863	CD368863 UI-H-F71-
C 26	600.8	36.0	628	12	BQ000991	BQ000991 UI-H-DH1-
C 27	594.8	35.6	660	12	BM840808	BM840808 K-EST0117
C 28	593	35.5	606	9	AW085560	AW085560 wv67c04.x
C 29	592.4	35.5	1623	29	AY415527	AY415527 Homo sapi
C 30	592	35.5	592	9	AI745575	AI745575 wc34f12.x
C 31	589.2	35.3	1623	29	AY415528	AY415528 Pan trogl
C 32	588.8	35.3	647	10	AW960501	AW960501 EST372572
C 33	581.2	34.8	811	12	BG170405	BG170405 602322736
C 34	579.4	34.7	615	9	AI801150	AI801150 t085h04.x
C 35	578.4	34.7	654	10	BE536247	BE536247 601062832
C 36	568	34.0	610	13	B0623654	B0623654 UI-H-FG1-
C 37	564	33.8	600	10	BF793767	BF793767 602254416
C 38	563.6	33.8	2826	11	BC058088	BC058088 Mus muscu
C 39	560.4	33.6	616	9	AI307810	AI307810 tb28q07.x
C 40	542	32.5	559	12	BQ010938	BQ010938 UI-1-BC1p
C 41	532.6	31.9	568	9	AA161113	AA161113 z058d05.s
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ALIGNMENTS

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LOCUS BX401255 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
DEFINITION CDNA clone CS0DK011Y17 3-PRIME, mRNA sequence.  
ACCESSION BX401255  
VERSION BX401255.1 GI:30610587  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL Contact: Genoscope  
COMMENT Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 4797.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DK011AE09NP1&cluster=4797.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paradise Avenue Genoscope sequence ID : CS0DK011AE09NP1.

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      /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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Query Match      61.9%; Score 1033.4; DB 13; Length 1201;
Best Local Similarity 97.0%; Pred. No. 6.3e-164;
Matches 1060; Conservative 6; Mismatches 25; Indels 2; Gaps 2;

QY 551 CATCACTGCTCTGGAATCAGCTTGGATAGCACCATTCTCGATCTCAAGGGCTGCA 610
DB 1093 CATCACTKTCCTGG-AATCAGCTGGGATAGCACCATTCT-GATCTCAAGGGCTGCA 1036

QY 611 TTCTGTGATCACAAGACCACTCCATGCTCTTCCAGCAATAATAATCACTCTCAACTGCA 670
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QY 671 GGAACCTCAGAACTGTGAGCTGTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAA 730
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QY 731 GACATGTGAAACCAATGACAGAGCCTGCTTAAACAGTCGCTAGATGCCCTCTGTCC 790
DB 915 GACATGTGAAACCAATGACAGAGCCTGCTTAAACAGTCGCTAGATGCCCTCTGTCC 856

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QY 1091 ATAAATCCGTGAGTATTAAAGCTTTTAAAGGTTCTTTGGGTAATAATTAGTCTCCCT 1150
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QY 1271 TTGTTTATAACAGTGCCTTTAAGGTATGATGATTTCTTGATGGAAGCCATTTCACATCA 1330
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DB 315 TGTCTTCATGGATATTATGTTACTTGTCTAAGATGCAAGTTGATTTATGAAGTATATA 256
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DB 255 CCCTTTACCCACAGACAGACAGTACAGATCCCTGCTTAAATCCAGGCTTAATTTGCC 196
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DB 135 GAATTCCTCTTTAAATATGATATTTCAAAGGTAAACAAATATATAAGAAAAATAA 76
QY 1571 ATATATTATACGGCTTCTGCTCCCATTTTAACTTCAGCTTCCCTTACTGTCCACAA 1630
DB 75 ATATATTATACGGCTTCTGCTCCCATTTTAACTTCAGCTTCCCTTACTGTCCACAA 16
QY 1631 CAACCAAGCTAAA 1643
DB 15 NAAAAAATAA 3

RESULT 2
LOCUS BM014010 834 bp mRNA linear EST 30-OCT-2001
DEFINITION 603639652F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5415612 5',
  mRNA sequence.
ACCESSION BM014010
VERSION BM014010.1 GI:16528364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 834)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
  Email: cgabbs@mail.nih.gov
  Tissue Procurement: DCTD/DTIP
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  plate: LLAM12060 row: h column: 13
  High quality sequence stop: 829.

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    Average insert size 1.383 kb. Library enriched for
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    Note: this is a NIH_MGC Library."

ORIGIN
Query Match      46.9%; Score 783; DB 12; Length 834;
Best Local Similarity 98.0%; Pred. No. 7.5e-122;
Matches 814; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

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QY 1532 TTTCAAAGGTAAACAATAACAATAAAGAAAAAATAATATATATTAATACCGGCTTCCT 1591
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QY 1592 GTCCCAATTTTAACTTCAGCTTCCTTCCCTACTGTGTCACCAACAACCAAGCTAAATAAGTCA 1651
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QY 1652 ACAGCCTGATGTGTAAAA 1669
Db |||||||
QY 18 ACAGCCTGATGTGTAAAA 1
Db |||||||

RESULT 4
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LOCUS EST390677 MAGE resequences, MAGP Homo sapiens cDNA, mRNA sequence.
ACCESSION AW978568
VERSION AW978568.1 GI:8169836
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 738)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 394
Seq primer: Forward.
Location/Qualifiers
1..738
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGP"
/note="Vector: pBluescript-SKm"

ORIGIN
Query Match 43.2%; Score 721; DB 10; Length 738;
Best Local Similarity 98.5%; Pred. No. 2e-111;
Matches 727; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 848 TCAAAGTCAGACAAATTACTAGACACTACTGACATCAAGAGAGAAATTTGCCAAAGTT 907
Db |||||||
QY 738 TCAAAGTCAGACAAATTACTAGACACTCTTGACATCAAGAGAGAAATTTGCCAAAGTT 679
Db |||||||
QY 908 ATAGTACAAAATTTGAAGATACAAACAAATGGGCTTTTACGGCTTACCCGGAAATACTT 967
Db |||||||
QY 678 ATAGTACAAAATTTGAAGATACAAACAAATGGGCTTTTACGGCTTACCCGGAAATACTT 619
Db |||||||
QY 968 GTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAAGTACTT 1027
Db |||||||
QY 618 GTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAAGTACTT 559
Db |||||||
QY 1028 TTTCAGAAGAAATGTGTTTCATAAAGGATATTTATATCTCTGTGCTTTGACTTTTTT 1087
Db |||||||
QY 558 TTTCAGAAGAAATGTGTTTCATAAAGGATATTTATATCTCTGTGCTTTGACTTTTTT 499
Db |||||||
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QY 1088 TATATAAAATCCGTGAGTATTAAAGCTTTATTGGAAGTTCTTTTGGGTAATAATTAGTCTC 1147
Db |||||||
QY 498 TATATAAAATCCGTGAGTATTAAAGCTTTATTGGAAGTTCTTTTGGGTAATAATTAGTCTC 439
Db |||||||
QY 1148 CTCCATGACACGTGAGTATTTTATTAATATACAGTAAAGAGTTTGAATTTTGCTA 1207
Db |||||||
QY 438 CTCCATGACACGTGAGTATTTTATTAATATACAGTAAAGAGTTTGAATTTTGCTA 379
Db |||||||
QY 1208 CATAGTTCAATTTTATGCTCTTTTGTAAACAGAAACCACTTTTAAAGGATAGTAATTA 1267
Db |||||||
QY 378 CATAGTTCAATTTTATGCTCTTTTGTAAACAGAAACCACTTTTAAAGGATAGTAATTA 319
Db |||||||
QY 1268 TTCTTGTATATAACAGTGCCTTAAAGTATCATGTATTTCTGATGGAAGCCATTTTCCAT 1327
Db |||||||
QY 318 TTCTTGTATATAACAGTGCCTTAAAGTATCATGTATTTTGTGTAAGGAGCCATTTTCCAT 259
Db |||||||
QY 1328 TCATGTTCTTCATGGATTTATTTGTTACTTGTCTTAAGATGCAATTTGATTTATGAAGTAT 1387
Db |||||||
QY 258 TCATGTTCTTCATGGATTTATTTGTTACTTGTCTTAAAGATGCAATTTGATTTATGAAGTAT 199
Db |||||||
QY 1388 ATACCTCTTTACCCACAGACAGACAGTACAGATCCCTGCCCTTAAATCCCAAGGCTTAATTTG 1447
Db |||||||
QY 198 ATACCTCTTTACCCACAGACAGACAGTACAGATCCCTGCCCTTAAATCCCAAGGCTTAATTTG 139
Db |||||||
QY 1448 CCTACAAAGGGTTATTAATTTAAACTCCATTTATAGGATTTACATTTTAAAGTTTATTT 1507
Db |||||||
QY 138 CCTACAAAGGGTTATTAATTTAAACTCCATTTATAGGATTTACATTTTAAAGTTTATTT 79
Db |||||||
QY 1508 TATGAATTCCTTTTAAAGATGATTTTCAAGGTAAACCAATACATATAAAGAAAAA 1567
Db |||||||
QY 78 TATGAATTCCTTTTAAAGATGATTTTCAAGGTAAACCAATCAATATAAAGAAAAA 19
Db |||||||
QY 1568 TAAATATATTAAATACCGG 1585
Db |||||||
QY 18 TAAATATATTAAATACCGG 1
Db |||||||

RESULT 5
BG393551
LOCUS 883 bp mRNA linear EST 12-MAR-2001
DEFINITION 602411943F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4540787 5',
mRNA sequence.
ACCESSION BG393551
VERSION BG393551.1 GI:13286999
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 883)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-f@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Prepared by: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10471 row: e column: 12
High quality sequence stop: 767.
Location/Qualifiers
1..883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4540787"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"

FEATURES
source
Location/Qualifiers
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/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 42.1%; Score 702.6; DB 12; Length 883;  
Best Local Similarity 98.6%; Pred. No. 2.2e-108;  
Matches 761; Conservative 0; Mismatches 5; Indels 6; Gaps 5;

QY 403 TCTAATCATGCTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGGAATAGTGG 462  
DB 1 TGTAAATCATGCTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGGAATAGTGG 60  
QY 463 TTCTCTGAAACTTCAAGGCTCCCTGCGACTCTCTCAAGACAATGATTTTATCTAGAAA 522  
DB 61 TTCTCTGAAACTTCAAGGCTCCCTGCGACTCTCTCAAGACAATGATTTTATCTAGAAA 120  
QY 523 AGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCAAGTTGGATAG 582  
DB 121 AGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCAAGTTGGATAG 180  
QY 583 CACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTCCATGCTCTTC 642  
DB 181 CACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTCCATGCTCTTC 240  
QY 643 AGCAATAATAAATCAACTCTCAACTGCAGAACTCAGAACTCTGCGACCTGGTATAGC 702  
DB 241 AGCAATAATAAATCAACTCTCAACTGCAGAACTCAGAACTCTGCGACCTGGTATAGC 300  
QY 703 CCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATCAAGAGCCCTGCCT 762  
DB 301 CCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATCAAGAGCCCTGCCT 360  
QY 763 TAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGGACTATGAAC 822  
DB 361 TAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGGACTATGAAC 420  
QY 823 TGTAGTACCAAGCTTACAGAGCACTCAAAAGTCAAGCAATTTACTAGACACTTACAT 882  
DB 421 TGTAGTACCAAGCTTACAGAGCACTCAAAAGTCAAGCAATTTACTAGACACTTACAT 480  
QY 883 CCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAAATGGG 942  
DB 481 CCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAAATGGG 540  
QY 943 TCTTCAGCCTTACCCGGAATATCTTGTGTTTCTAGATCACCATCTTTAAATTTACTTCA 1002  
DB 541 TCTTCAGCCTTACCCGGAATATCTTGTGTTTCTAGATCACCATCTTTAAATTTACTTCA 600  
QY 1003 AAATAAAGCATGTAAGTCACTGTTTTCAGAGAAATGTTTTCATAA - AAGGATATT 1061  
DB 601 AAATAAAGCATGTAAGTCACTGTTTTCAGAGAAATGTTTTCATAAACAGGATATT 660  
QY 1062 TATATCTCTGTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAGCTTTATTGA 1121  
DB 661 TATATCTCTGTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAGCTTTATTGA 718  
QY 1122 AGTTCTTTGGGTAAATATAGTCTCCCTCCATGACACTGCAGTATTTTTTT 1173  
DB 719 AGCT--CTTGGGTAACTATTAGTCT--CTCCATGACACTGCAGTATTTTTTT 767

RESULT 6  
BX343071/c  
LOCUS  
DEFINITION BX343071 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
Homo sapiens cDNA clone CS0DL009YCL19 3-PRIME, mRNA sequence.  
ACCESSION BX343071  
VERSION BX343071.1 GI:30334165  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: secre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 4797.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DL009AB1ONP1&cluster=4797.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DL009AB1ONP1.  
Location/Qualifiers  
1..1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DL009YCL19"  
/cell\_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"  
/cell\_line="RAMOS CELL LINE"  
/clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT  
25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 41.7%; Score 695.8; DB 13; Length 1201;  
Best Local Similarity 97.9%; Pred. No. 2.6e-107;  
Matches 693; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 390  
DB 710 AAAGTTACAGAGTGTTCAGAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 651  
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCA 450  
DB 650 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCA 591  
QY 451 TGAAAATAGTGTTCCTCTGAAACTTTCAAGTCCCTGCGAGTCTCTCAAGCAATGATTT 510  
DB 590 TGAAAATAGTGTTCCTCTGAAACTTTCAAGTCCCTGCGAGTCTCTCAAGCAATGATTT 531  
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCTGGAATCA 570  
DB 530 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCTGGAATCA 471  
QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCAAGAACCCAC 630  
DB 470 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCAAGAACCCAC 411  
QY 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTCTGAGGAAACTCAGAACGCTTGA 690  
DB 410 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTCTGAGGAAACTCAGAACGCTTGA 351  
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTTGAACCAATGAC 750  
DB 350 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTTGAACCAATGAC 291  
QY 751 AGAAGCCTGCCTTAAACAGTCCAGTCCAGTCCCTTCTGTCCAGGACTTGTGATCATGAAAG 810  
DB 290 AGAAGCCTGCCTTAAACAGTCCAGTCCAGTCCCTTCTGTCCAGGACTTGTGATCATGAAAG 231  
QY 811 GGACTATGAACCTGTTAGTACCAAGCCTCAAGAGACCTCAAAAGTCAAGCAATTTACTAGA 870  
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Db      230 GGACTATGAACCTGTAGTACCAAGGCTACCAAGGACBTCAAAAGTCAGACAATTAATTCAGA 171
QY      871 CACTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 930
Db      170 CACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 111
QY      931 CAACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGCTGGTTCTTAGATCACCATCTTT 990
Db      110 CADACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGCTGGTTCTTAGATCACCATCTTT 51
QY      991 AAATTTACTTCAAAATTAAGAGCATGTAAGTACCTGTTTTCAGAAGA 1038
Db      50 AAATTTACTTCAAAATTAAGAGCATGTAAGTACCTGTTTTCGCGWNGM 3

RESULT 7
LOCUS   CD365404/c
DEFINITION UI-H-FT2-bjj-h-03-0-UI.s1 NCI CGAP FT2 Homo sapiens CDNA clone
ACCESSION UI-H-FT2-bjj-h-03-0-UI 3', mRNA sequence.
VERSION   CD365404
KEYWORDS  EST.
SOURCE    CD365404.1 GI:311149494
ORGANISM  Homo sapiens (human)
REFERENCE 1. (bases 1 to 744)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgaps-r@mail.nih.gov
          Tissue Procurement: Dr. Gary W. Hunninghake, U of I
          CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Distribution information can be found at
          http://genome.uiowa.edu/distribution/cgap.html
          Seq primer: M13 FORWARD
          POLYA=Yes.
          Location/Qualifiers
            1..744
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="UI-H-FT2-bjj-h-03-0-UI"
              /tissue_type="Aveolar Macrophage"
              /dev_stage="Adult"
              /lab_host="DH10B (Life Technologies)"
              /clone_lib="NCI CGAP FT2"
              /notes="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a
              modified polylinker; Site: 1; Ecor I; Site: 2; Not I;
              NCI CGAP FT2 is a subtracted CDNA library constructed from
              a pool of 81 RNA samples from Alveolar Macrophages
              challenged with different treatments. The library was
              subtracted according to Bonaldo, Lennon and Soares, Genome
              Research, 6:791-806, 1996. The tissue was provided by Dr.
              Gary W. Hunninghake of the University of Iowa.
              TAG TISSUE=Human Lung Aveolar Macrophage
              TAG LIB=UI-H-FT2
              TAG_SEQ=GGCCATCGCG"

ORIGIN
Query Match 41.5%; Score 692.8; DB 14; Length 744;
Best Local Similarity 99.3%; Pred. No. 1.1e-106;
Matches 705; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY      331 ACAGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAGAAGAAAATGGAATTATC 390
Db      719 AAAGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAGAAGAAAATGGAATTATC 661

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QY      391 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCA 450
Db      660 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCA 601
QY      451 TGAATATAGTGTCTCTCTGAACTTCAAGTCCCTGCCAGCTCCCTCAAGACAATGATTT 510
Db      600 TGAATATAGTGTCTCTCTGAACTTCAAGTCCCTGCCAGCTCCCTCAAGACAATGATTT 541
QY      511 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTCACTGCTCTGGAATCA 570
Db      540 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTCACTGCTCTGGAATCA 481
QY      571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGGCTGCATTTCTGTGATCAAGAACCAC 630
Db      480 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGGCTGCATTTCTGTGATCAAGAACCAC 421
QY      631 TCCATGCTCTTTCAGCAATTAATAATCCACTCTCAACTGCAGGAACTCAGACGCTGCA 690
Db      420 TCCATGCTCTTTCAGCAATTAATAATCCACTCTCAACTGCAGGAACTCAGACGCTGCA 361
QY      691 GCCTGTATAGCCCGCAGCTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750
Db      360 GCCTGTATAGCCCGCAGCTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 301
QY      751 AGAAGCCTCCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGA 810
Db      300 AGAAGCCTCCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGA 241
QY      811 GGACTATGAACTTGTAGTACCAGGCTACAGGACCTCAAAAGTCAGACAATTAATCTAGA 870
Db      240 GGACTATGAACTTGTAGTACCAGGCTACAGGACCTCAAAAGTCAGACAATTAATCTAGA 181
QY      871 CACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 930
Db      180 CACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 121
QY      931 CAAACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGCTGGTTCTTAGATCACCATCTTT 990
Db      120 CAAACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGCTGGTTCTTAGATCACCATCTTT 61
QY      991 AAATTTACTTCAAAATTAAGAGCATGTAAGTACCTGTTTTCAGAAGAA 1040
Db      60 AAATTTACTTCAAAATTAAGAGCATGTAAGTACCTGTTTTCAGAAGAA 11

RESULT 8
LOCUS   CA413941/c
DEFINITION UI-H-EZ0-bau-f-07-0-UI.s1 NCI CGAP Chl Homo sapiens CDNA clone
ACCESSION UI-H-EZ0-bau-f-07-0-UI 3', mRNA sequence.
VERSION   CA413941
KEYWORDS  EST.
SOURCE    CA413941.1 GI:24776592
ORGANISM  Homo sapiens (human)
REFERENCE 1. (bases 1 to 709)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgaps-r@mail.nih.gov
          Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
          Orthopaedics
          CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Clone distribution information can be obtained
          from Dr. M. Bento Soares, bento-soares@uiowa.edu
          The following repetitive elements were found in this cDNA
          sequence: 1-64, >At_rich#Low_complexity (matched complement)

```



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Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
    source
        Location/Qualifiers
            1..709
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="UI-H-E20-bau-f-07-0-UI"
                /tissue_type="Chondrosarcoma Grade II"
                /dev_stage="Adult"
                /lab_host="DH10B (Life Technologies)"
                /clone_lib="NCI CGAP Ch1"
                /note="Organ: Left Pelvis; Vector: pVT3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch1 is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pVT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCGT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-E20
TAG_SEQ=ATCTAATG"

ORIGIN
Query Match 41.5%; Score 692; DB 14; Length 709;
Best Local Similarity 100.0%; Pred. No. 1.5e-106;
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 AAAAGCTCAAGCTGTTATTTATGAGCTGATCACTGCTCTGGAATCAAGTTGGGA 579
DB |||||
DB 709 AAAAGCTCAAGCTGTTATTTATGAGCTGATCACTGCTCTGGAATCAAGTTGGGA 650
QY 580 TAGCACCATTCTGGATCTCAAGGCGTCATTCTGTGATCAAGACCACTCCATGCTC 639
DB |||||
DB 649 TAGCACCATTCTGGATCTCAAGGCGTCATTCTGTGATCAAGACCACTCCATGCTC 590
QY 640 TTGAGCAATATAAATCCACTCTCACTCGAGGAACTCAGAACGCTGTCAGCCCTGGTAT 699
DB |||||
DB 589 TTGAGCAATATAAATCCACTCTCACTCGAGGAACTCAGAACGCTGTCAGCCCTGGTAT 530
QY 700 AGCCGAGCTGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAGCCCTG 759
DB |||||
DB 529 AGCCGAGCTGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAGCCCTG 470
QY 760 CCTTAACGAGTCGTAGATGCCCTCTGTCAGGAGCTTGTATCATGAAGAGGACTATGA 819
DB |||||
DB 469 CTTTACGAGTCGTAGATGCCCTCTGTCAGGAGCTTGTATCATGAAGAGGACTATGA 410
QY 820 ACTTGTAGTACCAAGCCCTACAGGACCTCAAAAGTCAGACAAATTAAGACACTACTGA 879
DB |||||
DB 409 ACTTGTAGTACCAAGCCCTACAGGACCTCAAAAGTCAGACAAATTAAGACACTACTGA 350
QY 880 CATCCAGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACAAACAAT 939
DB |||||
DB 349 CATCCAGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACAAACAAT 290
QY 940 GGGTCTTACGCTTACCCGGAATACTCTGGTCTTCTAGATCACCCTCTTTAAATTTACT 999
DB |||||
DB 289 GGGTCTTACGCTTACCCGGAATACTCTGGTCTTCTAGATCACCCTCTTTAAATTTACT 230
QY 1000 TCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTTTCAATAAAGGATA 1059
DB |||||
DB 229 TCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTTTCAATAAAGGATA 170
QY 1060 TTTATATCTGTGTTGCTTTTATATATAAATCCGTGAGTATTAAGCTTTTAT 1119
DB |||||

Db 169 TTTATATCTGTGTTGCTTTTATATATAAATCCGTGAGTATTAAGCTTTTAT 110
QY 1120 GAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGACGATTTTTTAAATTA 1179
DB |||||
DB 109 GAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGACGATTTTTTAAATTA 50
QY 1180 ATACAGTAAAAAGTTTGAATTTTGTCTACATA 1211
DB |||||
DB 49 ATACAGTAAAAAGTTTGAATTTTGTCTACATA 18

RESULT 9
BX337147/c
LOCUS
DEFINITION
    BX337147 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
    clone CS0DI037YA07 3-PRIME, mRNA sequence.
ACCESSION
    BX337147
VERSION
    BX337147.1 GI:30339578
KEYWORDS
    EST.
ORGANISM
    Homo sapiens (human)
SOURCE
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 1201)
AUTHORS
    Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE
    Full-length cDNA libraries and normalization
JOURNAL
    Unpublished (2001)
COMMENT
    Contact: Genoscope
    Genoscope - Centre National de Sequencage
    BP 191 91006 EVRY cedex - France
    Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
    Library was constructed by Life Technologies, a division of
    Invitrogen. This sequence belongs to sequence cluster 4797.f For
    more information about this cluster, see
    http://www.genoscope.cns.fr/
    cgi-bin/cluster.cgi?seq=CS0DI037AA04NP1&cluster=4797.f. Contact :
    Feng Liang Email : fliang@lifetech.com URL :
    http://fulllength.invitrogen.com/Invitrogen Corporation 1600
    Faraday Avenue Genoscope sequence ID : CS0DI037AA04NP1.

FEATURES
    source
        1..1201
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DI037YA07"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 41.4%; Score 691.4; DB 13; Length 1201;
Best Local Similarity 94.9%; Pred. No. 1.4e-106;
Matches 685; Conservative 23; Mismatches 14; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTTCAAGTGCCATTCCACTATGTGCAAGAGAAATGGAATATC 390
DB |||||
DB 722 AAAGTTACAGAGTGTTTCAAGTGCCATTCCACTATGTGCAAGAGAAATGGAATATC 663
QY 391 TGTGAACATACCTGTGAAATCATGGTCCCAAGAGAAATCATGTGGATCCTCTCAGCTCCA 450
DB |||||
DB 662 TGTGAACATACCTGTGAAATCATGGTCCCAAGAGAAATCATGTGGATCCTCTCAGCTCCA 603
QY 451 TGAATATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAATGATT 510
DB |||||
DB 602 TGAATATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAATGATT 543
QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCACTCACTGCTCGGAATCA 570
DB |||||
DB 542 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCACTCACTGCTCGGAATCA 483
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QY 571 CAGTGGGATAGCACCACCTTTCTGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 630
Db 482 CAGTGGGATAGCACCACCTTTCTGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 423
QY 631 TCATGCTCTTCAGCAATAAATCACTCTCACTGAGGAACTCAGAAGCTCTGCA 690
Db 422 TCATGCTCTTCAGCAATAAATCACTCTCACTGAGGAACTCAGAAGCTCTGCA 363
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGAC 750
Db 362 GCCTGGTATAGCCAGCAGTGGATCCAGGGAAGGGAAGACATTTGTGAACCAAAATGAC 303
QY 751 AGAAGCCTGCTTAAACAGTCGCTAGTAGCCCTTCTGTCCAGGACCTGATCATGAAGA 810
Db 302 AGAAGCCTGCTTAAACAGTCGCTAGTAGCCCTTCTGTCCAGGACCTGATCATGAAGA 243
QY 811 GGACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTACAGCAATTAAGTA 870
Db 242 GGACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTACAGCAATTAAGTA 183
QY 871 CACTACTGACATCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 930
Db 182 CACTACTGACATCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 123
QY 931 CAAACAAATGGGCTTTCAGGCTTACCCGGAATATCTGTGTTCTTAGATCACCATCTTT 990
Db 122 CAAACAAATGGGCTTTCAGGCTTACCCGGAATATCTGTGTTCTTAGATCACCATCTTT 63
QY 991 AATTTACTTCAAAATTAAGGATGTAAGTACCTGTTTTCAGAGAAATGTTTCAT 1050
Db 62 AATTTACTTCAAAATTAAGGATGTAAGTACCTGTTTTCAGAGAAATGTTTCAT 3
QY 1051 AA 1052
Db 2 AA 1

RESULT 10
BQ008463/c
LOCUS
DEFINITION
UT-H-ED1-ayk-k-19-0-UI.s1 NCI CGAP ED1 Homo sapiens CDNA clone
IMAGE:5840010 3', mRNA sequence.
BQ008463
VERSION
KEYWORDS
SOURCE
EST.
BQ008463.1 GI:19733364
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 734)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..734
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5840010"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"

FEATURES
source
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/clone_lib="NCI CGAP ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_ISSUE=chondrosarcoma
TAG_LIB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"

ORIGIN
Query Match 41.3%; Score 689; DB 12; Length 734;
Best Local Similarity 99.7%; Pred. No. 4.7e-106;
Matches 711; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 414 GTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGTCTCTGAAA 473
Db 729 GTCCACAGAGGAATCATGTGGA-CCTCTCAGCTCCATGAAATAGT-GTCTCTCTGAAA 672
QY 474 CTTCAAGTTCCTCCAGCTCCTCAAGCAATGATTTTTTATCTAGAAAGCTCAAGACT 533
Db 671 CTTCAAGTTCCTCCAGCTCCTCAAGCAATGATTTTTTATCTAGAAAGCTCAAGACT 612
QY 534 GTTATTTTATGAAGCTGCATCACTGTCCTGGAATCACAGTTGGGATAGCACCATTCTG 593
Db 611 GTTATTTTATGAAGCTGCATCACTGTCCTGGAATCACAGTTGGGATAGCACCATTCTG 552
QY 594 GATCTCAAAAGGGCTGCATTTCTGTGATCAACAAGACATCCATGCTCTTTCAGCAATAATAA 653
Db 551 GATCTCAAAAGGGCTGCATTTCTGTGATCAACAAGACATCCATGCTCTTTCAGCAATAATAA 492
QY 654 ATCCACTCTCACTGCAGGAACTCAGAACGCTGAGAGCTGTATAGCCAGCAGTGA 713
Db 491 ATCCACTCTCACTGCAGGAACTCAGAACGCTGAGAGCTGTATAGCCAGCAGTGA 432
QY 714 TCCAGAGCAAAAGGGAGACATTTGTGAACCAATGACAGAAGCCTGCCTTAAACAGTCGC 773
Db 431 TCCAGAGCAAAAGGGAGACATTTGTGAACCAATGACAGAAGCCTGCCTTAAACAGTCGC 372
QY 774 TAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGACTATGAATTTGTAGTACCA 833
Db 371 TAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGACTATGAATTTGTAGTACCA 312
QY 834 AGCTTCAAGGACCTCAAAAGTCAACAATTTACTAGACACTCTGACATCTCAAGGAGAAG 893
Db 311 AGCTTCAAGGACCTCAAAAGTCAACAATTTACTAGACACTCTGACATCTCAAGGAGAAG 252
QY 894 AATTTGCCAAAGTTATAGTACAAAATTGAAAGATAACAAATGGGTCTTCAGCCCTT 953
Db 251 AATTTGCCAAAGTTATAGTACAAAATTGAAAGATAACAAATGGGTCTTCAGCCCTT 192
QY 954 ACCCGAAATACCTGTGGTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCA 1013
Db 191 ACCCGAAATACCTGTGGTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCA 132
QY 1014 TGTAAGTGAATCTTTTTCAGAGAAATGTTTTCATAAAAGATATTTATATCTCTGTT 1073
Db 131 TGTAAGTGAATCTTTTTCAGAGAAATGTTTTCATAAAAGATATTTATATCTCTGTT 72
QY 1074 GCTTTGACTTTTTTTATATAAAATCCGTGAGTATTAAGCTTTTATTAAGGTTT 1126
Db 71 GCTTTGACTTTTTTTATATAAAATCCGTGAGTATTAAGCTTTTATTAAGGTTT 19
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```

RESULT 11
CB851847/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

CB851847
UI-CF-FN0-aem-o-20-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
UI-CF-FN0-aem-o-20-0-UI 3', mRNA sequence.
CB851847
CB851847.1 GI:30046667
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 715)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.regen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-24. >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..715
Location/Qualifiers
/mol_type="mRNA"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue="UI-CF-FN0-aem-o-20-0-UI"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FN0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-FN0 is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_SEQ=None found"

ORIGIN
Query Match 40.5%; Score 676.4; DB 14; Length 715;
Best Local Similarity 99.6%; Pred. No. 6.1e-104;
Matches 699; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 364 ATGTGACAGAGAGAAATGGAATTATCTCTGAACATACCTGTAATCATGGTCCACAAGA 423
DB 715 ATGTGACAGAGAGAAATGGAATGAA-TATCTCTGAACATACCTGTAATCATGGTCCACAAGA 657
QY 424 GGAATCATGTGATCTCTCAGCTCATGAAATAGTGGTTCTCTCGAAATCTCAAGGTC 483
DB 656 GGAATCATGTGATCTCTCAGCTCATGAAATAGT-GTTCTCTGAAATCTCAAGGTC 598
QY 484 CTGCGCAGCTCTCAAGCAATGATTTTATCTAGAAAGCTCAAGCTGATTTTAT 543
DB 597 CTTGCCAGCTCTCTCAAGCAATGATTTTATCTAGAAAGCTCAAGCTGATTTTAT 538

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QY 544 GAAGTCGATCAGTCTCTGGAAATCACAGTTGGATAGCACCATTCTTGGATCTCAAG 603
DB 537 GAAGTCGATCAGTCTCTGGAAATCACAGTTGGATAGCACCATTCTTGGATCTCAAG 478
QY 604 GGCTGCATTCTGTGATCACAAGACCACTCCATGTCTTTCAGCAATAATAAATCCACTCTC 663
DB 477 GGCTGCATTCTGTGATCACAAGACCACTCCATGTCTTTCAGCAATAATAAATCCACTCTC 418
QY 664 AACTGCAGGAAACTCAGAACCTCTGAGCCTGGTATATGCCAGCAGTGGATCCAGAGCAA 723
DB 417 AACTGCAGGAAACTCAGAACCTCTGAGCCTGGTATATGCCAGCAGTGGATCCAGAGCAA 358
QY 724 AAGGGAAGACATTTGTAACCAATACACAGAGCCCTTAACCAAGTCGATAGTGCCT 783
DB 357 AAGGGAAGACATTTGTAACCAATACACAGAGCCCTTAACCAAGTCGATAGTGCCT 298
QY 784 TCTGTCCAGGACCTTGATCATGAAGAGGACTATGAACCTTGTAGTACCAAGCCTTACAAG 843
DB 297 TCTGTCCAGGACCTTGATCATGAAGAGGACTATGAACCTTGTAGTACCAAGCCTTACAAG 238
QY 844 GACCTCAAAAGTCAGACAAATTTACTAGACACTACTGACATCCAAAGGAGAGAAATTTGCCAA 903
DB 237 GACCTCAAAAGTCAGACAAATTTACTAGACACTACTGACATCCAAAGGAGAGAAATTTGCCAA 178
QY 904 AGTTATAGTACAAAATTTGAAAGATTAACAACAATGGGTCTTCAGCCTTACCCGGAAT 963
DB 177 AGTTATAGTACAAAATTTGAAAGATTAACAACAATGGGTCTTCAGCCTTACCCGGAAT 118
QY 964 ACTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTGAC 1023
DB 117 ACTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTGAC 58
QY 1024 TGTTTTTCAGAGAAATGTGTTTTCATAAAAGGATATTATTA 1065
DB 57 TGTTTTTCAGAGAAATGTGTTTTCATAAAAGGATATTATTA 16

RESULT 12
BQ774940/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ774940
UI-H-PH0-bcd-1-20-0-UI.s1 NCI CGAP PH0 Homo sapiens cDNA clone
UI-H-PH0-bcd-1-20-0-UI 3', mRNA sequence.
BQ774940
BQ774940.1 GI:21983416
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 721)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-22. >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
1..721
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-PH0-bcd-1-20-0-UI"
/tissue_type="Human Chondrosarcoma Cell Line"

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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FH0"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_FH0 is a cDNA library containing the following
tissue(s): Human Grade 1 Chondrosarcoma Cell Line The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AGAATCCGGC. The cell line was provided by Dr
James Martin from University of Iowa
TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
Chondrosarcoma
TAG_LIB=UI-H-FH0
TAG_SEQ=AGAATCCGGC"

ORIGIN
Query Match 40.3%; Score 673; DB 13; Length 721;
Best Local Similarity 99.6%; Pred. No. 2.3e-103;
Matches 695; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 414 GTCCACAAGGAGGATCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCCTCGAAA 473
DB 711 GTCCACAAGGAGGATCATGT-GATCTCTCAGCTCCATGAAATAGT-GTTCCTCGAAA 654
QY 474 CTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAAAAGCTCAAGACT 533
DB 653 CTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAAAAGCTCAAGACT 594
QY 534 GTTATTTTATGAAGTCATCATCTGTCTCGAAATACAGTGGGATGAGCACCATTTCG 593
DB 593 GTTATTTTATGAAGTCATCATCTGTCTCGAAATACAGTGGGATGAGCACCATTTCG 534
QY 594 GATCTCAAGGGCTGATTTCTGTGATCACAGACCCTCATGCTCTTCAGCAATATAA 653
DB 533 GATCTCAAGGGCTGATTTCTGTGATCACAGACCCTCATGCTCTTCAGCAATATAA 474
QY 654 ATCCACTCTCAAGTCAAGAACTCAGAACTGTGACGCTGTATAGCCAGCAGTGA 713
DB 473 ATCCACTCTCAAGTCAAGAACTCAGAACTGTGACGCTGTATAGCCAGCAGTGA 414
QY 714 TCCAGACAAAGGAGAGACATTTGTGAACCAATGACAGAGGCTGCTTTAACAGTCG 773
DB 413 TCCAGACAAAGGAGAGACATTTGTGAACCAATGACAGAGGCTGCTTTAACAGTCG 354
QY 774 TAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACTATGAATTTGTAGTACCA 833
DB 353 TAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACTATGAATTTGTAGTACCA 294
QY 834 AGCCTACAAGGACCTCAAAAGTCAGACAAATTAAGTACACTACTGACATCAAGGAGAAG 893
DB 293 AGCCTACAAGGACCTCAAAAGTCAGACAAATTAAGTACACTACTGACATCAAGGAGAAG 234
QY 894 AATTGCGCAAGTTATAGTACAAAATTTGAAGATATAACAAATGGGCTTTCAGCCTT 953
DB 233 AATTGCGCAAGTTATAGTACAAAATTTGAAGATATAACAAATGGGCTTTCAGCCTT 174
QY 954 ACCGGGAATCTTGTGGTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCA 1013
DB 173 ACCGGGAATCTTGTGGTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCA 114
QY 1014 TGTAAAGTGAATGTTTTTCAAGAGAAATGTGTTTTCATAAAGGATATTTATATCTCTGTT 1073
DB 113 TGTAAAGTGAATGTTTTTCAAGAGAAATGTGTTTTCATAAAGGATATTTATATCTCTGTT 54
QY 1074 GCTTTGACTTTTTTATATAAATCCGCGAGTATATAA 1111
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53 GCTTTCACATTTTTTTATATAAATCCGTGATTTAAA 16

RESULT 13
BI257472
LOCUS
DEFINITION
BI257472 812 bp mRNA linear EST 17-JUL-2001
602967861F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5107310 5',
mRNA sequence.
ACCESSION
BI257472.1 GI:14812879
VERSION
EST.
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 812)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11259 row: j column: 15
High quality sequence stop: 806.
Location/Qualifiers
1..812
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5107310"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH MGC 12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
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Query Match 39.5%; Score 660; DB 12; Length 812;
Best Local Similarity 97.8%; Pred. No. 3.2e-101;
Matches 691; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
QY 331 ACAGTTTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGGAATATC 390
DB 107 AAAGTTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGGAATATC 166
QY 391 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGATCTCTCAGTCCA 450
DB 167 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGATCTCTCAGTCCA 226
QY 451 TGAATAAGTGGTTCCTCTGAAACTTCAAGTCCCTGCCAGCTCTCAAGACAATGATTT 510
DB 227 TGAATAAGTGGTTCCTCTGAAACTTCAAGTCCCTGCCAGCTCTCAAGACAATGATTT 286
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCGGAATCA 570
DB 287 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCGGAATCA 346
QY 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCACAAAGACCAC 630
DB 347 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCACAAAGACCAC 406
QY 631 TCCATGCTCTTCAGCAATAATAAATCCACTCACTCACTGAGGAACTCAGAACGTCGTGCA 690
DB 407 TCCATGCTCTTCAGCAATAATAAATCCACTCACTCACTGAGGAACTCAGAACGTCGTGCA 466
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QY 691 GCTGTATAGCCACAGTGGATCAGAGCAAAAGGGAAGACATTTGTGAACCAATATGAC 750  
|||||  
Db 467 GCTGTATAGCCACAGTGGATCAGAGCAAAAGGGAAGACATTTGTGAACCAATATGAC 526  
|||||  
QY 751 AGAGCGCTGCTTAAACAGTGGATGAGTGGCTTCTGTCCAGGAGTTCATCATGAAGA 810  
|||||  
Db 527 AGAGCGCTGCTTAAACAGTGGATGAGTGGCTTCTGTCCAGGAGTTCATCATGAAGA 585  
|||||  
QY 811 GGAATATGAATTTAGTACCAAGCTTACAGGACCTCAAGGACCTCAAAAGTTCAGACAAATTTACTAGA 870  
|||||  
Db 586 GGAATATGAATTTAGTACCAAGCTTACAGGACCTCAAGGACCTCAAAAGTTCAGACAAATTTACTAGA 645  
|||||  
QY 871 CACTACTGATCAATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 930  
|||||  
Db 646 CACTACTGATCAATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 704  
|||||  
QY 931 CAAACAAATGGGTCTTACGCTTACCGGAAATACCTTGTGGTTCTTAGATACCAATCTTT 990  
|||||  
Db 705 CAAACAAATGGGTCTTACGCTTACCGGAAATACCTTGTGGTTCTTAGATACCAATCTTT 764  
|||||  
QY 991 AAATTTACTTCAAAATAAAGCATGTAAAGTGAAGTCTGTTTTCAGGAAGA 1038  
|||||  
Db 765 AAATTTACTTCAAAATAAAGCATGTAAAGTGAAGTCTGTTTTCAGGAAGA 812  
|||||

RESULT 14  
BE875947  
LOCUS 601486423F1 NIH\_MGC\_59 Homo sapiens cDNA clone IMAGE:388965 5',  
DEFINITION mRNA sequence.  
ACCESSION BE875947  
VERSION BE875947.1 GI:10324723  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.  
AUTHORS Email: cgabs-remail.nih.gov  
TITILE Tissue Procurement: DCTD/DTF/Gazdar  
JOURNAL cDNA Library Preparation: Life Technologies, Inc.  
COMMENT cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9669 row: n column: 06  
High quality sequence stop: 795.  
Location/Qualifiers  
1. 828  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:388965"  
/tissue\_type="large cell carcinoma, undifferentiated"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 69"  
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Average insert size 1.1 kb. Library constructed by Life  
Technologies."

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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."

ORIGIN  
Query Match 39.4%; Score 657.2; DB 10; Length 828;  
Best Local Similarity 96.8%; Pred. No. 9.5e-101;  
Matches 726; Conservative 0; Mismatches 13; Indels 11; Gaps 5;  
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Db 4 TGTAATCATGGTCCAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGG 63  
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Db 64 TTCTCTGAAACTTCAAGGTCCCTGSCAGCTCCTCAAGACAATGATTTTTTATCTAGAAA 123  
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QY 583 CACCAATTTCTGATCTCAAGGGCTGCATTTCTGTATCAAGAGACACTCCATGCTCTTC 642  
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|||||  
Db 304 CCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCTGCT 363  
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ACCESSION CB852764  
VERSION CB852764.1 GI:30047800  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
TITILE 1 (bases 1 to 683)  
Normalizaton and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: McCray, PB  
McCray Lab

University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171

Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

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normalized Human lung epithelial cell libraries (EN1 and  
DUI) The library was subtracted according to  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. For additional information, contact:  
bento-soares@uiowa.edu  
TAG\_SEQ=None found"

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Query Match 39.3%; Score 656.6; DB 14; Length 683;  
Best Local Similarity 99.3%; Pred. No. 1.3e-100;  
Matches 670; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
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QY 726 GGAAGACATTTGCAACCAATAGCAGAAGCTCGCTTAAACAGTCCGCTAGATGCCCTTC 785  
DB 324 GGAAGACATTTGCAACCAATAGCAGAAGCTCGCTTAAACAGTCCGCTAGATGCCCTTC 265  
QY 786 TGTCACGGGACTTGATCATGAAAGAGGACTATGAACTTTGTAGTACCAAGCCTACAGGA 845  
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QY 846 CCTCAAGAGTCAGACAAATTAAGTACACTGACATCCAGGAGAGAAATTTGCCAAG 905  
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Search completed: April 1, 2004, 06:17:29  
Job time : 4694 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:13:27 ; Search time 81.5 Seconds  
(without alignments)

11572.314 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
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Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
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- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1182	41.0	478	3	AAY59405 Human RIC
3	1182	41.0	531	3	AAY59404 Human RIC
4	1182	41.0	540	2	AAY92795 Human BI
5	1182	41.0	540	3	AAY68774 Amino aci
6	1182	41.0	540	4	AAM93621 Human pol
7	1182	41.0	540	5	Aau80369 Human cel
8	1182	41.0	540	5	Aae27882 Human rec
9	1182	41.0	544	3	Ab43570 Human can
10	1176	40.8	540	2	AAY31140 Human CAR

11	1176	40.8	540	4	AAB20079	Aab20079 Human CAR
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13	1176	40.8	540	5	AAO22107	Aao22107 Protein o
14	1176	40.8	540	6	ABU56269	Abu56269 Human cas
15	1176	40.8	540	7	ADB81362	Adb81362 Human cas
16	1027	35.7	510	7	ADC99079	Adc99079 Human KPP
17	867	30.1	167	3	AAY59407	Aay59407 Human RIC
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19	632	21.9	131	6	ABU56271	Abu56271 Human cas
20	548	19.0	110	6	ABU56272	Abu56272 Human CAR
21	544	18.9	109	5	AAO22110	Aao22110 Protein o
22	461	16.0	92	5	ABJ04754	Abj04754 RICK prot
23	125	4.3	959	4	AAM79473	Aam79473 Human pro
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34	122.5	4.3	409	6	ABU56299	Abu56299 Human cas
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36	122.5	4.3	953	2	AAY31141	Aay31141 Human CAR
37	122.5	4.3	953	3	AAB15552	Ab15552 Apoptosis
38	122.5	4.3	953	4	AAM78489	Aam78489 Human pro
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## ALIGNMENTS

RESULT 1

AAY59406  
ID AAY59406 standard; protein; 284 AA.

AC AAY59406;

XX XX 21-MAR-2000 (first entry)

XX XX Human RICK protein sequence residues 248-531.

DE DE RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW KW CIDE-A; CIDE-B; DRBP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.

OS Homo sapiens.

XX XX WO9955134-A2.

XX XX 04-NOV-1999.

XX XX 27-APR-1999; 99WO-US009183.

XX XX 27-APR-1998; 98US-00069023.

XX XX (UNMI ) UNIV MICHIGAN.

XX XX Nunez G, Inohara N, Koseki T;

XX XX WPI; 2000-072163/06.

PT PT Compositions for identifying apoptosis signaling pathway inhibitors  
PT PT useful for treating diseases.



XX PS Claim 6; Page: 93pp; English.

XX CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP

CC CC kinase) protein of the invention. RICK acts as a positive regulator of

CC CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

CC CC during CD95 signalling. The invention provides methods for identifying

CC CC apoptosis signalling pathway inhibitors and activators, and methods and

CC CC compositions for screening compounds which will modulate the interactions

CC CC of the various compositions identified: RICK, and the CIDE family of

CC CC activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening

CC CC assays for agents, useful in the diagnosis, prognosis or treatment of

CC CC disease associated with excess cell growth and dysregulation of

CC CC apoptosis. Complexes containing RICK and CLARP can be used in drug

CC CC screening assays to identify inhibitor molecules blocking CD95-mediated

CC CC apoptosis. Overexpression of ARC in an in vitro cell system can be used

CC CC to identify inhibitors of the enzymatic activity of caspase-8.

CC CC Identification of ARC-like inhibitory compounds may be useful for gene

CC CC therapy treatment of disease with increased cell death in muscle tissue

CC CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to

CC CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,

CC CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies

CC CC can be used as reagents for the preparation of affinity chromatography

CC CC media, and for diagnostically measuring RICK levels. A specific inhibitor

CC CC of an essential step in the biochemistry of apoptosis is needed. RICK

CC CC interaction with intracellular factors such as CLARP and FADD appears to

CC CC be essential for apoptosis, inhibitors of RICK binding to intracellular

CC CC apoptosis factors are potential drug candidates. Note: This sequence was

XX CC created using information given in the specification

SQ Sequence 284 AA;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
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Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	41.04%	Indels:	0
DB:	3	Gaps:	0

US-09-771-161A-2 (1-1669) x AAY59406 (1-284)

QY 332 CAGTTACAGAGTGTTCAGAGTCCCAATTCACCTATGTGACAGAGAAATGAAATATCT 391

DB 57 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 76

QY 392 CTGAACATACCTGTAATCATGTCACAGAGGATCATGTGGATCTCTCAGCTCCAT 451

DB 77 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 96

QY 452 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTGCCAGCTCCCTCAAGACAAATGATTTT 511

DB 97 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 116

QY 512 TTATCTAGAAAAGCTCAAGACTGTATTTATGAGCTGTCATCATCTGCTCGGAATCAC 571

DB 117 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 136

QY 572 AGTTGGGATGACCACTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACT 631

DB 137 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 156

QY 632 CCATGCTCTTCAGCAATAAATCACTCTCAACTGCGAGAACTCAGAACGCTCGAC 691

DB 157 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 176

QY 692 CTGTGTATAGCCAGAGTGGATCCAGACAAAGGAGACATTTGTGAACCAATGACA 751

DB 177 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 196

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QY 872 ACTACTGACATCAAGAGAGAAATTTGCGAAATTTATAGTACAAAAATTTGAAGATAAC 931

DB 237 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 256

QY 932 AAACAAATGGCTCTTCAAGCTTACCCGGAATACTTGTGTTTCTAGATCACCACATCTTTA 991

DB 257 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 276

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DB 277 AsnLeuLeuGlnAsnLysSerMet 284

RESULT 2

AAY59405

ID AAY59405 standard; protein; 478 AA.

XX AAY59405;

XX 21-MAR-2000 (first entry)

Human RICK protein sequence residues 54-531.

RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;

caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;

CIDE-A; CIDE-B; DRP-1; diagnosis; cell growth; apoptosis dysregulation;

gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;

aplastic anaemia; ischaemic injury; toxin-induced liver disease.

OS Homo sapiens.

XX WO9955134-A2.

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-US009183.

XX 27-APR-1998; 98US-00069023.

XX (UNMI) UNIV MICHIGAN.

PI Nunez G, Inohara N, Koseki T;

XX WPI; 2000-072163/06.

PT Compositions for identifying apoptosis signalling pathway inhibitors

XX useful for treating diseases.

PS Claim 6; Page: 93pp; English.

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CC CC kinase) protein of the invention. RICK acts as a positive regulator of

CC CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

CC CC during CD95 signalling. The invention provides methods for identifying

CC CC apoptosis signalling pathway inhibitors and activators, and methods and

CC CC compositions for screening compounds which will modulate the interactions

CC CC of the various compositions identified: ARC, RICK, and the CIDE family of

CC CC activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening

CC CC assays for agents, useful in the diagnosis, prognosis or treatment of

CC CC disease associated with excess cell growth and dysregulation of

CC CC apoptosis. Complexes containing RICK and CLARP can be used in drug

CC CC screening assays to identify inhibitor molecules blocking CD95-mediated

CC CC apoptosis. Complexes containing RICK and CLARP can be used in drug

CC CC screening assays to identify inhibitor molecules blocking CD95-mediated

CC CC apoptosis. Overexpression of ARC in an in vitro cell system can be used

CC CC to identify inhibitors of the enzymatic activity of caspase-8.

CC CC Identification of ARC-like inhibitory compounds may be useful for gene

CC CC therapy treatment of disease with increased cell death in muscle tissue

CC CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to

CC CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,

CC CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies





Db 304 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 323  
 QY 392 CTGAACATACCTTAATCATGTGCACAAAGAGAAATCATGTGATCTCTCAGCTCCAT 451  
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 AC AAW92795;  
 XX 07-MAY-1999 (first entry)  
 DT Human B1 protein.  
 XX B1 protein; intracellular mediator; modulator; inflammation; cell death;  
 KW cell survival pathway; intracellular signalling; AIDS; cancer; human.  
 OS Homo sapiens.  
 XX WO9855507-A2.  
 PN 10-DEC-1998.  
 PD 01-JUN-1998; 98WO-IL000255.  
 PF 05-JUN-1997; 97IL-00121011.  
 PR 30-JUN-1997; 97IL-00121199.  
 PR 11-SEP-1997; 97IL-00121746.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX

PI Wallach D, Boldin M, Malinin N;  
 XX WPI; 1999-070258/06.  
 DR N-PSDB; AAX02558.  
 XX New B1 protein regulates cell death and cell survival pathways -  
 PT derivatives, DNA and antibodies, also regulate intracellular inflammation  
 PT ; for treating AIDS, cancer.  
 XX Claim 4; Fig 3A; 90pp; English.  
 PS This invention describes the isolation of a novel human B1 protein which  
 CC can interact with, intracellular mediators or modulators of inflammation,  
 CC cell death and/or cell survival pathways, directly or indirectly. Cells  
 CC can be modulated or mediated in inflammation, cell death or cell survival  
 CC pathways or another intracellular signalling activity using B1.  
 CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
 CC oligonucleotides and ribozymes can also be used to regulate the above  
 CC pathways  
 XX Sequence 540 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 3.3e-119 Length: 540  
 Score: 1182.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.56% Mismatches: 0  
 Query Match: 41.04% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-771-161A-2 (1-1669) x AAW92795 (1-540)  
 QY 332 CAGTTACAGAGTGTTCCTCAAGTCCCATTCACCTATGTGCAAGAGAAATGAATATCT 391  
 Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332  
 QY 392 CTGAACATACCTGTTAAATCATGTGTCACAAAGAGAAATCATGTGATCTCTCAGCTCCAT 451  
 Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352  
 QY 452 GAAATAGTGGTCTCTCAAGTCCCTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTT 511  
 Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 372  
 QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGCTCTGGAATCAC 571  
 Db 373 LeuSerArgLysAlaGlnAspCysIlePheMetLysLeuHisCysProGlyAsnHis 392  
 QY 572 AGTTGGATAGACCACTTTCTGATCTCAAGGCTGCATCTCTGATCACAAGACCACT 631  
 Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 412  
 QY 632 CCATGCTCTTACGAATAATAATCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAG 691  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CCTGTGTATAGCCAGCTGGATCCAGACCAAGGAGACAAATGATTCGACCAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCCTGCCTTAACCAAGCTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAATCTTTAGTACCAAGCTCACAAGGCTCAAAAGTCAAGAAATTTACTAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAATAATGAAGATAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAAATGGGTCTTACCGCTTACCGGAAATCTTGTGTTTCTAGATCACCATCTTTA 991

Db 513 LysGlnMetGlyLeuGlnProTyrProGlnLeuValSerArgSerProSerLeu 532  
 QY 992 AATTTACTTCAAAATAAAGCATG 1015  
 Db 533 AenLeuLeuGlnAsnLysSerMet 540  
 RESULT 5  
 AAY68774  
 ID AAY68774 standard; protein; 540 AA.  
 XX AC AAY68774;  
 XX DT 16-MAY-2000 (first entry)  
 XX DE Amino acid sequence of a human phosphorylation effector PHSP-6.  
 XX KW Human; phosphorylation effector; PHSP; proliferative disorder;  
 XX KW immune disorder; neuronal disorder.  
 XX OS Homo sapiens.  
 XX FH Key  
 XX FT Region.  
 FT FT Location/Qualifiers  
 FT 18 287  
 FT /note= "protein kinase family signature sequence"  
 FT 23  
 FT /note= "potential phosphorylation site"  
 FT 34  
 FT /note= "potential phosphorylation site"  
 FT 58  
 FT /note= "potential phosphorylation site"  
 FT 100  
 FT /note= "potential glycosylation site"  
 FT 102  
 FT /note= "potential phosphorylation site"  
 FT 180  
 FT /note= "potential phosphorylation site"  
 FT 183  
 FT /note= "potential phosphorylation site"  
 FT 207  
 FT /note= "potential phosphorylation site"  
 FT 224  
 FT /note= "potential phosphorylation site"  
 FT 267  
 FT /note= "potential phosphorylation site"  
 FT 296  
 FT /note= "potential phosphorylation site"  
 FT 301  
 FT /note= "potential phosphorylation site"  
 FT 360  
 FT /note= "potential phosphorylation site"  
 FT 374  
 FT /note= "potential phosphorylation site"  
 FT 391  
 FT /note= "potential glycosylation site"  
 FT 401  
 FT /note= "potential phosphorylation site"  
 FT 428  
 FT /note= "potential phosphorylation site"  
 FT 442  
 FT /note= "potential phosphorylation site"  
 FT 457  
 FT /note= "potential glycosylation site"  
 FT 478  
 FT /note= "potential phosphorylation site"  
 FT 484  
 FT /note= "potential phosphorylation site"  
 FT 537  
 FT /note= "potential glycosylation site"  
 XX PN W0200006728-A2.

XX PD 10-FEB-2000.  
 XX PF 28-JUL-1999; 99WO-US017132.  
 XX PR 28-JUL-1998; 98US-0155213P.  
 XX PR 14-SEP-1998; 98US-0155213P.  
 XX PR 14-OCT-1998; 98US-0155239P.  
 XX PR 03-NOV-1998; 98US-0106889P.  
 XX PR 19-NOV-1998; 98US-0109093P.  
 XX PR 22-DEC-1998; 98US-0113796P.  
 XX PR 12-JAN-1999; 99US-0155233P.  
 XX FA (INCY-) INCYTE PHARM INC.  
 XX FI Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
 PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
 PI Reddy R, Lu DAM, Shih LL;  
 XX WPI; 2000-183125/16.  
 DR N-PSDB; AAZ46143.  
 XX New human phosphorylation effectors useful for the diagnosis, treatment  
 and prevention of proliferative, immune and neuronal disorders.  
 XX Claim 1; Page 84-85; 142pp; English.  
 XX AAY68769-95 and AAY68797-99 represent human phosphorylation effectors  
 (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
 given in the specification). The sequences were isolated from cDNA  
 libraries prepared from various human tissues. The PHSP proteins are  
 useful for the diagnosis, treatment and prevention of proliferative  
 disorders, immune disorders and neuronal disorders. The PHSP proteins  
 form pharmaceutical compositions which useful for treating or preventing  
 disorders associated with decreased PHSP expression/activity. PHSP  
 antagonists are useful for treating or preventing disorders associated  
 with increased PHSP expression/activity  
 XX SQ Sequence 540 AA;  
 Alignment Scores:  
 Pred. No.: 3.3e-119 Length: 540  
 Score: 1182.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.56% Mismatches: 0  
 Query Match: 41.04% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-771-161A-2 (1-1669) x AAY68774 (1-540)  
 QY 332 CAGTTACAGAGTGTTCAGTCCATTCACCTATGTGACAGAGAAATGAAATATCT 391  
 Db 313 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 332  
 QY 392 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCAT 451  
 Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352  
 QY 452 GAAATAGTGTCTCTCTGAACTTCAAGTCCCTGCGAGCTCTCTCAAGACAATGATTT 511  
 Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 372  
 QY 512 TTATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCATCTGTCTGGAATCAC 571  
 Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
 QY 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 631  
 Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 412  
 QY 632 CCATGCTTTCAGCAATAATAATATCCACTCTCACTGCGAGAACTCAGAACGCTGCGAG 691  
 Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432





US-09-771-161A-2 (1-1669) x AAE27882 (1-540)

QY 332 CAGTTACAGAGTGTTCACAGTGCATTACCTATGTGACAGAGAAATGGAATATCT 391

Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332

QY 392 CTGAACATACCTGTAAATCATGTGCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 451

Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352

QY 452 GAAATAGTGTTCCTCCTGAACTTCAAGTTCCTGCCAGCTCCTCAAGACAAATGATTTT 511

Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372

QY 512 TTATCTAGAAAGCTCAAGACTGTATTATTTATGAGCTGCATCTCTCGAATATCAC 571

Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392

QY 572 AGTTGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAC 631

Db 393 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 412

QY 632 CATGCTCTTCAGCAATATAATCCACTCTCACTGAGGAACTCAGAACTGCTGGAG 691

Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

QY 692 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAGGAGACATTTGTGAACCAATGACA 751

Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgLysIleValAsnGlnMetThr 452

QY 752 GAAGCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCAGGAGCTGTGATGAAGAG 811

Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472

QY 812 GACTATGAAGTGTGTAGTACCAAGCTCAGAGCAAGCACTCAAGTCAAGTACTAGAC 871

Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492

QY 872 ACTACTGACATCCAGGAGGAAGATTTGCCAAGTTATAGTACAAAATTTGAAAGATAAC 931

Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512

QY 932 AAACAAATGGTCTTCAGCTTACCGGAAATCTTGTGTTCTTGTAGATCACCATCTTTA 991

Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532

QY 992 AATTTACTTCAAAATAAAGCATG 1015

Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9

AAB43570

ID AAB43570 standard; protein; 544 AA.

XX AC AAB43570;

XX DT 08-FEB-2001 (first entry)

XX DE Human cancer associated protein sequence SEQ ID NO:1015.

XX KW Human; cancer associated gene; cancer antigen; detection; cancer;

KW diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;

KW antidiabetic; antihistaminic; antirheumatic; antiarthritic; antiviral;

KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;

KW dermatological; neuroprotective; thrombolytic; coagulant; neotropic;

KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;

KW immune disorder; haematopoietic cell disorder; autoimmune disorder;

KW allergic reaction; graft versus host disease; organ rejection;

KW haemostatic; thrombolytic; cardiovascular disorder; infection;

KW neurological disease; drug screening.

OS Homo sapiens.

XX WO200055350-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005882.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587533/55.

XX N-PSDB; AAC77779.

XX Novel isolated nucleic acids comprising sequences encoding peptides

XX useful for treating or diagnosing e.g. cancer.

XX Claim 11; Page 1595-1597; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in

XX AAB43398 to AAB44239. The proteins can have activities based on the

XX tissues and cells the genes are expressed in. Example of activities

XX include: cytostatic; proliferative; vulnerable; immunomodulator;

XX antidiabetic; antihistaminic; antirheumatic; antiarthritic;

XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;

XX dermatological; neuroprotective; cardiac; thrombolytic; coagulant;

XX polynucleotides and polypeptides can be used for preventing, treating or

XX ameliorating medical conditions and diagnosing pathological conditions.

XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from

XX the present invention may be used to treat immune disorders by activating

XX or inhibiting the proliferation, differentiation or mobilisation of

XX immune cells, to treat disorders of haematopoietic cells, autoimmune

XX disorders, allergic reactions, graft versus host disease and organ

XX rejection, modulate haemostatic or thrombolytic activity, modulate

XX inflammation, cancers, cardiovascular disorders, neurological disease and

XX bacterial or viral infections. The peptides, nucleotides, antibodies,

XX agonists and antagonists may be also used in drug screens. AAC78449 to

XX AAC78457 and AAB44240 represent sequences used in the exemplification of

XX the present invention

XX SQ Sequence 544 AA;

Alignment Scores:

Pred. No.: 3,31e-119 Length: 544

Score: 1182.00 Matches: 227

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.56% Mismatches: 0

Query Match: 41.04% Indels: 0

DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x AAB43570 (1-544)

QY 332 CAGTTACAGAGTGTTCACAGTGCATTACCTATGTGACAGAGAAATGGAATATCT 391

Db 317 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 336

QY 392 CTGAACATACCTGTAAATCATGTGCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 451

Db 337 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 356

QY 452 GAAATAGTGTTCCTCCTGAACTTCAAGTTCCTGCCAGCTCCTCAAGACAAATGATTTT 511

Db 357 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 376

QY 512 TTATCTAGAAAGCTCAAGACTGTATTATTTATGAGCTGCATCTCTCGAATATCAC 571

Db 377 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 396

QY 572 AGTTGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAC 631

Db 397 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 416  
 QY 632 CCATCTCTTACGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAAAGCTGTCGAG 691  
 Db 417 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 436  
 QY 692 CCGTGTATAGCCACAGCTGATCCAGACCAAGGGAAGACATTTGTCAACCAATGACA 751  
 Db 437 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 456  
 QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCACGGGACTTGCATCATGAAAGAG 811  
 Db 457 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 476  
 QY 812 GACTATGAAGTGTGTAGTACCAAGCTTCAAGGACTCAAGAGTCCAGCAATTTACTAGAC 871  
 Db 477 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 496  
 QY 872 ACTACTGCATCCAGGAGAGAGATTTGCCAAGTTATAGTACAAAATTTGAAGATTAAC 931  
 Db 497 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 516  
 QY 932 AAACAATGGGTCTTACAGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 991  
 Db 517 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 536  
 QY 992 AATTTACTTCAAAATAAAGCATG 1015  
 Db 537 AsnLeuLeuGlnAsnLysSerMet 544  
 RESULT 10  
 ID AAY311140 standard; protein; 540 AA.  
 AC AAY311140;  
 XX 25-OCT-1999 (first entry)  
 DE Human CARD-3 protein.  
 KW CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
 KW caspase activation; detection; screening; therapy; diagnosis; disease;  
 KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
 KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
 KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;  
 KW myelodysplastic syndrome; myocardial infarction; cell proliferation;  
 KW cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;  
 KW human.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..300  
 FT /note= "predicted kinase domain"  
 FT Domain 301..431  
 FT /note= "predicted linker domain"  
 FT Domain 432..540  
 FT /note= "predicted CARD domain"  
 XX  
 FN WO9940102-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 05-FEB-1999; 99WO-US002544.  
 XX  
 PR 06-FEB-1998; 98US-00019942.  
 PR 17-JUN-1998; 98US-00099041.  
 PR 08-DEC-1998; 98US-00207359.  
 XX  
 FA (MILL-) MILLENNIUM PHARM INC.

XX Bertin J;  
 FI WPI; 1999-494269/41.  
 DR N-PSDB; AAZ09246.  
 XX  
 PT Novel CARD-3 and CARD-4 genes and polypeptides used or treating  
 PT regulation of cellular proliferation and differentiation and cell  
 PT survival.  
 XX  
 PS Example 2; Fig 2; 181pp; English.  
 XX  
 CC This invention describes the isolation of novel human caspase recruitment  
 CC domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial  
 CC murine CARD-4L protein and genes. The genes and proteins of the invention  
 CC are involved in the regulation of caspase activation. The caspase  
 CC recruitment domain (CARD) polynucleotides, polypeptides, homologues and  
 CC antibodies can be used in screening assays, detection assays, predictive  
 CC medicine and therapeutic and prophylactic methods of treatment. The  
 CC methods may be used to diagnose and treat patients which are suffering  
 CC from a disorder associated with abnormal level or rate of apoptotic cell  
 CC death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
 CC activity of the TNF receptor complex, or abnormal activity of a caspase.  
 CC Diseases that may be treated include cancer (particularly follicular  
 CC lymphoma, carcinomas associated with mutations in p53 and hormone-  
 CC dependent tumours), autoimmune disorders (e.g. systemic lupus  
 CC erythematosus, immune-mediated glomerulonephritis), viral infections,  
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
 CC retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,  
 CC anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.  
 CC CARD-3 protein interacts with other cellular proteins, and so can be used  
 CC for regulation of cellular proliferation and differentiation and cell  
 CC survival. The CARD proteins may also be used to for screen drugs or  
 CC compounds which modulate their activity. The CARD-4 gene can express a  
 CC long transcript that encodes CARD-4L, a short transcript that encodes  
 CC CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence  
 CC represents the human CARD-3 protein described in the method of the  
 CC invention  
 XX  
 SQ Sequence 540 AA;  
 Alignment Scores:  
 Pred. NO.: 1.49e-118 Length: 540  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 40.83% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-771-161A-2 (1-1669) x AAY311140 (1-540)  
 QY 332 CAGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCT 391  
 Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332  
 QY 392 CTGAACATACCTGTAAATCATGTGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451  
 Db 333 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 352  
 QY 452 GAAATATAGTGTCTCTCTGAAACTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTT 511  
 Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372  
 QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGATCATCTCTCTGGAATCAC 571  
 Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 392  
 QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTCATTTCTGTGATCAAGACCACT 631  
 Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412  
 QY 632 CCATGCTCTTCAGCAATAATAATTCACCTCTCAACTCAGGAAACTCAGAAAGCTGTCGAG 691



Db 413 ProCysSerSerAlaIleleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CTGTGTATAGCCAGCAGTGGATCCAGACCAAGGAGACATTGTGAACCAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAACCTGTGTAGTACCAAGCTCAGAGCACTCAAAAGTCAGCAATTAAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAGGAGCAAGATTGTCCAAGTTATAGTACAAATAATGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAAATGGGTCTTCAGCCTTACCCGGAATACTGTGGTTCTAGATCAACATCTTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532  
 QY 992 AATTACTTCAAAATAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 11

AAB20079 standard; protein; 540 AA.

XX AAB20079;  
 AC AAB20079;  
 XX  
 DT 23-APR-2001 (first entry)  
 XX Human CARD-3 protein.  
 DE  
 XX CARD-3; caspase recruitment domain; human; cancer; infection;  
 KW autoimmune disease; neurological disease; haematological disease;  
 KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
 KW antiinflammatory; apoptosis; diagnosis; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..400 /note= "kinase domain"  
 FT Domain 401..431 /note= "linker domain"  
 FT Domain 432..540 /note= "CARD"  
 FT  
 XX WO200100826-A2.  
 PN  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 28-JUN-2000; 2000WO-US017691.  
 XX  
 PR 28-JUN-1999; 99US-00340620.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Bertin J;  
 PI  
 XX WPI; 2001-061973/07.  
 DR  
 DR N-PSDB; AAF30001.  
 XX  
 XX Isolated intracellular proteins predicted to be involved in regulating  
 PT caspase activation are used for diagnosis and treatment of e.g. cancer,  
 PT viral infections, autoimmune diseases, neurological diseases and  
 PT hematological disorders.  
 XX  
 XX Claim 9; Fig 2; 208pp; English.  
 PS  
 XX

CC The present sequence is that of human caspase recruitment domain 3 (CARD-  
 CC 3), an intracellular protein predicted to be involved in regulating  
 CC caspase activation. The sequence is predicted from an isolated cDNA clone  
 CC (see AAF30001). Methods of diagnosing and treating patients suffering  
 CC from a disorder associated with an abnormal level or rate of apoptotic  
 CC cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
 CC activity of the tumour necrosis factor receptor complex or abnormal  
 CC activity of a caspase involve administering a compound that modulates the  
 CC expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using  
 CC gene therapy methods. Such disorders include cancer, viral infection,  
 CC autoimmune disorders, neurological diseases, haematological disorders,  
 CC inflammatory disorders and immune disorders. CARD-3, -4, -5 and -6  
 CC proteins can be used to regulate cell proliferation, cell survival and  
 CC cell growth. They can also be used to screen drugs or compounds that  
 CC modulate their activity or expression and to treat disorders associated  
 CC with insufficient or excessive production of CARD-3, -4, -5 or -6  
 CC protein, or production of an aberrant protein  
 XX

SQ Sequence 540 AA;

Alignment Scores:  
 Pred. No.: 1,49e-118 Length: 540  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 40.83% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x AAB20079 (1-540)

QY 332 CAGTTACAGAGTGTTCAGTGGCCATTCACTATGTGCAAGAGAAATGAATTATCT 391  
 Db 333 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 332  
 QY 392 CTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451  
 Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352  
 QY 452 GAAAAATAGTGGTTCCTCAAACTTCAAGGTCCCTCCAGCTCTCTCAAGACAAATGATTTT 511  
 Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372  
 QY 512 TTATCTAGAAAGCTCAAGACTGTATTATTTATGAGCTGCATCTGCTCCCTGGAATACAC 571  
 Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
 QY 572 AGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCCT 631  
 Db 393 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412  
 QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCGAGAACTCAGAACTCTGCGAG 691  
 Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CCTGTATAGCCAGCAGCTGGATCCAGAGCAAGGAGAGACATTGTGAACCAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAACCTGTGTAGTACCAAGCTCAGAGCACTCAAAAGTCAGCAATTAAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAGGAGCAAGATTGTCCAAGTTATAGTACAAATAATGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAAATGGGTCTTCAGCCTTACCCGGAATACTGTGGTTCTAGATCAACATCTTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532



QY 992 AATTTACTCAAAATAAAGCATG 1015  
 DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 12  
 ABO31075  
 ID ABO31075 standard; protein; 540 AA.  
 AC ABO31075;  
 XX 21-OCT-2002 (first entry)  
 XX Human caspase recruitment domain protein CARD-3.  
 XX Human; caspase recruitment domain; CARD-3; CARD-4; LRR;  
 KW leucine rich repeat; LPS; lipopolysaccharide; NF-KB;  
 KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis;  
 KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;  
 KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;  
 KW gastrointestinal allergy; insulin-dependent diabetes;  
 KW bacterial infection; tuberculosis; lepromatous leprosy;  
 KW cell signalling disorder; tissue disorder.  
 XX Homo sapiens.  
 OS WO200253765-A1.  
 PN 11-JUL-2002.  
 PD 20-DEC-2001; 2001WO-US049798.  
 PF 29-DEC-2000; 2000US-0258724P.  
 PR (MILL-) MILLENNIUM PHARM INC.  
 PA Bertin J, Philpott D, Sansonetti P, Girardin S;  
 XX WPI; 2002-583627/62.  
 DR N-PSDB; ABK89280.  
 XX Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.  
 XX Example 2; Fig 2; 139pp; English.  
 XX The invention relates to identifying (MI) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-KB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-KB activation, where altered NF-KB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-KB. Modulators identified by (MI) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and

CC disorders of tissues. The present sequence represents human CARD-3  
 CC protein  
 XX  
 SQ Sequence 540 AA;  
 Alignment Scores:  
 Pred. NO.: 1.49e-118 Length: 540  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 40.83% Indels: 0  
 DB: 5 Gaps: 0

US-09-771-161A-2 (1-1669) x ABO31075 (1-540)

QY 332 CAGTTACAGAGTGTTCACAGTCCATTCACTATGTGACAGAGAAATGCAATTTATCT 391  
 DB 313 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 332  
 QY 392 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451  
 DB 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352  
 QY 452 GAAATAGTGGTCTCTGAACTTCAAGGTCCCTCCAGCTCCTCAAGACAATGATTT 511  
 DB 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372  
 QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGTGCATCACTGTCTCTGGAATACAC 571  
 DB 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
 QY 572 AGTTGGATAGACACCATTTCTGGATCTCAAGGGCTCATTTCTGTGATCAACAAGACCACT 631  
 DB 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412  
 QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCACTCAGAGAACTCAGAACGCTGCGAG 691  
 DB 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CTTGGTATAGCCACGAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATGACA 751  
 DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCTGCTTAACACAGTCGCTAGATGCCCTTCTGTCCAGGGGACTTGATCATCAAGAG 811  
 DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATCAACTTGTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGCAATTTACTAGAC 871  
 DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTCACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 DB 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAAATGGTCTTCAGCCTTACCCCGAAATACTTGTGTTTCTAGATCACCATCTTTA 991  
 DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
 QY 992 AATTTACTCAAAATAAAGCATG 1015  
 DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 13  
 ABO22107  
 ID ABO22107 standard; protein; 540 AA.  
 XX ABO22107;  
 AC ABO22107;  
 XX 27-SEP-2002 (first entry)  
 XX Protein of human CARD-3 SEQ ID No 2.  
 XX



DR N-PSDB; ABX75869, ABX74870.

XX Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z

PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,

PT detection assays, predictive medicine, and in therapeutic applications.

XX

XX Example 2; Fig 2; 99pp; English.

XX The invention relates to an isolated polypeptide, comprising at least 25

CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,

CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)

CC polypeptide. Also included is an isolated fusion protein, comprising the

CC CARD polypeptide covalently linked by a peptide bond to a heterologous

CC polypeptide. The CARD polypeptide is useful in screening assays,

CC detection assays (e.g. chromosomal mapping, tissue typing and forensic

CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,

CC monitoring clinical trials and pharmacogenomics), and in therapeutic and

CC prophylactic treatments (in diseases associated with apoptotic cell death

CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and

CC immune related glomerulonephritis), viral infections, AIDS (acquired

CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's

CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis

CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),

CC haematological diseases (e.g. anaemia, neutropenia and myelodysplastic

CC syndromes), myocardial infarction and stroke). The CARD polypeptide is

CC useful as bait protein in a two-hybrid assay or three hybrid assay to

CC identify other proteins, which bind to or interact with other CARD

CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for

CC human CARD-4 is located on chromosome 7. The present sequence is a human

CC CARD protein

XX

SQ Sequence 540 AA;

Alignment Scores:

Pred. No.:	1.49e-118	Length:	540
Score:	1176.00	Matches:	226
Percent Similarity:	99.56%	Conservative:	1
Best Local Similarity:	99.12%	Mismatches:	0
Query Match:	40.83%	Indels:	0
DB:	6	Gaps:	0

US-09-771-161A-2 (1-1669) x ABUS6269 (1-540)

QY 332 CAGTTACAGAGTGTTCAGTGCCTACCTACCTATGTGACAGAAAGTAATATCT 391

DB 333 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332

QY 392 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451

DB 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352

QY 452 GAAATAGTGGTTCCTGAAACTTCAAGGTCCTCCAGGCTCCTCAAGACAATGATTTT 511

DB 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspHe 372

QY 512 TTATCTAGAAAGCTCAACAGCTGTTATTTATGAAGCTGCATCATGTCTCGGAATCAC 571

DB 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 392

QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTGTGATCACAAGACCACT 631

DB 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412

QY 632 CCATCTCTTTCAGCAATATAATCCACTCTCACTCAGGAAATCTCAGAACGCTCGAG 691

DB 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

QY 692 CTGTGTATAGCCAGAGTGGATTCAGAGCAAAAGGGAAGACATTTGTGAACAAATGACA 751

DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452

QY 752 GAAGCTCCCTTAACAGCTGCATGATCCCTCTCTCCAGGACTTCATCATGAAAGAG 811

DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472

QY 812 GACTATGAACCTGTGTAGTACCAAGCCTACAGAGCCTCAAAAGTCAGACAATTACTAGAC 871

DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492

QY 872 ACTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGATTATAGTACAAAATTTGAAAGATAAC 931

DB 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512

QY 932 AAACAAATGGTCTTTCAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTTA 991

DB 513 LysGlnMetGlyLeuGlnProTyrProGluLeuValValSerArgSerProSerLeu 532

QY 992 AATTACTTCAAAATAAAGCATG 1015

DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 15

ADB81362

ID ADB81362 standard; protein; 540 AA.

XX

AC ADB81362;

DT 04-DEC-2003 (first entry)

XX Human caspase recruitment domain 3 (CARD-3) protein.

DE

XX human; CARD-3; CARD-4; caspase recruitment domain; apoptosis; p75;

KW tumour necrosis factor; TNF; neutrophin receptor; cancer;

KW autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;

KW viral infection; neurological; retinitis pigmentosa; haematologic;

KW chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.

XX Homo sapiens.

Key	Location/Qualifiers
Domain	1..300
Domain	/label = Kinase_domain
Domain	301..431
Domain	/label = Linker_domain
Domain	432..540
Domain	/label = CARD
Domain	/note = Caspase recruitment domain

US2002061833-A1.

XX 23-MAY-2002.

XX 26-DEC-2000; 2000US-00748537.

XX 06-FEB-1998; 98US-00019942.

PR 17-JUN-1998; 98US-00099041.

XX (BERT/) BERTIN J.

PA (CHAO/) CHAO M V.

PI Bertin J, Chao MV;

XX WPI: 2003-657125/62.

DR N-PSDB; ADB81363.

XX

PT Detecting compounds which alter binding of the caspase recruitment domain

PT (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful

PT to provide compounds for treating CARD-3 mediated disorders.

XX Disclosure; Fig 1; 40pp; English.

XX This invention relates to two novel genes CARD-3 and CARD-4 (caspase

CC recruitment domains), which are mediators of apoptosis and are useful in

CC the identification of compounds that modulate apoptosis. Specifically,

CC CARD-3 (also known as RIP2, RICK and CARDIAK) is known to be a mediator

CC of p75 (a member of the tumour necrosis factor (TNF) family), and is

CC believed to provide the switch for cell survival and cell death decisions  
CC mediated by this p75 neurotrophin receptor. Accordingly these genes, and  
CC the proteins encoded thereof, are linked to certain disorders associated  
CC with an increased number of cells surviving and proliferating when  
CC apoptosis is inhibited. These include cancer, autoimmune disorders e.g.  
CC systemic lupus and immune mediated glomerulonephritis, viral infections  
CC such as those caused by the herpesvirus, neurological disorders such as  
CC retinitis pigmentosa, haematologic diseases including chronic  
CC neutropenia, as well as myocardial infarction and strokes. The present  
CC invention further describes a novel method for determining whether a test  
CC compound alters the binding of CARD-3 to p75, which comprises measuring  
CC the binding of a polypeptide containing the CARD domain of CARD-3 to a  
CC polypeptide comprising the death domain of p75 in the presence and  
CC absence of the test compound, and determining if binding is altered. This  
CC polypeptide is the human CARD-3 protein sequence of the invention.

XX  
SQ Sequence 540 AA;

Alignment Scores:  
Pred. No.: 1.49e-118 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: 7 Gaps: 0

US-09-771-161A-2 (1-1669) x ADB81362 (1-540)

QY	332	CAGTTACAGAGTCTTTCAAGTGCCTACCTATGTGACAAAGAAATGGAATTATCT	391
DB	313	LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	332
QY	392	CTGAACATACCTGAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT	451
DB	333	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis	352
QY	452	GAAATAGTGTCTCTCTGAAACTTCAGGTCCTCCAGCTCCTCAAGACAAATGATTTT	511
DB	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	372
QY	512	TTATCTAGAAAGCTCAAGACTGTGTTATTTTATGAAGCTGCATCAGCTCTGGAATCAC	571
DB	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	392
QY	572	AGTGGGATAGCACCATTCTGGATCTCAAGGGCTGCTTCTGTGATCACAAGACCACT	631
DB	393	SerTrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrIle	412
QY	632	CCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACCTCTGCAG	691
DB	413	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432
QY	692	CTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAATGACA	751
DB	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	452
QY	752	GAAGCCCTGCTTACCAAGTCCGTAGATGCCCTTCTGTCAGGGACTTGATCATCAAGAG	811
DB	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472
QY	812	GACTATGAACCTGTTAGTACCAAGCCCTACAGGACCTCAAAAGTCAGACAAATTACTAGAC	871
DB	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492
QY	872	ACTACTGACATCCAGAGAGAGATTTCCTCAAGTTATAGTACAAAATTGAAGATAAC	931
DB	493	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512
QY	932	AAACAAATGGGTCTTACGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA	991
DB	513	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	532
QY	992	AATTACTTCAAAATAAAGCATG	1015

Db 533 AsnLeuLeuGlnAsnLysSerMet 540  
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Job time : 93.5 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:16:28 ; Search time 24.5 Seconds  
(without alignments)  
7033.775 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 778828

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES			
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2	1182	41.0 478 4	US-09-069-023-4 Sequence 4, Appli
3	1182	41.0 530 4	US-09-069-023-3 Sequence 3, Appli
4	1182	41.0 531 4	US-09-069-023-1 Sequence 1, Appli
5	1182	41.0 540 4	US-09-069-023-27 Sequence 27, Appli
6	1182	41.0 540 4	US-09-345-473E-28 Sequence 28, Appli
7	1176	40.8 540 3	US-09-019-942-1 Sequence 1, Appli
8	1176	40.8 540 4	US-09-099-041A-2 Sequence 2, Appli
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11	1176	40.8 540 4	US-09-207-359B-2 Sequence 2, Appli
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20	632	21.9	131	4	US-09-865-364-5	Sequence 5, Appli
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29	122.5	4.3	164	4	US-09-340-620A-41	Sequence 41, Appli
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32	122.5	4.3	249	4	US-09-207-359B-39	Sequence 39, Appli
33	122.5	4.3	249	4	US-09-340-620A-39	Sequence 39, Appli
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39	122.5	4.3	953	4	US-09-207-359B-8	Sequence 8, Appli
40	122.5	4.3	953	4	US-09-340-620A-8	Sequence 8, Appli
41	122.5	4.3	953	4	US-09-865-364-8	Sequence 8, Appli
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44	119	4.1	100	4	US-09-207-359B-10	Sequence 10, Appli
45	119	4.1	100	4	US-09-340-620A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1  
US-09-069-023-5  
; Sequence 5, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-5

SUMMARIES			
Alignment Scores:	6,75E-132	Length:	284
Pred. No.:	1182.00	Matches:	227
Score:	100.00%	Conservative:	1
Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	41.04%	Indels:	0
DB:	4	Gaps:	0

US-09-771-161A-2 (1-1669) x US-09-069-023-5 (1-284)

QY	332	CAGTTACAGAGTGGTTTCAAGTGCCTATTCACCTATGTGACAGAGAAATGAATATCT	391
Db	57	LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	76
QY	392	CTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT	451

Db	77	LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis	96
Qy	452	GRAAATAGTGGTCTCCTGAAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTT	511
Db	97	GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	116
Qy	512	TTATCTAGAAAAGCTCAAGACTCTTATTTATGAAGCTGCATCTGCTCTGGAATCAC	571
Db	117	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	136
Qy	572	AGTTGGATAGCACCATTCTCGATCTCAAGGCTGCATCTCTGTCATCACAAGACCACT	631
Db	137	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr	156
Qy	632	CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG	691
Db	157	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	176
Qy	692	CTGTGTATAGCCAGCTAGTGCAGAGCAAAAGGAAGACATTGTGAACCAATGACA	751
Db	177	ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	196
Qy	752	GAAGCTGCTTACCAAGTGCAGTCCCTCTGTCAGGACCTTGATCATCAAGAGAG	811
Db	197	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	216
Qy	812	GACTATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACAAATTA	871
Db	217	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	236
Qy	872	ACTACTGACATCCAGGAGAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC	931
Db	237	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	256
Qy	932	AAACAAATGGCTCTTACGCTTACCGGAAATCTTGTGGTTCTAGATCACCATCTTTA	991
Db	257	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	276
Qy	992	AATTACTTCAAAATAAAAGCATG 1015	
Db	277	AsnLeuLeuGlnAsnLysSerMet 284	
RESULT 2			
US-09-069-023-4			
; Sequence 4, Application US/09069023A			
; Patent No. 6348573			
; GENERAL INFORMATION:			
; APPLICANT: Nunez, Gabriel			
; APPLICANT: Inohara, Naohiro			
; APPLICANT: Koseki, Takeyoshi			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS			
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS			
; FILE REFERENCE: UM-03333			
; CURRENT APPLICATION NUMBER: US/09/069,023A			
; CURRENT FILING DATE: 1998-04-27			
; NUMBER OF SEQ ID NOS: 38			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 4			
; LENGTH: 478			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-069-023-4			
Alignment Scores:			
Pred. No.:	8,79e-132	Length:	478
Score:	1182.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	41.04%	Indels:	0
DB:	4	Gaps:	0
US-09-771-161A-2 (1-1669) x US-09-069-023-4 (1-478)			

Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-3 (1-530)

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QY 332 CAGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAAAGAAATGAATATCT 391
DB 303 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 322
QY 392 CTGAACATACCTGTAATCATCGTCCACAGAGGATCATGTGGATCCCTCAGTCCAT 451
DB 323 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 342
QY 452 GAAATAGTGGTTCCTCAAGTCCCTCAAGTCCCTCAAGTCCCTCAAGTCCCTCAAGTCCAT 511
DB 343 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 362
QY 512 TTATCTAGAAAGCTCAAGTGTATTATTTATGAAGTGCATCATGTCTCGAATATCAT 571
DB 363 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 382
QY 572 AGTTGGATAGCACCATTTCTGATCTCAAGGCTGCTATCTGTGATCACAAGACCAT 631
DB 383 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 402
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691
DB 403 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 422
QY 692 CTGTGTATAGCCAGCAGTGTGATCCAGACCAAGGAAAGACATTTGTGAACCAATGACA 751
DB 423 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 442
QY 752 GAAGCTGCTTAACAGTCCGTAGTGCCTTCTGTCAGGAGCTTGTATCATGAAGAG 811
DB 443 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 462
QY 812 GACTATGAATCTGTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAAGAAATTTACTAGAC 871
DB 463 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 482
QY 872 ACTACTGACATCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAGATAC 931
DB 483 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 502
QY 932 AAACAATGGTCTTCAGCTTACCGGAAATATGTGTTTCTAGATCACCATCTTTA 991
DB 503 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 522
QY 992 AATTTACTTCAAAATAAAAGCATG 1015
DB 523 AsnLeuLeuGlnAsnLysSerMet 530
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## RESULT 4

US-09-069-023-1

; Sequence 1, Application US/09069023A

; Patent No. 6348573

; GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 531

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-1

Alignment Scores:

Pred. No.: 9 27e-132 Length: 531

Score: 1182.00 Matches: 227

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.56% Mismatches: 0

Query Match: 41.04% Indels: 0

DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-1 (1-531)

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QY 332 CAGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAAAGAAATGAATATCT 391
DB 304 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 323
QY 392 CTGAACATACCTGTAATCATCGTCCACAGAGGATCATGTGGATCCCTCAGTCCAT 451
DB 324 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 343
QY 452 GAAATAGTGGTTCCTCAAGTCCCTCAAGTCCCTCAAGTCCCTCAAGTCCCTCAAGTCCAT 511
DB 344 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 363
QY 512 TTATCTAGAAAGCTCAAGTGTATTATTTATGAAGTGCATCATGTCTCGAATATCAT 571
DB 364 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 383
QY 572 AGTTGGATAGCACCATTTCTGATCTCAAGGCTGCTATCTGTGATCACAAGACCAT 631
DB 384 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 403
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691
DB 404 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 423
QY 692 CTGTGTATAGCCAGCAGTGTGATCCAGACCAAGGAAAGACATTTGTGAACCAATGACA 751
DB 424 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 443
QY 752 GAAGCTGCTTAACAGTCCGTAGTGCCTTCTGTCAGGAGCTTGTATCATGAAGAG 811
DB 444 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 463
QY 812 GACTATGAATCTGTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAAGAAATTTACTAGAC 871
DB 464 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 483
QY 872 ACTACTGACATCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAGATAC 931
DB 484 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 503
QY 932 AAACAATGGTCTTCAGCTTACCGGAAATATGTGTTTCTAGATCACCATCTTTA 991
DB 504 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 523
QY 992 AATTTACTTCAAAATAAAAGCATG 1015
DB 524 AsnLeuLeuGlnAsnLysSerMet 531
```

## RESULT 5

US-09-069-023-27

; Sequence 27, Application US/09069023A

; Patent No. 6348573

; GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
 ; FILE REFERENCE: 35800/183781  
 ; CURRENT FILING DATE: 1998-04-27  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 27  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-069-023-27  
 ; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
 ; FILE REFERENCE: 35800/183781  
 ; CURRENT FILING DATE: 1999-06-30  
 ; NUMBER OF SEQ ID NOS: 62  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-345-473E-28

Alignment Scores:  
 Pred. No.: 9,35E-132 Length: 540  
 Score: 1182.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.56% Mismatches: 0  
 Query Match: 41.04% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-27 (1-540)

QY	332	CAGTTACAGAGTGTTC	CAAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCT	391
DB	313	LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer		332
QY	392	CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT		451
DB	333	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis		352
QY	452	GAATAATAGTGTTCCTGTAACCTCAAGTCCCTGCAGCTCTCTCAAGACAATGATTTT		511
DB	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe		372
QY	512	TTATCTAGAAAGCTCAAGACTGTATTATTAAGCTGCATCACTCTCTCGGAAATCAC		571
DB	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis		392
QY	572	AGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCCTGTGATCAAGACCACT		631
DB	393	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr		412
QY	632	CCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG		691
DB	413	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln		432
QY	692	CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACA		751
DB	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr		452
QY	752	GAAGCTGCTTAACCACTGCTAGATGCCCTTCTGTCAGGACTTGCATCATGAAAGAG		811
DB	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu		472
QY	812	GACTATGACTTGTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTTACTAGAC		871
DB	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp		492
QY	872	ACTACTGACATCAAGGAGAAATTTGCCAAAGTATAGTACAAAAATTTGAAGATTAAC		931
DB	493	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn		512
QY	932	AAACAAATGGCTTCCTCAGCTTACCCGGAAATCTTGTGTTCTTAGATCACCATCTTTA		991
DB	513	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu		532
QY	992	AATTTACTTCAAAATAAAGCATG 1015		
DB	533	AsnLeuLeuGlnAsnLysSerMet 540		

RESULT 6  
 US-09-345-473E-28  
 ; Sequence 28, Application US/09345473E  
 ; Patent No. 6558903  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hodge, Martin

Alignment Scores:  
 Pred. No.: 9,35E-132 Length: 540  
 Score: 1182.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.56% Mismatches: 0  
 Query Match: 41.04% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-345-473E-28 (1-540)

QY	332	CAGTTACAGAGTGTTC	CAAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCT	391
DB	313	LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer		332
QY	392	CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT		451
DB	333	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis		352
QY	452	GAATAATAGTGTTCCTGTAACCTCAAGTCCCTGCAGCTCTCTCAAGACAATGATTTT		511
DB	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe		372
QY	512	TTATCTAGAAAGCTCAAGACTGTATTATTAAGCTGCATCACTCTCTCGGAAATCAC		571
DB	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis		392
QY	572	AGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCCTGTGATCAAGACCACT		631
DB	393	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr		412
QY	632	CCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG		691
DB	413	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln		432
QY	692	CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACA		751
DB	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr		452
QY	752	GAAGCTGCTTAACCACTGCTAGATGCCCTTCTGTCAGGACTTGCATCATGAAAGAG		811
DB	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu		472
QY	812	GACTATGACTTGTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTTACTAGAC		871
DB	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp		492
QY	872	ACTACTGACATCAAGGAGAAATTTGCCAAAGTATAGTACAAAAATTTGAAGATTAAC		931
DB	493	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn		512
QY	932	AAACAAATGGCTTCCTCAGCTTACCCGGAAATCTTGTGTTCTTAGATCACCATCTTTA		991
DB	513	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu		532
QY	992	AATTTACTTCAAAATAAAGCATG 1015		
DB	533	AsnLeuLeuGlnAsnLysSerMet 540		

RESULT 7  
 US-09-019-942-1  
 ; Sequence 1, Application US/09019942



Patent No. 6033855  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
DOMAIN POLYPEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/019,942  
FILING DATE: 06-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meikiejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/068001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-019-942-1

Alignment Scores:  
Pred. No.: 4,85e-131 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-019-942-1 (1-540)

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QY 332 CAGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAGAGAAATGAATATCT 391
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTCAAGTCCCTCCAGTCCCTCAAGACCAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTCCTCGAAATACAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAATCTCAAGACGCTGCAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
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QY 692 CCTGTATAGCCACAGTGGATCCAGACAAAAGGAGACATTGTGAACCAATGACA 751
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAACAGTCCGTAGATGCCCTTCTGTCAGGACTTGATCATGAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTGTTAGTACCAAGCTCAAGGACTCAAAAGTCAGACAAATTTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCAGCTTACCCTCCGGAATATCTTGTTGTTCTAGATCCACCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTTACTTCAAAATAAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540
RESULT 8
US-09-099-041A-2
; Sequence 2, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-2
Alignment Scores:
Pred. No.: 4,85e-131 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 4 Gaps: 0
US-09-771-161A-2 (1-1669) x US-09-099-041A-2 (1-540)
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Db 393 SerTrpAspSerThrIleSerGlnArgAlaAlaPheCysAspHisLysThrIle 412  
QY 632 CCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAAAGCTCTGCAG 691  
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 751  
Db 433 ProGlyIleAlaGlnInrIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAGCCTGCTTAAACCACTGCTAGATGCCCTCTCTCCAGGACTTGCATCATGAAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACCTGTGTAGTACCAAGCCCTACAAGGACCTCAAAAGCTCAGACAAATTTACTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCCAGGAGAAATTGGCCAAAGTTATAGTACAAAAATTTGAAGATAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGCTTTCAGCCTTACCCTGGAATATCTGTGTGTCTTCTAGATCACCATCTTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTACTTCAAAATAAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9  
US-09-245-281-2  
; Sequence 2, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/09/245,281  
; EARLIER FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-245-281-2

Alignment Scores:  
Pred. No.: 4,85e-131 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-245-281-2 (1-540)

QY 332 CAGTTACAGAGTGTTCAGTGCCTTACCTATGTCAGAGAAATGGAATATCT 391  
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332  
QY 392 CTGAACATACCTGTAATCATGTGTCACAGAGGAAATCATGTGGATCTCTCAGCTCCAT 451  
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 352

QY 452 GAAATAGTGGTTCTCTGAAACTTCAAGGTCTCTGCAGCTCTCTCAAGACAATGATTTT 511  
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372  
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTCTCTCGGAATCAC 571  
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
QY 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCAAGACCACT 631  
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412  
QY 632 CCATGCTCTTTCAGCAATAAATAATCCACTCTCAACTGCAGGAACTCAGAAAGCTCTGCAG 691  
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 751  
Db 433 ProGlyIleAlaGlnInrIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAGCCTGCTTAAACCACTGCTAGATGCCCTCTCTCCAGGACTTGCATCATGAAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACCTGTGTAGTACCAAGCCCTACAAGGACCTCAAAAGCTCAGACAAATTTACTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCCAGGAGAAATTGGCCAAAGTTATAGTACAAAAATTTGAAGATAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGGTCTTTCAGCCTTACCCTGGAATATCTGTGTGTCTTCTAGATCACCATCTTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTACTTCAAAATAAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 10  
US-09-470-271-1  
; Sequence 1, Application US/09470271  
; Patent No. 6410689  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/470,271  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/019,942  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-470-271-1

Alignment Scores:  
Pred. No.: 4,85e-131 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-470-271-1 (1-540)

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QY 332 CAGTTACAGAGTGTTCCTCAAGTGCCTTCACTATGTGACAGAGAAATGGAATTATCT 391
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DB 313 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTCACAAAGGAAATCATGTGGATCTCTCAGCTCCAT 451
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTGCGAGCTCCTCAAGCAATGATTTT 511
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTCCTCACTGTCTCGAAATCAC 571
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAAGACCCT 631
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTACCAAGTGCCTAGATGCCCTTCTGTCCAGGAACTCAAGAACTGAC 691
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTTGGTATAGCCAGAGTGCATCCAGACAAAGGAAAGACATTTGTGAACCAATGACA 751
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGAACTTGATCAATGAAAG 811
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACTTGTAGTACCAAGCTTCAAGCACTCAAAAGTCCAGCAATTTACTAGAC 871
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAGTTATAGTCAAAAATTTGAAAGATAAC 931
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DB 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTACCGCTTACCGGAAATCTTGTGGTTTCTAGATCACCATTCTTA 991
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532
QY 992 AATTACTCAAAATAAAGCATG 1015
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RESULT 11

US-09-207-359B-2

; Sequence 2, Application US/09207359B

; Patent No. 6469140

; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/207,359B  
; CURRENT FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-207-359B-2

Alignment Scores:

Pred. No.: 4,85e-131 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-207-359B-2 (1-540)

```
QY 332 CAGTTACAGAGTGTTCCTCAAGTGCCTTCACTATGTGACAGAGAAATGGAATTATCT 391
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 313 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTCACAAAGGAAATCATGTGGATCTCTCAGCTCCAT 451
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTGCGAGCTCCTCAAGCAATGATTTT 511
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTCCTCACTGTCTCGAAATCAC 571
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAAGACCCT 631
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTACCAAGTGCCTAGATGCCCTTCTGTCCAGGAACTCAAGAACTGAC 691
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTTGGTATAGCCAGAGTGCATCCAGACAAAGGAAAGACATTTGTGAACCAATGACA 751
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QY 752 GAAGCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGAACTTGATCAATGAAAG 811
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DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACTTGTAGTACCAAGCTTCAAGCACTCAAAAGTCCAGCAATTTACTAGAC 871
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DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAGTTATAGTCAAAAATTTGAAAGATAAC 931
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DB 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTACCGCTTACCGGAAATCTTGTGGTTTCTAGATCACCATTCTTA 991
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; Sequence 2, Application US/09340620A					
; Patent No. 6482933					
; GENERAL INFORMATION:					
; APPLICANT: Bertin, John					
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF					
; FILE REFERENCE: 07334-124001					
; CURRENT FILING DATE: 1999-06-28					
; PRIOR FILING DATE: 1999-02-05					
; PRIOR APPLICATION NUMBER: US 09/245,281					
; PRIOR FILING DATE: 1998-12-08					
; PRIOR APPLICATION NUMBER: US 09/099,041					
; PRIOR FILING DATE: 1998-06-17					
; PRIOR APPLICATION NUMBER: US 09/019,942					
; PRIOR FILING DATE: 1998-02-06					
; NUMBER OF SEQ ID NOS: 71					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 2					
; LENGTH: 540					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-09-340-620A-2					
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Percent Similarity:	99.56%	Conservative:	1		
Best Local Similarity:	99.12%	Mismatches:	1		
Query Match:	40.83%	Indels:	0		
DB:	4	Gaps:	0		
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Db	313	LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 332	Db	313	LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 332
QY	392	CTGAACATACCTGTAATCATGTGCCAAGAGAAATCATGTGCATCTCTCAGCTCCAT 451	QY	392	CTGAACATACCTGTAATCATGTGCCAAGAGAAATCATGTGCATCTCTCAGCTCCAT 451
Db	333	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352	Db	333	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY	452	GAATAAGTGTTCTCTGAAACTTCAAGTGCCTCCAGTCTCTCAAGCAATGATTTT 511	QY	452	GAATAAGTGTTCTCTGAAACTTCAAGTGCCTCCAGTCTCTCAAGCAATGATTTT 511
Db	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372	Db	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY	512	TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTCTCGGAAATCAC 571	QY	512	TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTCTCGGAAATCAC 571
Db	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392	Db	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY	572	AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACT 631	QY	572	AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACT 631
Db	393	SerTrpAspSerThrIleSerGlnArgAlaAlaPheCysAspHisLysThrIle 412	Db	393	SerTrpAspSerThrIleSerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY	632	CCATGCTCTTACGATTAATAATCCACTCTCAACTGCAGAAACTCAGACGCTCCAG 691	QY	632	CCATGCTCTTACGATTAATAATCCACTCTCAACTGCAGAAACTCAGACGCTCCAG 691
Db	413	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432	Db	413	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY	692	CTGTGTATAGCCACAGCTGGATTCAGAGCAAAAGGGAAGCAATTTGTAACCAATGACA 751	QY	692	CTGTGTATAGCCACAGCTGGATTCAGAGCAAAAGGGAAGCAATTTGTAACCAATGACA 751
Db	433	ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452	Db	433	ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY	752	GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 811	QY	752	GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 811
Db	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472	Db	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY	812	GACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTACTAGAC 871	QY	413	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432





GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:19:33 ; Search time 76 Seconds  
(without alignments)  
11492.462 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 2130338

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	1182	41.0	540	9	US-09-771-161A-184	Sequence 184, Appl
3	1182	41.0	540	9	US-09-862-027-28	Sequence 28, Appl
4	1182	41.0	540	10	US-09-981-397A-14	Sequence 14, Appl
5	1182	41.0	544	9	US-09-925-301-1015	Sequence 1015, Ap
6	1176	40.8	540	9	US-09-748-537-1	Sequence 1, Appl
7	1176	40.8	540	9	US-09-728-721-2	Sequence 2, Appl
8	1176	40.8	540	13	US-10-133-780-1	Sequence 1, Appl
9	1176	40.8	540	13	US-10-105-931-2	Sequence 2, Appl
10	1176	40.8	540	13	US-10-118-984-2	Sequence 2, Appl
11	1176	40.8	540	14	US-10-295-981-2	Sequence 2, Appl
12	632	21.9	131	9	US-09-728-721-5	Sequence 5, Appl
13	632	21.9	131	13	US-10-105-931-5	Sequence 5, Appl
14	632	21.9	131	13	US-10-118-984-5	Sequence 5, Appl
15	632	21.9	131	14	US-10-295-981-5	Sequence 5, Appl
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17	544	18.9	109	13	US-10-105-931-6	Sequence 6, Appl
18	544	18.9	109	13	US-10-118-984-6	Sequence 6, Appl
19	544	18.9	109	14	US-10-295-981-6	Sequence 6, Appl
20	461	16.0	92	13	US-10-014-269-21	Sequence 21, Appl
21	461	16.0	92	13	US-10-002-974-21	Sequence 21, Appl
22	461	16.0	92	14	US-10-314-506-21	Sequence 21, Appl
23	451	15.7	90	9	US-09-841-879B-10	Sequence 10, Appl
24	447	15.5	89	9	US-09-931-071-11	Sequence 11, Appl
25	145.5	5.2	109	9	US-09-728-721-71	Sequence 71, Appl
26	145.5	5.2	109	14	US-10-295-981-71	Sequence 71, Appl
27	143.5	5.0	95	9	US-09-841-879B-12	Sequence 12, Appl
28	122.5	4.3	164	9	US-09-728-721-41	Sequence 41, Appl
29	122.5	4.3	164	13	US-10-118-984-41	Sequence 41, Appl
30	122.5	4.3	164	14	US-10-295-981-41	Sequence 41, Appl
31	122.5	4.3	249	9	US-09-728-721-39	Sequence 39, Appl
32	122.5	4.3	249	13	US-10-118-984-39	Sequence 39, Appl
33	122.5	4.3	249	14	US-10-295-981-39	Sequence 39, Appl
34	122.5	4.3	507	15	US-10-401-194-3	Sequence 3, Appl
35	122.5	4.3	953	9	US-09-728-721-8	Sequence 8, Appl
36	122.5	4.3	953	13	US-10-105-931-8	Sequence 8, Appl
37	122.5	4.3	953	13	US-10-118-984-8	Sequence 8, Appl
38	122.5	4.3	953	14	US-10-013-477-12	Sequence 12, Appl
39	122.5	4.3	953	14	US-10-295-981-8	Sequence 8, Appl
40	122.5	4.3	953	14	US-10-028-374-4	Sequence 4, Appl
41	122.5	4.3	953	14	US-10-183-770-4	Sequence 4, Appl
42	119	4.1	100	9	US-09-728-721-10	Sequence 10, Appl
43	119	4.1	100	13	US-10-105-931-10	Sequence 10, Appl
44	119	4.1	100	13	US-10-118-984-10	Sequence 10, Appl
45	119	4.1	100	14	US-10-295-981-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-09-771-161A-93  
; Sequence 93, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 93  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-93

RESULT 3  
US-09-862-027-28  
; Sequence 28, Application US/09862027  
; Patent No. US20020142428A1  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin R.

RESULT 2  
US-09-771-161A-184  
; Sequence 184, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619



US-09-981-397A-14

Sequence 14, Application US/09981397A  
Publication No. US20030082519A1  
GENERAL INFORMATION:  
APPLICANT: Axxina Pharmaceuticals AG  
APPLICANT: Schubart, Daniel  
APPLICANT: Habenberger, Peter  
APPLICANT: Stein-Gerlach, Matthias  
APPLICANT: Bevec, Dorian  
TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
TITLE OF INVENTION: Inhibition  
FILE REFERENCE: AXM-004.1 US  
CURRENT APPLICATION NUMBER: US/09/981,397A  
CURRENT FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/240,750  
PRIOR FILING DATE: 2000-10-16  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-981-397A-14

## Alignment Scores:

Pred. No.: 6.64e-114 Length: 540  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 10 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-981-397A-14 (1-540)

QY	332	CAGTTACAGAGTGTTC	CAAGTGCCTTACCTATCTGACAAAGAAATGGAATATCT	391
DB	313	LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	332	
QY	392	CTGAACATACCTGTAAATCATGTC	CAAGAGGAATCATGTGGATCTCTCAGCTCCAT	451
DB	333	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	352	
QY	452	GAAATAGTGGTTCCTCGAACTTCAAGTCC	CAAGTCCCTCCACAGCAATGATTTT	511
DB	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	372	
QY	512	TTATCTAGAAAGCTCAAGACTGTTATTTAT	TATGAAGCTGCATCTGTCTCGAAATCAC	571
DB	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlnAsnHis	392	
QY	572	AGTTGGGATAGCACCATTTCTGGATCTCAA	GGGCTGCATCTCTGTATCACAAGACCAT	631
DB	393	SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	412	
QY	632	CCATGCTCTTACGAATTAATTAATCCTCA	CTCTCAACTCAGGAACTCAGAACGCTGCGAG	691
DB	413	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432	
QY	692	CCTGTATAGCCACAGTGCATCCAGACAA	AGGAGACATTTGTGAACCAATGACA	751
DB	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgLysAlaValAsnGlnMetThr	452	
QY	752	GAAAGCTGCTTAAACAGTCCGCTAGATGC	CTCTCTCTCAGGAGCTTGATCATGAAGAG	811
DB	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472	
QY	812	GACTATGAACCTTGTAGTACCAAGCTCA	AGGACTCAAAAGTCAAGCAATTACTAGAC	871
DB	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492	
QY	872	ACTACTGACATCCAAAGGAGAAATTTGC	CAAGTTTAGTAGTACAAAATTTGAAAGATAAC	931
DB	493	ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512	

US-09-771-161A-2 (1-1669) x US-09-862-027-28 (1-540)

Sequence 14, Application US/09981397A  
Publication No. US20030082519A1  
GENERAL INFORMATION:  
APPLICANT: Axxina Pharmaceuticals AG  
APPLICANT: Schubart, Daniel  
APPLICANT: Habenberger, Peter  
APPLICANT: Stein-Gerlach, Matthias  
APPLICANT: Bevec, Dorian  
TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
TITLE OF INVENTION: Inhibition  
FILE REFERENCE: AXM-004.1 US  
CURRENT APPLICATION NUMBER: US/09/981,397A  
CURRENT FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/240,750  
PRIOR FILING DATE: 2000-10-16  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-862-027-28

## Alignment Scores:

Pred. No.: 6.64e-114 Length: 540  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-862-027-28 (1-540)

QY	332	CAGTTACAGAGTGTTC	CAAGTGCCTTACCTATCTGACAAAGAAATGGAATATCT	391
DB	313	LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	332	
QY	392	CTGAACATACCTGTAAATCATGTC	CAAGAGGAATCATGTGGATCTCTCAGCTCCAT	451
DB	333	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	352	
QY	452	GAAATAGTGGTTCCTCGAACTTCAAGTCC	CAAGTCCCTCCACAGCAATGATTTT	511
DB	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	372	
QY	512	TTATCTAGAAAGCTCAAGACTGTTATTTAT	TATGAAGCTGCATCTGTCTCGAAATCAC	571
DB	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	392	
QY	572	AGTTGGGATAGCACCATTTCTGGATCTCAA	GGGCTGCATCTCTGTATCACAAGACCAT	631
DB	393	SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	412	
QY	632	CCATGCTCTTACGAATTAATTAATCCTCA	CTCTCAACTCAGGAACTCAGAACGCTGCGAG	691
DB	413	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432	
QY	692	CCTGTATAGCCACAGTGCATCCAGACAA	AGGAGACATTTGTGAACCAATGACA	751
DB	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgLysAlaValAsnGlnMetThr	452	
QY	752	GAAAGCTGCTTAAACAGTCCGCTAGATGC	CTCTCTCTCAGGAGCTTGATCATGAAGAG	811
DB	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472	
QY	812	GACTATGAACCTTGTAGTACCAAGCTCA	AGGACTCAAAAGTCAAGCAATTACTAGAC	871
DB	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492	
QY	872	ACTACTGACATCCAAAGGAGAAATTTGC	CAAGTTTAGTAGTACAAAATTTGAAAGATAAC	931
DB	493	ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512	
QY	932	AAACAAATGGTCTCAGCTTACCGGAAAT	CTGTGTCTTAGATCACCATCTTTA	991
DB	513	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	532	
QY	992	AATTTACTTCAAAATAAAGCATG	1015	
DB	533	AsnLeuLeuGlnAsnLysSerMet	540	

RESULT 4

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QY 932 AAACAAATGGTCTTACAGCTTACCGGAAATCTTGTGTTCTAGATCACCATTCTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 5
US-09-925-301-1015
; Sequence 1015, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1015
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1015

Alignment Scores:
Pred. No.: 6,66e-114 Length: 544
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-925-301-1015 (1-544)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAGAGAAATGGAATTATCT 391
Db 317 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 336
QY 392 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
Db 337 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 356
QY 452 GAAATAGTGGTTCCTCGAAACTTCAAGGTCCTCCAGCTCCCTCAAGACAATGATTTT 511
Db 357 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 376
QY 512 TTATCTAGAAAGCTCAGACTGTTATTTATGAGCTGCACTACTGCTGGAAATCAC 571
Db 377 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 396
QY 572 AGTTGGATAGCACCATTCTCGATCTCAAAGGCTGCATCTGTGATCACAAGACCACT 631
Db 397 SerTyrAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrThr 416
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGAGGAACTCAGAACGCTTGAG 691
Db 417 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 436
QY 692 CCTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATGACA 751
Db 437 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 456
QY 752 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG 811
Db 457 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 476
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QY 812 GACTATGAACCTGTTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAGACAATTACTAGAC 871
Db 477 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 496
QY 872 ACTACTGATCATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTCAGAAAGATAAC 931
Db 497 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 516
QY 932 AAACAAATGGTCTTACAGCTTACCGGAAATCTTGTGTTCTAGATCACCATTCTTTA 991
Db 517 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 536
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 537 AsnLeuLeuGlnAsnLysSerMet 544

RESULT 6
US-09-748-537-1
; Sequence 1, Application US/09748537
; Patent No. US20020061833A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THEREOF
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-537-1

Alignment Scores:
Pred. No.: 2,8e-113 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-748-537-1 (1-540)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAGAGAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTCGAAACTTCAAGTCCCTCCAGCTCCCTCAAGACAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAGCTCAGACTGTTATTTATGAAGCTGCATCTACTGCTGGAAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTCTGGAATCTCAAAGGCTGCATCTTGTGATCACAAGACCACT 631
Db 393 SerTyrAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrThr 412
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGAGGAACTCAGAACGCTTGAG 691
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-133-780-1

Alignment Scores:
Pred. No.: 2,8e-113 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-133-780-1 (1-540)
QY 332 CAGTTACAGAGTGTTCCTCAAGTCCCAATTCACCTATGTGACAAAGAAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GMAAATAGTGTTCCTCAAGTCCCAATTCACCTATGTGACAAAGAAAATGGAATTATCT 511
Db 353 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTCTGGAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGCACCATTCTGGAATCTCAAGGCTGCATTCGTGATCAAGAGCACT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnAAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATAAATCAACTCTCAAGTCCAGGAAACTCAGAACGCTGCAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGTTATAGCCAGCAGTGCATCCAGAGCAAAAGGAGACATTTGTGATCAGAACATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTCCCTTAACCACTGCTAGATGCCCTTCTGCTCCAGGACTTGCATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTGTGTAGTACCAAGCTTACCAAGGCTCAAGAGCAAAAGTCAACAATTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTCAGAAAGTAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTCAGCCTTACCCGGAAATACCTTGTGGTTCTPAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9
US-10-105-931-2
; Sequence 2, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
;

; CURRENT APPLICATION NUMBER: US/10105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-105-931-2

Alignment Scores:
Pred. No.: 2,8e-113 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-105-931-2 (1-540)
QY 332 CAGTTACAGAGTGTTCCTCAAGTCCCAATTCACCTATGTGACAAAGAAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GMAAATAGTGTTCCTCAAGTCCCAATTCACCTATGTGACAAAGAAAATGGAATTATCT 511
Db 353 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTCTGGAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGCACCATTCTGGAATCTCAAGGCTGCATTCGTGATCAAGAGCACT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnAAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATAAATCAACTCTCAAGTCCAGGAAACTCAGAACGCTGCAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGTTATAGCCAGCAGTGCATCCAGAGCAAAAGGAGACATTTGTGATCAGAACATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTCCCTTAACCACTGCTAGATGCCCTTCTGCTCCAGGACTTGCATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTGTGTAGTACCAAGCTTACCAAGGCTCAAGAGCAAAAGTCAACAATTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTCAGAAAGTAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTCAGCCTTACCCGGAAATACCTTGTGGTTCTPAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 10
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692 CTTGGTATGCCAGCAGTGATCCAGACAAAAGGAGACATTTGTGAACCAATGACA 751  
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433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
Qy 752 GAAGCCTGCTTAAACCAAGTCGTAGATGCCCTTCTCTCCAGGAGACTTGTATCATGAAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
Qy 812 GACTATGAACCTTGTAGTACCAAGCCTTCAAGGACCTCAAAAGTCCAGAAATCTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
Qy 872 ACTACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
Qy 932 AAACAAATGGTCTTACAGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeu 532  
Qy 992 AATTACTTCAAAATAAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540  
RESULT 12  
US-09-728-721-5  
; Sequence 5, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; TYPE: PRT  
; LENGTH: 131  
; ORGANISM: Homo sapiens  
US-09-728-721-5  
Alignment Scores:  
Pred. No.: 8,84e-57 Length: 131  
Score: 632.00 Matches: 117  
Percent Similarity: 99.16% Conservative: 1  
Best Local Similarity: 98.32% Mismatches: 1  
Query Match: 21.94% Indels: 0  
Gaps: 0  
DB:  
US-09-771-161A-2 (1-1669) x US-09-728-721-5 (1-131)  
Qy 332 CAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATCT 391  
Db 13 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 32  
Qy 392 CTGAACATACCTCTAAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451  
Db 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52  
Qy 452 GAAATAGTGGTTCTCCTGAAACTTCAAGTCCCTGCCAGTCTCTCAAGACATGATTTT 511  
Db 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 72  
Qy 512 TTATCTAGAAAAGCTCAAGACTCTTATTTATCAAGCTGCATCATCTCTCGAAATCAC 571  
Db 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92  
Qy 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGATCAAGACCAT 631  
Db 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112  
Qy 632 CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCG 688  
Db 113 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131  
RESULT 14  
US-10-118-984-5  
; Sequence 5, Application US/10118984  
; Publication No. US20020197693A1  
; GENERAL INFORMATION:

73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92  
Qy 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGATCAAGACCAT 631  
Db 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112  
Qy 632 CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCG 688  
Db 113 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131  
RESULT 13  
US-10-105-931-5  
; Sequence 5, Application US/10105931  
; Publication No. US20020150987A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/10/105,931  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-931-5  
Alignment Scores:  
Pred. No.: 8,84e-57 Length: 131  
Score: 632.00 Matches: 117  
Percent Similarity: 99.16% Conservative: 1  
Best Local Similarity: 98.32% Mismatches: 1  
Query Match: 21.94% Indels: 0  
Gaps: 0  
DB:  
US-09-771-161A-2 (1-1669) x US-10-105-931-5 (1-131)  
Qy 332 CAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATCT 391  
Db 13 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 32  
Qy 392 CTGAACATACCTCTAAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451  
Db 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52  
Qy 452 GAAATAGTGGTTCTCCTGAAACTTCAAGTCCCTGCCAGTCTCTCAAGACATGATTTT 511  
Db 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 72  
Qy 512 TTATCTAGAAAAGCTCAAGACTCTTATTTATCAAGCTGCATCATCTCTCGAAATCAC 571  
Db 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92  
Qy 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGATCAAGACCAT 631  
Db 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112  
Qy 632 CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCG 688  
Db 113 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131  
RESULT 14  
US-10-118-984-5  
; Sequence 5, Application US/10118984  
; Publication No. US20020197693A1  
; GENERAL INFORMATION:

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; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-5

Alignment Scores:
Pred. No.:      8,84e-57      Length:      131
Score:          632.00      Matches:      117
Percent Similarity: 99.16%      Conservative: 1
Best Local Similarity: 98.32%      Mismatches: 1
Query Match:      21.94%      Indels:      0
DB:              13          Gaps:          0

US-09-771-161A-2 (1-1669) x US-10-118-984-5 (1-131)
QY 332 CAGTTACAGAGTGTTCCTCAAGTGCCATTACCTATGTGACAAAGAAATGGAATTATCT 391
DB 13 LysLeuGlnSerValSerSerAlaLeHisLeuCysAspLysLysMetGluLeuSer 32
QY 392 CTGAACATACCTGTAATCATCGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
DB 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 52
QY 452 GAAATAGTGGTTCCTGAAACTTCAGGTCCTCCAGCTCCCTCAAGACAATGATTTT 511
DB 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 72
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTCGAAATCAC 571
DB 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGATAGCACCATTCTCGGATCTCAAAGGGCTGCATTCTGTGATCACAAAGACCACT 631
DB 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATATAATCCACTCTCAACTGCGAGGAACTCAGAACGCTCTG 688
DB 113 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

RESULT 15
US-10-295-981-5
; Sequence 5, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-5

Alignment Scores:
Pred. No.:      8,84e-57      Length:      131
Score:          632.00      Matches:      117
Percent Similarity: 99.16%      Conservative: 1
Best Local Similarity: 98.32%      Mismatches: 1
Query Match:      21.94%      Indels:      0
DB:              14          Gaps:          0

US-09-771-161A-2 (1-1669) x US-10-295-981-5 (1-131)
QY 332 CAGTTACAGAGTGTTCCTCAAGTGCCATTACCTATGTGACAAAGAAATGGAATTATCT 391
DB 13 LysLeuGlnSerValSerSerAlaLeHisLeuCysAspLysLysMetGluLeuSer 32
QY 392 CTGAACATACCTGTAATCATCGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
DB 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 52
QY 452 GAAATAGTGGTTCCTGAAACTTCAGGTCCTCCAGCTCCCTCAAGACAATGATTTT 511
DB 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 72
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTCGAAATCAC 571
DB 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGATAGCACCATTCTCGGATCTCAAAGGGCTGCATTCTGTGATCACAAAGACCACT 631
DB 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATATAATCCACTCTCAACTGCGAGGAACTCAGAACGCTCTG 688
DB 113 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

Search completed: March 29, 2004, 14:28:31
Job time : 86 secs
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:15:32 ; Search time 31.5 Seconds  
(without alignments)  
10193.248 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880  
Sequence: 1 acctagttataccagata.....caacagcgtgatgtgtaaaa 1669

Scoring table:

BLASUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=klp  
-O=/cpn2.1/USPTO spoal\_p/US09771161/runat\_29032004.124825.13694/app\_query.fasta\_1.1863  
-DB=PIR\_78 -QPMT=fstasn -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blasmus62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09771161 @CCN 1.1.44 @runat\_29032004.124825.13694 -NCPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 78.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	3.5	943	2 S44636	f22b7.5 protein -
2	99.5	3.5	830	2 T00029	Miranda protein -
3	98	3.4	618	2 S68450	apoptosis inhibito
4	95	3.3	731	2 A99106	hypothetical prote
5	93	3.2	692	2 T32980	hypothetical prote
6	90.5	3.1	956	2 T40953	hypothetical prote
7	90	3.1	597	2 F82935	DNA polymerase III
8	90	3.1	708	2 JQ1148	killer toxin KHS p
9	90	3.1	1205	2 T41987	hypothetical prote
10	90	3.1	2288	2 T29999	hypothetical prote
11	89.5	3.1	2368	2 S46005	BSR1 protein - yea
12	89	3.1	242	2 S71757	MADS box protein D
13	89	3.1	283	2 B81996	RNA polymerase sig
14	89	3.1	1360	2 T33922	hypothetical prote

15	89	3.1	1944	2 A55117	tsg24 protein - mo
16	88	3.0	133	2 H71190	hypothetical prote
17	88	3.1	358	2 J55964	apoptosis inhibito
18	88	3.1	397	2 E82876	hypothetical prote
19	88	3.1	524	2 S35551	transcription fact
20	88	3.1	1019	2 E90097	hypothetical prote
21	88	3.1	1135	2 T30561	Scythe protein - A
22	88	3.1	1758	2 T30560	resistance protein
23	87.5	3.0	340	2 T27389	hypothetical prote
24	87.5	3.0	406	2 S44842	K06H7.2 protein -
25	87	3.0	147	2 F84869	hypothetical prote
26	87	3.0	294	2 T21474	hypothetical prote
27	87	3.0	340	2 E70121	hypothetical prote
28	86.5	3.0	407	2 S27774	transforming protei
29	86.5	3.0	528	2 T52092	DNA-binding protei
30	86.5	3.0	1203	2 T17415	mycelial surface a
31	86	3.0	371	2 E88986	protein C50H11.13
32	86	3.0	721	2 S31824	gene Mx protein -
33	86	3.0	3169	2 T00296	toxin B - Escheric
34	85.5	3.0	212	2 G75458	conserved hypothet
35	85.5	3.0	455	1 J43338	tryptophan dimethy
36	85.5	3.0	1095	2 T20528	hypothetical prote
37	85.5	3.0	3898	1 GNWVHC	genome polyprotein
38	85	3.0	690	2 A24545	triacylglycerol li
39	85	3.0	721	2 S31820	gene Mx protein -
40	85	3.0	721	2 A37472	interferon-inducib
41	85	3.0	1121	2 F71613	hypothetical prote
42	84.5	2.9	224	2 S23728	MADS box protein T
43	84.5	2.9	362	2 E71637	hypothetical prote
44	84.5	2.9	644	2 A42220	helix-loop-helix p
45	84.5	2.9	810	2 S69652	hypothetical prote

ALIGNMENTS

RESULT 1

S44636  
f22b7.5 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Dec-1997  
C:Accession: S44636  
R:Anderson, K.  
Submitted to the ENBL Data Library, March 1993  
A:Description: Sequence of the C. elegans cosmid F22B7.  
A:Reference number: S44628  
A:Accession: S44636  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-943 <AND>  
A:Cross-references: EMBL:L12018; NID:g156298; PID:g156307  
C:Genetics:  
A:Introns: 83/2; 250/2; 453/1; 484/2; 519/1; 553/3; 580/3; 632/3; 729/3; 830/2; 905/1  
C:Superfamily: dnaJ amino-terminal homology  
F:531-595/Domain: dnaJ amino-terminal homology <DNJ>

Alignment Scores:  
Pred. No.: 0.376 Length: 943  
Score: 100.50 Matches: 45  
Percent Similarity: 38.36% Conservative: 44  
Best Local Similarity: 39.40% Mismatches: 84  
Query Match: 3.49% Indels: 59  
DB: 2 Gaps: 10

US-09-771-161A-2 (1-1669) x S44636 (1-943)

QY	392	CTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCTCTCAGCTCCAT	451
DB	349	IIeAspValAlaMetAsnGlnGluArgSerGluThrAlaThrAspGlnAspValCysLeu	368
QY	452	GAATAATAGTGGTCTCCCGAAACTTCAGAGTCCCTCCAGCTCCCTCAAGACAAATGATTTT	511
DB	369	AlaIleAspSerSerProAspProThrSerSer-----AsnAspMet	382

QY	512	TTATCTAGAAAAGCTCAAGACTCTTATTTATGACGCTGCATCTGCTCTGGAATCAC	571
Db	383	IleAsnLys-----PheValValGluLeuGluHisAlaThrAsnValGlu	397
QY	572	AGTTGGGATAGCACCATTCTGCA-----	595
Db	398	ThrTrpGluMetIleValAsnGlyIleIleAspAspGlnLysLysProValAlaIleGlu	417
QY	596	-----TCTCAAGGGCTGCA	610
Db	418	LysLysGluAsnGluGluProValAspMetMetAspLeuIlePheSerMetSerArg	437
QY	611	TTCTGTGATCACAAGACCCTCATCTCTTCAGCAATAATA-----AATCCACTCTCA	664
Db	438	MetAspAspGlnArgThrGluLeuProAlaAargPheIleProProArgProValSer	457
QY	665	ACTGCAGGA-----AACTCAGAACGCTCTGCAGCTCGTATAGCCAGCAGTGG	712
Db	458	SerAlaSerLysLysThrThrLysSerHisArgIleLeuProGlyLeuArgAlaAsnTrp	477
QY	713	ATCCAGACCAAGGGAGACATTGTGAACCAATGACAGAACGCTGCCTTAACCAAGTCG	772
Db	478	ThrLysValGlnSerMetLysValLeuGlyMetPheVal-----LeuAsnArgSer	494
QY	773	CTAGATGCCCTTCTGTCAGGACTTCATCATGAAAGAGGACTATGAACCTTGTAGTACC	832
Db	495	---SerGlyLeuIleHisAargSerValProLeuLeuAlaGln-----ValSerThr	510
QY	833	AAGCCTACAGGAGCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAAGGAGAA	892
Db	511	ProThrThrSerThrThrLysLeuAlaGlnLeuHisThrThrHisAlaLeuSerLysGlu	530
QY	893	GAATTGCCAAAGTATA---GTCAAAAATTGAACATAACAA-----	934
Db	531	AspTyrTyrLysThrLeuGlyValAspLysLysSerAspAlaLysAlaIleLysLysAla	550
QY	935	-----CAATGGGTCTTCAGCCTTACCCGGAATA	964
Db	551	TyrPheGlnLeuAlaLysLysTyrHisProAspVal	562
RESULT 2			
T00029			
Miranda protein - fruit fly ( <i>Drosophila melanogaster</i> )			
C/Species: <i>Drosophila melanogaster</i>			
C/Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 17-Nov-2000			
C/Accession: T00029			
R/Ikeshima-Kataoka, H.; Skeath, J.B.; Nabeshima, Y.; Doe, C.Q.; Matsuzaki, F.			
Nature 390, 625-629, 1997			
A/Title: Miranda directs Prospero to a daughter cell during <i>Drosophila</i> asymmetric division			
A/Reference number: Z14067; MUID:98065952; PMID:9403694			
A/Accession: T00029			
A/Status: preliminary; translated from GB/EMBL/DBJ			
A/Molecule type: mRNA			
A/Residues: 1-830 <IKE>			
A/Cross-references: EMBL:AB005661; NID:g2749776; PIDN:BAA24111.1; PID:g2749777			
A/Experimental source: strain Canton-S			
C/Genetics:			
A/Cross-references: FlyBase:FBgn0021776			
A/Map position: 92B-C			
Alignment Scores:			
Pred. No.:	0.462	Length:	830
Score:	99.50	Matches:	59
Percent Similarity:	37.50%	Conservative:	49
Best Local Similarity:	20.4%	Mismatches:	111
Query Match:	3.45%	Indels:	69
DB:	2	Gaps:	10
US-09-771-161A-2 (1-1669) x T00029 (1-830)			
QY	353	GCATTCACCTATGTGACAGAAGAAATGAATTATCTCTGAACATACCTGTAATCAT	412
Db	64	AlaValArgPheAlaSerSerSerLysGluAlaLysGluPheAlaIlePro-----	80

QY	413	GGTCACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAAATAGTGGTTCTCTCTGAA	472
Db	81	---LysGluAspLysLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGln	99
QY	473	ACTTCAAGGTCCTGCCAGCTCTCAGACAATGATTTTTTATCTAGAAAAGCTCAAGAC	532
Db	100	ArgLeuArgPheArgProThrProSerHisThrAspThrAlaThrGlySerGly-----	117
QY	533	TGTTATTTTGAAGCTGCATCAGCTGCTGGAATCACAGTGGGATAGCACCATTCT	592
Db	118	-----Ser	118
QY	593	GGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATA	652
Db	119	GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr	133
QY	653	AATCCACTCTCACTGCAGGAACTCAGAACTCAGAACTGTCAGCCTGCTGATATACCCAGCAGTGG	712
Db	134	ThrProValLysGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnTyr	153
QY	713	---ATCCAGACCAAGGAGAGACATTGTGAACCAATGACAGAAAGCC---TGCCTTAAC	766
Db	154	GluIleArgHisLysAsnGluLeuIleGluSerGlnLeuSerGlnLeuAspValLeuArg	173
QY	767	CAGTCGTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAGACTATGAACCTTGT	826
Db	174	ArgHisValAspGlnLeuLysGluAlaLysLeuArgGluGluHisGluLeuAla	193
QY	827	AGTACCAAGCTTACAGG-----ACCTCAAAAGTCAGACAAATTACTAGAC	871
Db	194	ThrSerLysThrAspArgLeuIleGluAlaLeuThrSerGluAsnLeuSerHisLysAla	213
QY	872	ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTGAAAGATAAAC	931
Db	214	LeuAsnGluGlnMetGlyGlnGluHisAlaAsp---LeuLeuGluArgLeuAlaAlaMet	232
QY	932	AAACAAATGGTCTTCAGCCTTACCCGAA-----ATCTTGTGTTTCT	976
Db	233	GluGlnGlnLeuGlnGlnHisAspGluHisGluArgGlnValGluAlaLeuValAla	252
QY	977	AGATCACCATTCTTA-----AATTACTTCAAAATAAAAGCATGTAAGTGACT	1024
Db	253	GluSerGluLeuArgLeuAlaAsnGluLeuGlnThrAlaAsnGluAspArgGln	272
QY	1025	GTTTTTCAAGAGAAATGTCTTTCATAAAAGGATATTTATCTCTGTTGCTTTGACTTT	1084
Db	273	LysValGluGluGln-----	277
QY	1085	TTTTATATAAATCCGTGAGTATTAAAGCTTTATTCAGGTTCTTTGGTAAATATTAGT	1144
Db	278	-----LeuGlnAlaGlnLeuSerAlaLeuGlnAlaAspValAla	290
QY	1145	CTCCTCCATGACACTGCAGTATT	1168
Db	291	GlnAlaArgGluHisCysSerLeu	298
RESULT 3			
S68450			
apoptosis inhibitor hiap-2 - human			
C/Species: <i>Homo sapiens</i> (man)			
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000			
C/Accession: S68450			
R/Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, A.; Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP			
Nature 379, 349-353, 1996			
A/Reference number: A58182; MUID:96149249; PMID:8552191			
A/Accession: S68450			
A/Status: nucleic acid sequence not shown			
A/Molecule type: mRNA			
A/Residues: 1-618 <LIS>			
A/Cross-references: EMBL:U45879; NID:g1184317; PIDN:AA50372.1; PID:g1184318			
C/Function:			

A:Description: apoptotic suppressor  
C:Superfamily: RING finger homology  
C:Keywords: apoptosis; zinc finger  
F:567-611/Domain: RING finger homol

Alignment Scores:

Pred. No.:	0.623	Length:	618
Score:	98.00	Matches:	31
Percent Similarity:	44.78%	Conservative:	29
Best Local Similarity:	23.13%	Mismatches:	58
Query Match:	3.40%	Indels:	16
DB:	2	Gaps:	3

US-09-771-161A-2 (1-1669) x S68450 (1-618)

713	ATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAGAGCGCTGCCTTAAACCAAGTCG	772
Qy		
Db		
461	IieATGLyAsnArgMetAlaLeuPheGlnLeuThr-----CysValLeuProile	478
Qy		
Db		
773	CTAGATGCCCTTCGTCCAGGACATTGATCATGAAGAGGACATGTAACCTTGTGTAGTACC	832
Qy		
Db		
479	LeuAspAsnLeuLeuLeuLysAlaAsnValIleAsnLysGlnGluHisAspIleIleLysGln	498
Qy		
Db		
833	AAGCCTACAGGACCTCCAAAAGTCAGACAAATTACTAGACACTACTGCACTCCAGAGAGAA	892
Qy		
Db		
499	LysThrGlnIleProLeuGlnAlaArgGluLeuIleAspThrIleTrpValLysGlyAsn	518
Qy		
Db		
893	GAATTTGCCAAAGTTATAGTACAAAATTGAAAGAT-----	928
Qy		
Db		
519	AlaAlaAlaAsnIlePheLysAsnCysLeuLysGluIleAspSerThrLeuTyLysAsn	538
Qy		
Db		
929	-----AACAAACAATGGCTTCACAGCCTTACCCGGAATACTGTGGTTCTTAGA	979
Qy		
Db		
539	LeuPheValAspLysAsnMetLysTyIleProThrGluAspValSerGlyLeuSerLeu	558
Qy		
Db		
980	TCACCATCTTTAAATTTACTCCAAAATAAAGACATGTAAGTAGCTGTTTTTTCAGAGAGAA	1031
Qy		
Db		
559	GluGluGlnLeuArgGluGlnGluGluArgThrCysLysValCysMetAspLysGlu	578
Qy		
Db		
1040	ARGTGTTTCATA-----AAAGGATATTTATATCTCTGT	1072
Qy		
Db		
579	ValSerValValPheIleProCysGlyHisLeuValValCys	592
Qy		
Db		

## RESULT 4

A99106  
hypothetical protein orf731 [imported] - Guillardia theta nucleomorph  
C:Species: nucleomorph Guillardia theta  
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
C:Accession: A99106  
R:Bougas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reif  
Nature 410, 1091-1096, 2001  
A:Title: The highly reduced genome of an enslaved algal nucleus.  
A:Reference number: A99082; MUID:11323671; PMID:11323671  
A:Accession: A99106  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-731 <DOU>  
A:Cross-references: GB:AJ010592; NID:q12580677; PIDN:CAC36995.1; GSPDB:GN00151

Alignment Scores:

Pred. No.:	1.22	Length:	731
Score:	95.00	Matches:	109
Percent Similarity:	37.47%	Conservative:	78
Best Local Similarity:	21.84%	Mismatches:	179
Query Match:	3.30%	Indels:	133
DB:	2	Gaps:	23

US-09-771-161A-2 (1-1669) x A99106 (1-731)

Qy	206	CTCAACTCTTTATATATTTCTTTCCATGATATTTTGTACAAACATATATAAAATGTGTTAGATT	265
Db	118	LeuAsnIleIlePheAspThrLysMetTyrPhe-----ArgPheAsnLeuArgIleLeu	135
Qy	266	GTATTTTACCTTCTATATATTTCTTAATCATCTCC-----AGTTAAAGTGTATATATA	316
Db	136	LysSerPheIleHisLysPheLeuLeuThrSerAlaIleIleSerAsnIleAsnTyrPhe	155
Qy	317	TTTATGTTATTCATACAGTTTACAGAGTGTTCCTCAAGTGCCATTCCCTCATGTGCAAGAAG	376
Db	156	PheIleTyrLysLeuSerTyrAsnCysIleGlnThrLeuLysLysIleCysPheLysLys	175
Qy	377	AAATGGAATTATCTCTGAACATACCTCTGTAATCATGTGTCACCAAGAGGAATCATGTGGA	436
Db	176	PheIleIleIle-----	179
Qy	437	TCCTCTCAGCTCCATGAAATAGTGTTCCTCGAAACTTCAAGGTCCTCGCCAGCTCCT	496
Db	180	-----LeuAsnGlnHisSerGlyLys-LeuSerPheGluLysSerAsnAsnIle--	195
Qy	497	CAAGACAATCATTTTATCTAGAAAAGCTCAAGACTG-----	534
Db	196	-----PheValPheTyrIle-PheSerSerValLeuIleLeuIlePhePheAsnTyrT	213
Qy	535	--TTATTTTATGAAGCTGCATCACTGCTCGGAAATCACAGTTTGGGATAGCACCATTCT	592
Db	213	yrLeuPheTyrAsnLysPheIleLeuAspMetLysSerGlnLeuPheSerSerPhePheP	233
Qy	593	GGATCTCAAAAGGCTGCATCTGTGATCACAAGACCACCTCCATGCTCTTCAGC-----	645
Db	233	heIleAspLysAsnIleIlePheSerIleProGlnSerAsnTyrIleIleAsnThrAspI	253
Qy	646	--AATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGCTGCAGCCTGGTATAGCC	703
Db	253	leAsnAsnIleIleTyrIleLeuIleLeuAsnPheThrAsnSerIleLeuPhe-SerLeu	272
Qy	704	CAGCAGTGGATC-----CAGAGCAAAAGGGAAGACATTTGTAACCAAAATGACAGAA	757
Db	273	LysLysTrpIlePheLeuLeuLysLysThrGluTyrMetArgAsnAsnIleIleLeuIle	292
Qy	758	TGCCTTAACAGTCGCTAGATGCCCTCTCTGTCAGGAGACTTGATCATGAAGAGGACTAT	817
Db	293	LeuThrPheSerLysLeuSerAsnLysLeuAsnLysAsnValVal-----Tyr	308
Qy	818	GAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGCTCAGACAAATTAAGTACTAG	877
Db	309	AsnLeuPheAsnLeu-----LysValPheGluLeuLeuLysLysArg	322
Qy	878	GACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGAGATAACA	937
Db	323	PheIleAspAsnAsnHisTyrThrArgLeuLeuPheAspPheIle-----	337
Qy	938	ATGGGTCTTCAGCCTTACCCGGAATACTGTGTTTCTAGATCACCATTCTTTAAATTTA	997
Db	338	-----ValGluIleIleIleLysSerLysAsnTyrLysIle-IleAs	351
Qy	998	CTTCAAAATAAAGCATGTAAGTCACTGTTTTTCAAGAGAAATGTGTTTCATAAAAGGA	1057
Db	351	nGlnLysIleSerThr-IleAsnIleCysPheArgLeuPhePheIlePheHisGluLys-	370
Qy	1058	TATTTATATCTGTGCTTGACTTTTTTATATAAATCCGTGAG-----T	1105
Db	371	-----LeuIleLysIleAsnGluIleLysPheArgT	381
Qy	1106	ATTAAAGCTTTATTGAAGGTTCTTTGGGT---AAATATTAGTCTCCCTCC---ATG	1159
Db	381	yrPheGlyPheIleLysTrpLeuLeuAsnPheLysTyrAsnAsnThrGluValLeuThrI	401
Qy	1160	TGCAGTATTTTTTTTAAATTAATCAAGTAAAAAGTTTGAATTTTGTCTACATAGTCAAT-	1218
Db	401	IeTyrPheIleLeuArgLeuIleLysPheLysTyrIleLysAspAsnLysPheSerL	421



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QY 76 GATTTTCAGGATGAAGCTCTGAGACACTGAGAGAAGGTAAACAAATTAATATATGAGCCAGGA 135
Db 76 GATTTTCAGGATGAAGCTCTGAGACACTGAGAGAAGGTAAACAAATTAATATATGAGCCAGGA 135
QY 262 LysPheGluAsnGluLeuLeuTyrThrAlaMetHisThrSerLeuPheLysSerVal 281
Db 262 LysPheGluAsnGluLeuLeuTyrThrAlaMetHisThrSerLeuPheLysSerVal 281
QY 136 TTCAAAGTCTGGTTCNCTAAAGTATTTCCTCGTCTACACTGCTTTTCCCTTC----- 189
Db 136 TTCAAAGTCTGGTTCNCTAAAGTATTTCCTCGTCTACACTGCTTTTCCCTTC----- 189
QY 282 PheAsnIleLeuGlySer-----PheTyrThrMetArgLeuLeuArgAsn 296
Db 282 PheAsnIleLeuGlySer-----PheTyrThrMetArgLeuLeuArgAsn 296
QY 190 -----AGTTATATGTTATATCTCAACTCTTTATATTT----- 222
Db 190 -----AGTTATATGTTATATCTCAACTCTTTATATTT----- 222
QY 297 LysHisAspGlyAspSerTyrGluLeuValPro-----ValPheAlaLysAsnPro 313
Db 297 LysHisAspGlyAspSerTyrGluLeuValPro-----ValPheAlaLysAsnPro 313
QY 223 -----TCTTTCCATGTTATTTTGACAAACATATAAATGTG 258
Db 223 -----TCTTTCCATGTTATTTTGACAAACATATAAATGTG 258
QY 314 SerLysThrProProCysAsnAspAsnPheLysIlePheSerAspAspIle-----LysLeu 332
Db 314 SerLysThrProProCysAsnAspAsnPheLysIlePheSerAspAspIle-----LysLeu 332
QY 259 TTAGATTGTTATTTTACTTCTATAATTTCTCAATCATCTCCAGTAAAGTGTATATATT 318
Db 259 TTAGATTGTTATTTTACTTCTATAATTTCTCAATCATCTCCAGTAAAGTGTATATATT 318
QY 333 IleGlyCys-----LysIlePheAla 339
Db 333 IleGlyCys-----LysIlePheAla 339
QY 319 TATGTTATTCATTACAGTTCACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAA 378
Db 319 TATGTTATTCATTACAGTTCACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAA 378
QY 340 GlyVal-SerLeuAsnPheSerSerProLysProAlaHisArgPheTyrGluLeuAsnLys 359
Db 340 GlyVal-SerLeuAsnPheSerSerProLysProAlaHisArgPheTyrGluLeuAsnLys 359
QY 379 AATGGAATTATCTCTGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATC 438
Db 379 AATGGAATTATCTCTGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATC 438
QY 359 sThrSerSerAsnLeuSerIleProValLeuGlnLysProSerAsnPheHisSerSerSe 379
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QY 439 CTCTAGCTCCATGAATAAGTGGTCTCTCTCAAACTTCAAGTCCCTGCCAGCTCCCTCA 498
Db 439 CTCTAGCTCCATGAATAAGTGGTCTCTCTCAAACTTCAAGTCCCTGCCAGCTCCCTCA 498
QY 379 rThrGluLeuSerAspAsn-----SerIleHisGlnGlyArgArgAlaValAspProVa 397
Db 379 rThrGluLeuSerAspAsn-----SerIleHisGlnGlyArgArgAlaValAspProVa 397
QY 499 AGACAATGATTTTTTATCTAGAAAAGCTCAAGACTGCTTTATTTATGAAGCTGCATCACTG 558
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QY 397 lValAsnGlnAsnAsnProSerAsnPheGluGluMetIleMetAsnLysLeuAsnLysLe 417
Db 397 lValAsnGlnAsnAsnProSerAsnPheGluGluMetIleMetAsnLysLeuAsnLysLe 417
QY 559 TCTTGAATACAGTTGGATGAGCACCATTCTTGGATCTCAAAAGGCTGCAATCTGTGGA 618
Db 559 TCTTGAATACAGTTGGATGAGCACCATTCTTGGATCTCAAAAGGCTGCAATCTGTGGA 618
QY 417 uPro-----ThrIleAspLysGlnIleLeuLeuGlyThrSerSerLeuThrHisPheGl 434
Db 417 uPro-----ThrIleAspLysGlnIleLeuLeuGlyThrSerSerLeuThrHisPheGl 434
QY 619 TCACAGACCACT----- 631
Db 619 TCACAGACCACT----- 631
QY 434 nAspLysThrThrAlaIleGluHisSerIleAsnLysSerAsnSerLysGlnProProAr 454
Db 434 nAspLysThrThrAlaIleGluHisSerIleAsnLysSerAsnSerLysGlnProProAr 454
QY 632 -----CCATGCTCTTCAGCAATA---ATAAATCCA----- 658
Db 632 -----CCATGCTCTTCAGCAATA---ATAAATCCA----- 658
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Db 454 gPheLysPheGlnLeuProProArgProThrSerAsnThrLeuProLeuGluProGluGl 474
QY 659 -----CTCTCAACTGCAGGAAC----- 676
Db 659 -----CTCTCAACTGCAGGAAC----- 676
QY 474 uGluLeuValThrArgTyrSerValSerSerAspGlyAsnThrValAspGluAlaIleTh 494
Db 474 uGluLeuValThrArgTyrSerValSerSerAspGlyAsnThrValAspGluAlaIleTh 494
QY 677 -----TCAGACGCTCTCAGCCTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGGA 729
Db 677 -----TCAGACGCTCTCAGCCTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGGA 729
QY 494 rLysGlnSerGlnThrPheGluLeuValAsnSerAsnGluPheAsnGluValAsnAlaAs 514
Db 494 rLysGlnSerGlnThrPheGluLeuValAsnSerAsnGluPheAsnGluValAsnAlaAs 514
QY 730 AGACATTGTGAACCAATCAGACAGCCTGCCTTAAACCAGTCGCTAGATGCGCTCTCTGTC 789
Db 730 AGACATTGTGAACCAATCAGACAGCCTGCCTTAAACCAGTCGCTAGATGCGCTCTCTGTC 789
QY 514 nAspValHisLysSerLeuArgGlnAsnCysAlaLysLeuAspPheAspAspSerLysSe 534
Db 514 nAspValHisLysSerLeuArgGlnAsnCysAlaLysLeuAspPheAspAspSerLysSe 534
QY 790 CAGGGACTTGATCATGAAGAGGACTATCAACTTGTGTAGTACCAAGCCTPACAAGGACCTC 849
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QY 554 oLysSerGlySerLeuThrProSerIleAspMetLys----- 566
Db 554 oLysSerGlySerLeuThrProSerIleAspMetLys----- 566
QY 910 AGTACAAAATTTGAAAGATAAACAAATGGTCTTTCAGCTTACCTCCCGGAAATACTTGT 969
Db 910 AGTACAAAATTTGAAAGATAAACAAATGGTCTTTCAGCTTACCTCCCGGAAATACTTGT 969
QY 567 -PheLeuArgLeuGlnAspGluLysMetAspAspLeuGlyAspAsnTyrThrIleLeu 586
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Db 586 uMetSerSerAsnProValSerSerTyrGlyValGlySerLeuTyrLeuPheGlnProLy 606
QY 1009 AAGCATGTAAAGTACTGTTTTCAGAGAAATGTGTTTCATAAAAGGATATTTATATCT 1068
Db 1009 AAGCATGTAAAGTACTGTTTTCAGAGAAATGTGTTTCATAAAAGGATATTTATATCT 1068
QY 606 s-----II 607
Db 606 s-----II 607
QY 1069 CTGTTGCTTTCAGCTTTTATAT-----ATAAAATCCGTGAGTATTTAAAGCTTT 1116
Db 1069 CTGTTGCTTTCAGCTTTTATAT-----ATAAAATCCGTGAGTATTTAAAGCTTT 1116
QY 607 eValCysSerGluLysTyrIleAsnHisGluGluLeuAspAsnMetAsnLeuLysSerLe 627
Db 607 eValCysSerGluLysTyrIleAsnHisGluGluLeuAspAsnMetAsnLeuLysSerLe 627
QY 1117 ATTGAAG----- 1123
Db 1117 ATTGAAG----- 1123
QY 627 uHisArgTrpLeuSerArgSerLeuHisValLeuGlnSerPheSerGlyGluIleGluLe 647
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QY 1124 -----GTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAG 1164
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C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: F82935
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A:Reference number: A82870
A:Accession: F82935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-597 <GLA>
A:Cross-references: GB:AF222894; GB:AF222894; NID:g6899034; PIDN:AAF30492.1; GSPDB:GN001;
A:Experimental source: serovar 3; biovar 1
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A:Gene: dnaX; U0087
A:Genetic code: SGC3
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Pred. No.: 3.59 Length: 597
Score: 90.00 Matches: 67
Percent Similarity: 34.58% Conservative: 53
Best Local Similarity: 19.31% Mismatches: 98
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US-09-771-161A-2 (1-1669) x F82935 (1-597)
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QY 247 ATATAAAATGTTAGATTGTTATTTTACTTCTAT----- 280
Db 247 ATATAAAATGTTAGATTGTTATTTTACTTCTAT----- 280
QY 284 lIleIleAsnValLeu-IleAspTyrLeuIleTyrLeuLysThrAsnAspIleAsnAsnLe 303
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QY 281 -----AATTT 285
Db 281 -----AATTT 285
QY 303 uLysLysValSerValAspGluLeuLysLysMetLeuLeuIleAsnPheAsnGlyAsnTy 323
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QY 286 CCTAATCATCTCCAGTTAAAGTGTATAT-----ATATT 318
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Db 862 LysLeuGluAsnGluLeuGluLysLeuArgAsnGluAsnLysGluValGlyLysGlu 881  
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 Db 882 AlaArgAlaArgAspAlaAlaAsnGlnGlnLeuSerArgAlaAsnLeuLeuAsnLysGlu 901  
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 C;Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 29-Oct-1999  
 C;Accession: S46005; S46578; S46663; S47954; S84650  
 R;Becan, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.  
 submitted to the Protein Sequence Database, August 1994  
 A;Reference number: S45995  
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 A;Experimental source: strain S289C  
 R;Becan, A.M.; Cullin, C.; Grzybowski, E.; Lacroite, F.; Nasr, F.; Ozier-Kalogeropoulos,  
 Yeast 10(Suppl.A), S1-S11, 1994  
 A;Title: The sequence of 29.7kb from the right arm of chromosome II reveals 13 complete  
 A;Reference number: S46569; MUID:94378717; PMID:8091856  
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 A;Experimental source: strain S289C  
 R;Kato, R.; Ogawa, H.  
 submitted to the EMBL Data Library, May 1992  
 A;Description: An essential gene, ESR1, is required for mitotic cell growth, DNA repair  
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 A;Molecule type: DNA  
 A;Residues: 1-196, 'D', 198-2368 <KAT>  
 A;Cross-references: EMBL:D11089; NID:G506874; PIDN:BAA01860.1; PID:d1002337; PID:G506876  
 R;Kato, R.; Ogawa, H.  
 Nucleic Acids Res. 22, 3104-3112, 1994  
 A;Title: An essential gene, ESR1, is required for mitotic cell growth, DNA repair and me  
 A;Reference number: S47953; MUID:94344772; PMID:8065923  
 A;Accession: S47954  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 195-196, 'D', 198-322; 671-744; 848-1796; 1803-2003; 2004-2368 <KA2>  
 A;Cross-references: EMBL:D11088  
 R;Weinert, I.A.; Harlow, D.  
 submitted to the EMBL Data Library, July 1995  
 A;Reference number: S64650  
 A;Accession: S64650  
 A;Molecule type: DNA  
 A;Residues: 1-715, 'P', 717-1254, 'Q', 1256-1275, 'G', 1277-2368 <WE1>  
 A;Cross-references: EMBL:U31109; NID:G950172; PIDN:AAA74482.1; PID:G950173  
 C;Genetics:  
 A;Gene: SGD:ESR1; MEC1  
 A;Cross-references: SGD:S0000340; MIPS:YBR136W  
 A;Map position: 2R  
 C;Function:  
 A;Description: required for mitotic cell growth, DNA repair, and meiotic recombination  
 C;Keywords: ATP; P-loop; purine nucleotide binding; transmembrane protein  
 F;74-90/Domain: transmembrane #status predicted <TM1>  
 F;218-234/Domain: transmembrane #status predicted <TM2>  
 F;717-787/Domain: transmembrane #status predicted <TM3>  
 F;922-938/Domain: transmembrane #status predicted <TM4>  
 F;1152-1169/Domain: transmembrane #status predicted <TM5>  
 F;1288-1304/Domain: transmembrane #status predicted <TM6>  
 F;1315-1331/Domain: transmembrane #status predicted <TM7>

F;1682-1689/Region: nucleotide-binding motif A (P-loop)  
 F;1918-1934/Domain: transmembrane #status predicted <TM8>  
 F;2126-2142/Domain: transmembrane #status predicted <TM9>  
 F;1688/Binding site: ATP/GTP (Lys) #status predicted  
 Alignment Scores:  
 Pred. No.: 4.63 Length: 2368  
 Score: 89.50 Matches: 64  
 Percent Similarity: 36.36% Conservative: 44  
 Best Local Similarity: 21.55% Mismatches: 126  
 Query Match: 3.11% Indels: 63  
 DB: 2 Gaps: 13  
 US-09-771-161A-2 (1-1669) x S46005 (1-2368)  
 QY 359 CACCTATGTGCAAGAGAA-----ATGGAATTATCTCTGAACATACCT 403  
 Db 491 HisLeuGluAspIleGluLysThrGlyAsnProPheValArgIleAsnProAsnArgPro 510  
 QY 404 GTAAATCATGTGTCACAGAGGAATCATGTGATCTCTCAG-----CTCCAT 451  
 Db 511 -----GluAlaGlyLysSerGluIlePheArgIleLeuHis 523  
 QY 452 GAAATAGTGTCTCTCAAACTTCAAGTCCCTCCAGCTCTCAAGACATGATTT 511  
 Db 524 SerAsn-----PheLeuSerHisProAsnIleAspGluPhe 535  
 QY 512 TTATCTAGAAAAAGCTCAAGACTGTTATTATTATGAAGCTGCATCAC----- 556  
 Db 536 ---SerGluSerLeuLeuSerGlyIleLeuPheSerLeuHisArgIlePheSerHisPhe 554  
 QY 557 -----TGCTCTGAAATCACAGTGGGATAGCACCATTCTTGATCTCAA 601  
 Db 555 GlnProProLysLeuThrAspGlyAsnGlyGlnIleAsnLysSerPheLysLeuValGln 574  
 QY 602 AGGGCTGCATTCTGTGATCACAGACCATCTCCATGCTCTTCAGCAATAATAATCCACTC 661  
 Db 575 LysCysPheMetAsnSerAsnArgTyrLeuArgLeuLeuSerThrArgIleLeuProLeu 594  
 QY 662 -----TCAACTGCAGGAAATCAGAACCTGTGACGCTGTGTATAGCCAGAGTGG 712  
 Db 595 PheAsnIleSerAspSerHisAsnSerGluAspGluHisThrAlaThrLeuIleLysPhe 614  
 QY 713 ATCCAGAGCAAAAGGAGACATTTGTG-----AACCAATG 748  
 Db 615 LeuGlnSerGlnLysLeuProValValLysGluAsnLeuValIleAlaTrpThrGlnLeu 634  
 QY 749 ACAGAGCTGCTTAACACAGTCGTAGATGCCCTTCTGTCTCCAG-----GACTTGATC 802  
 Db 635 ThrLeuThrThrSerAsnAspValPheAspThrLeuLeuLeuLysLeuIleAspIlePhe 654  
 QY 803 ATGAAAGAGAGACTATGAACCTTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCAGACAA 862  
 Db 655 AsnSerAspAspTyrSerLeuArgIleMetMetThrLeuGlnIleLysAsnMetAlaLys 674  
 QY 863 TTACTAGACACTACTGACATCCAA---GGAGAGAATTTGCCAAAGTATAGTACAAAAA 919  
 Db 675 IleLeuLysLysThrProTyrGlnLeuLeuSerProIleLeuProValLeuLeuArgGln 694  
 QY 920 TTCAAGATTAAC-----AAACAAATGGGTCTTCAGCCTTTACCCGGAAATACTTGTG 970  
 Db 695 LeuGlyLysAsnLeuValGluArgLysValGlyPheGlnAsnLeuIleGluLeuLeuGly 714  
 QY 971 GTTCTAGATCACCATCTTTAAATTTACTTTCAAAATAAAAGCATGTAAGTACTGTTTT 1030  
 Db 715 TyrSerLysThrIleLeuAspIlePheGlnArgTyrIleIleProTyrAlaIle 734  
 QY 1031 CAA-----GAAGAAATGTTTTCATAAAAGGATATTTATATCTCTGT 1072  
 Db 735 GlnTyrLysSerAspValLeuSerGluIleAlaLysIle-----MetCys 749  
 QY 1073 TGCTTTGACCTTTTATATAAAATCCGTGATGATTAAAGCTTTATTGAAG 1123



Db 750 AspGlyAspThrSerLeulleAsnGlnMetLysValAsnLeuLeuLysLys 766  
RESULT 12  
MADS box protein DRFH200 - garden snapdragon  
C:Species: Antirrhinum majus (garden snapdragon)  
C:Date: 11-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 20-Jun-2000  
C:Accession: S71757  
EMBO J. 15, 4330-4343, 1996  
R: Davies, B.; Egea-Cortines, M.; de Andrade Silva, E.; Saedler, H.; Sommer, H.  
A: Title: Multiple interactions amongst floral homeotic MADS box proteins.  
A: Reference number: S71756; MUID: 970151333; PMID: 8861961  
A: Accession: S71757  
A: Status: nucleic acid sequence not shown  
A: Molecule type: mRNA  
A: Residues: 1-242 <DAV>  
A: Cross-references: EMBL: X95469; NID: g1239958; PIDN: CAA64743.1; PID: g1239959  
C: Superfamily: transcription factor squa; serum response factor DNA-binding domain homolog  
C: Keywords: DNA binding; transcription regulation  
F: 2-57/Domain: serum response factor DNA-binding domain homology <SRF>  
F: 94-159/Domain: domain K <KDO>  
  
Alignment Scores:  
Pred. No.: 4.07 Length: 242  
Score: 89.00 Matches: 48  
Percent Similarity: 34.36% Conservative: 30  
Best Local Similarity: 21.15% Mismatches: 65  
Query Match: 3.09% Indels: 84  
DB: 2 Gaps: 7  
  
US-09-771-161A-2 (1-1669) x S71757 (1-242)  
  
QY 362 CTATGTGCAAGCAAGAAATGGAATTTATCTCTCAACATACCTGTAATCATGGTCCACAA 421  
Db 38 LeuCysAsp-----AlaGluValAlaLeuIlellePheSerAsnArgGlyLysLeu 54  
  
QY 422 GAGGAATCATGTGGATCTCTCAGCTCCATGAA-----AAT 457  
Db 55 TyrGluPheCysSerSerThrSerMetLeuAsnThrLeuGluArgTyrGlnLysCysAsn 74  
  
QY 458 AGTGGTCTCTCAAGTTCAGAGTTCAGAGTCCCTCCAGACAAATGATTTTATCT 517  
Db 75 TyrGlyProGluThrAsnValSer----- 83  
  
QY 518 AGAAAGCTCAAGACTGTTATTTATGAAGTGCATCTGCTCTGGAATCACAGTTGG 577  
Db 83 ----- 83  
  
QY 578 GATAGACCACTTTCTGGATCTCAAGGGTGCATCTCTGTGATCACAGACCCTCATGC 637  
Db 83 ----- 83  
  
QY 638 TCTTCAGCAATAAATCCACTCTCAACTGCGAGGAATCTCAGAGCTCTGCGAGCTGCT 697  
Db 84 -----ThrArgGluAlaLeuGluLeuSer 91  
  
QY 698 ATAGCCAGCAGTGGATCCAGACGAAA---AGGGAAGACATTGTGAACCAAAATGACAGAA 754  
Db 92 SerGlnGlnGluTyrLeuLysLeuLysAlaArgTyrGluAlaLeuGlnArgSerGlnArg 111  
  
QY 755 GCCTGCTTAACAGCTCGCTAGATGCCCTTCTGTCAGGAGCTTGTATGATGAAGAGGAC 814  
Db 112 AsnLeuLeuGlyGluAspLeuGlyProLeuAsnSerLysGluLeuLeuSerLeuGluArg 131  
  
QY 815 TATGAACCTTTAGTACCAGCTCAAGGACCTCAAAAGTCAGACAAATTACTAGACACT 874  
Db 132 GlnLeuAspMetSerLeuLysGlnIleArgSerThrArgThrGlnAlaMetLeuAspThr 151  
  
QY 875 ---ACTGACATCCAGGAGAAATTTGCC-----AAAGCTTATAGTACAA 916  
Db 152 LeuThrAspLeuGlnArgLysGluHisAlaLeuAsnGluAlaAsnArgSerLeuLysHis 171  
  
QY 917 AAATTGAAGATAACAAACAAATGGGTCTTTCAGCCTTACCCG-----GAAATACTT 967

Db 172 ArgLeuMetAspGlySerGlnIleSerLeuGlnTrpAsnProAsnAlaGluAspHisVal 191  
QY 968 GTGGTTTCTAGATCACCATCT 988  
Db 192 GlyTyrGlyArgGlnProSer 198  
  
RESULT 13  
B81996  
RNA polymerase sigma factor NMA0049 [imported] - Neisseria meningitidis (strain Z2491 ser  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: B81996  
R: Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A: Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A: Reference number: B81775; MUID: 20222556; PMID: 10761919  
A: Accession: B81996  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-283 <PAR>  
A: Cross-references: GB: AL162752; GB: AL157959; NID: g7378778; PIDN: CAB83366.1; PID: g7378824  
A: Experimental source: serogroup A, strain Z2491  
C: Genetics:  
A: Gene: NMA0049  
  
Alignment Scores:  
Pred. No.: 4.14 Length: 283  
Score: 89.00 Matches: 53  
Percent Similarity: 35.68% Conservative: 28  
Best Local Similarity: 23.35% Mismatches: 86  
Query Match: 3.09% Indels: 60  
DB: 2 Gaps: 9  
  
US-09-771-161A-2 (1-1669) x B81996 (1-283)  
  
QY 500 GACAAATGATTTTATCTAGAAAAGCTCAAGAC-----TGT 535  
Db 42 AspAsnProLeuLeuGluArgLysAspThrAspGluPheSerAspAlaGluPheSerHis 61  
  
QY 536 TATTTTATGAAGTGCATCCTGCTGGAATCACAGTTGGAT-----AGCACCATT 589  
Db 62 TyrThrAlaProAlaArgGlnIleGlyGlyAspGlyGlyGluAspMetLeuSerAsnIle 81  
  
QY 590 TCTGGATCTCAA-----AGGGTGCATCTCTGTGATCACAAGACCACT 631  
Db 82 AlaGlyGluGlnAspPheLysGlnTyrLeuHisAlaGlnValCysGluHisProLeuSer 101  
  
QY 632 CCATGCTCTTTCAGCAATAATAATCCACTCTCACTGAGGAACTCAGAACGTCGTGCAG 691  
Db 102 AspGlnGluSerAlaCysValHisIleLeuIleAspPheLeuAspGlu----- 117  
  
QY 692 CTGTGTATAGCCACAGTGGATCCAGACCAAGGAGACATTTGTGAAC----- 742  
Db 118 -----GlnGlyTyrLeuThrAspSerIleGluAspIleLeuAspHisThrPro 133  
  
QY 743 -----CAATGACAGAACCTGCTTAACTACAGTCTGATGCTGCTT----- 784  
Db 134 LeuGluTrpMetLeuAspGluAlaMetLeuLysGlnAlaLeuThrAlaLeuLysLysPhe 153  
  
QY 785 -----CTGTCCAGGACTTCATCATGAAA---GAGGAC 814  
Db 154 AspProAlaGlyValAlaAlaAlaAspLeuAsnGluSerLeuIleLeuGlnIleGluArg 173  
  
QY 815 TATGAACCTTTAGTACCAGCTCAAGGACCTCAAAAGTCAGACAAATTACTAGACACT 874  
Db 174 SerGlyGluCysAlaAlaLysProSerAlaLeuHisIleValArgAsnAlaLeuAspSer 193  
  
QY 875 ACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATACAAA 934  
Db 194 IleAspGlyAsnArgSerGlnThrLeuAlaArgIleLysLysArgLeuProGlnThrAsp 213

QY 935 CAA-----ATGGGCTTCAGCTTACCCGGAAATA 964  
Db 214 SerGlyThrLeuGluAlaLeuAspLeuLeuAlaSerLeuAsnProPheProAlaVal 233  
QY 965 CTTGTGTTTCTAGATCACCATCT-----TTAAATTTACTTTCAA 1003  
Db 234 GlyPheAlaSerSerThrProThrProTyrSerAspGluAlaLeuAlaAsnLeuLeuAla 253  
QY 1004 AATAAAGCATGTAAAGTACT 1024  
Db 254 PheArgGlyMetGluValSer 260  
RESULT 14  
T33922  
hypothetical protein Y8A9A.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T33922  
R: Courtney, L.; Langston, Y.; Drone, K.; Mead, K.  
submitted to the EMBL Data Library, February 1999  
A:Description: The sequence of C. elegans cosmid Y8A9A.  
A:Reference number: Z21439  
A:Accession: T33922  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1360 <COU>  
A:Cross-references: EMBL:AF125461; PIDN: AAD12852.1; GSPDB: GNO0020; CESP: Y8A9A.2  
A:Experimental source: strain Bristol N2; clone Y8A9A  
C:Genetics:  
A:Gene: CESP: Y8A9A.2  
A:Map position: 2  
A:Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3; 848/2; 944/2; 1044/2; 1

Alignment Scores: 4.87 Length: 1360  
Pred. No.: 89.00 Matches: 39  
Score: 33.68% Conservative: 25  
Best Local Similarity: 20.53% Mismatches: 68  
Query Match: 3.09% Indels: 58  
Gaps: 7  
DB:

US-09-771-161A-2 (1-1669) x T33922 (1-1360)

QY 341 AGTGTTCACAGTTCACCTATGTGACAGAGAAATGGAATTTATCTCTGAACATA 400  
Db 972 ThrValSerGlyThrGlnHisLeuGlyProGlnPro-----AsnTyr 986  
QY 401 CCTGTAATCATGTGTCACAGAGATCATCTGTGATCCTCTCAGCTCCATGAAAT--- 457  
Db 987 ThrThrProTyrAlaProTyrAspProThrCysThrAspAsnCysCysProGluThrGly 1006  
QY 458 -----AGTGGTTCCTCGAAACTTCAAGCTCCCTGCCAGCTCCTCTCAAGAC 502  
Db 1007 IleTrpSerAspTrpThrSerThrProAsnGlnCysArgAspTyrCysGlySerCysGly 1026  
QY 503 AATGATTTTTTATCTAGAAAAGCTCAAGAC----- 532  
Db 1027 AsnGlnThrArgThrArgThrCysThrSerAspAlaAspGlyCysProCysGlnGlyPro 1046  
QY 533 -----TGTTATTTTATGAAGCTGCATCACTGT 559  
Db 1047 ThrThrIleThrGluProCysGlyThrGlyValCysTyrPheProArgLeuSerCysCys 1066  
QY 560 CTTGGAATACAGTGTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGAT 619  
Db 1067 ProGly-----TyrThrAlaThrValGluGlyAsnGln----- 1077  
QY 620 CACAGACCATCTCCATGTCTTTCAGCAATAATAATCCA-----CTCTCACTGCAGGA 673  
Db 1078 HisIleCysGlyProLeuThrThrAlaValAlaAspProAspLysLeuAsnThrCysGly 1097  
QY 674 AACTCAGACGCTGTCAGCGCTTGATAGCCAGCAGTGGATCCAG----- 718

Db 1098 ValSerCysCysProSerAlaGlyIleTrpGlyGluTrpValSerValSerGlyCysAsn 1117  
QY 719 -----AGCAAAAGGGAAGACATTGTGCAACCAAAATG 748  
Db 1118 AspThrCysGlySerCysGlyGlnGluThrArgLysArgLysCysLeuSerLeuGlnTyr 1137  
QY 749 ACAGAAGCTGCTTTAACACGATCGCTAGAT 778  
Db 1138 GlyCysAlaCysThrGlyAsnAlaThrAsp 1147  
RESULT 15  
A55117  
tsq24 protein - mouse  
N:Alternate names: bime protein homolog  
C:Species: Mus musculus (house mouse)  
C>Date: 28-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 17-Mar-2000  
C:Accession: A55117  
R: Starborg, M.; Brundell, E.; Gell, K.; Hoeoeg, C.  
J. Biol. Chem. 269, 24133-24137, 1994  
A:Title: A novel murine gene encoding a 216-kDa protein is related to a mitotic checkpoint  
A:Reference number: A55117; MUID: 95014147; PMID: 7929068  
A:Accession: A55117  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1944 <STR>  
A:Cross-references: GB: X80169; NID: g562764; PIDN: CAA56450.1; PID: g642252  
C:Genetics:  
A:Gene: tsq24  
C:Superfamily: bime protein

Alignment Scores: 5.06 Length: 1944  
Pred. No.: 89.00 Matches: 52  
Score: 37.56% Conservative: 25  
Best Local Similarity: 25.37% Mismatches: 72  
Query Match: 3.09% Indels: 56  
Gaps: 10  
DB:

US-09-771-161A-2 (1-1669) x A55117 (1-1944)

QY 326 TCATTACAGTTACAGAGTGTTCAGTGCCATT-----CACTATGTGACAGAGAA 379  
Db 291 ThrLeuGlnAsnAlaThrThrSerSerSerLeuThrAlaHisLeuArgSerLeuSerLys 310  
QY 380 ATGGAATTTCTCTGAACATACCTGTAATCAT-----GGTCCACAAGAGGAA 427  
Db 311 GlyGluSerProValAlaSerProPheGlnAsnTyrSerSerIleHisSerArg 330  
QY 428 TCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCTCTGAAACTTCAAGGTCCCTG 487  
Db 331 SerThrSerSerProSerLeuHisSerArgSer----- 341  
QY 488 CCAGCTCCTCAAGACAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAG 547  
Db 342 ProSerIleSerAsnMetGlyValLeuSerArgAla----- 353  
QY 548 CTGCATCATGTCTCT-----GGAATACAGTTGGATAGCACCATTTCTGGATCTCAA 601  
Db 354 -----HisSerProAlaLeuGlyValHisSerPhe-----SerGlyAlaGln 367  
QY 602 AGGCTGCATTTCTGTGATCAAGACCATCTCCATGCTCTTCACAATAATAATCCACTC 661  
Db 368 ArgPheAsnLeuSerSerHisSerGlnSerProLysArgHisSerIleSerHisSerPro 387  
QY 662 TCAACTCCAGAAACTCAGAACCTCTGCAGCTGGTATACCCCGCAGTGGATCCAGAGC 721  
Db 388 SerGlySerPheAsnAspSerPheLeuAlaPro----- 398  
QY 722 AAAAGGAAGACATTTGTGAACCAAAATGACAGAGACCTGCTTAACCAAGTCGTAGATGCC 781  
Db 399 GluThrGluProIleVal-----ProGluLeuCysIle----- 409  
QY 782 CTTCTGTCCAGGAGCTTGATCATGAAAGAGGACTATGAATCTGTTAGTACCAGCCTACA 841

```

Db      410 -----AspHisLeuTrpThrGluThrLeuProAsnIleArgGluLysAsnSer 425
Qy      842 AGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGAGGAGAGAATTGCCC 901
Db      426 GlnAlaSerLysVal-----PheIleThrThrAspLeuCysGlyGlnLysPheLeu 442
Qy      902 AAAGTTATAGTACAA 916
Db      443 CysPheLeuValGlu 447

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Search completed: March 29, 2004, 14:24:54  
Job time : 50.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:14:22 ; Search time 20.5 Seconds

(without alignments)  
8478.545 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880  
Sequence: 1 acctgtttatccagata.....caacagcgtgatgtgtaaaa 1669

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-O=/cpn2.1/USPTO.spool.p/US09771161/runat.29032004.124824.13664/app.query.fasta\_1.1863  
-DB=SwissProt 42 -OPMT=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=blosum62 -TRANS=human40.cdi  
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-MODES=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09771161 @CGN 1 1 19 @runat.29032004.124824.13664 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt 42.2

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182	41.0	540	1 RIK2_HUMAN	O43353 h receptor-
2	839.5	29.1	539	1 RIK2_MOUSE	P58801 mus musculus
3	122.5	4.3	953	1 CAR4_HUMAN	Q9Y239 homo sapien
4	100.5	3.5	943	1 YLW5_CAEEL	P34408 caenorhabdi
5	98	3.4	618	1 BIR2_HUMAN	Q13490 homo sapien
6	96.5	3.4	953	1 CAR4_MOUSE	Q8bnb0 mus musculus
7	94	3.3	357	1 REP1_ZYGBA	P13776 zygosacchar
8	92	3.2	612	1 BIR2_MOUSE	Q62210 mus musculus
9	90	3.1	708	1 KHS1_YEAST	P38690 saccharomyc
10	89.5	3.1	2368	1 ESR1_YEAST	P38111 saccharomyc
11	89.5	3.1	3130	1 DPOZ_HUMAN	O60573 homo sapien
12	89	3.1	1944	1 ANCL_MOUSE	P53995 mus musculus
13	88	3.1	358	1 PIAP_PIG	O62640 sus scrofa
14	88	3.1	524	1 T2FA_XENLA	Q04870 xenopus lae
15	88	3.1	8797	1 SNE1_HUMAN	Q8nf91 homo sapien
16	87.5	3.0	406	1 YMX2_CAEEL	P34510 caenorhabdi
17	87	3.0	341	1 Y173_BORBU	O51195 borrelia bu
18	87	3.0	400	1 RT0A_DICDI	P54681 dictyostell

19	86.5	3.0	365	1 SYAP_MOUSE	Q9d5v6 mus musculu
20	86.5	3.0	407	1 MYC_ASTVU	Q17103 asterias vu
21	86.5	3.0	976	1 YBS4_YEAST	P38244 saccharomyc
22	86.5	3.0	1088	1 MRTB_HUMAN	Q9ulh7 homo sapien
23	85.5	3.0	513	1 MATK_CYRRA	Q8wlv4 cyrilla rac
24	85.5	3.0	3898	1 POLG_HCVA	P19712 hog cholera
25	85	3.0	627	1 ABPX_YEAST	Q08641 saccharomyc
26	85	3.0	690	1 LIP_STAAN	P10335 staphylococ
27	85	3.0	721	1 MX_ANAPL	P32338 anas platyr
28	84.5	2.9	224	1 AGI9_LYCES	Q42464 lycopersico
29	84.5	2.9	733	1 ACE1_TIRE	Q9p8w3 trichoderma
30	84	2.9	690	1 LIP_STAAN	Q8n5v2 staphylococ
31	83.5	2.9	266	1 KUR5_MOUSE	Q60852 mus musculu
32	83.5	2.9	486	1 ZASA_HUMAN	Q15172 h serine/th
33	83.5	2.9	604	1 BIR3_HUMAN	Q13489 homo sapien
34	83.5	2.9	805	1 HIPA_XENLA	Q918a9 xenopus lae
35	83.5	2.9	1822	1 SC72_SCHPO	Q9p7v5 schizosacch
36	83.5	2.9	2567	1 M18B_HUMAN	Q8iugs homo sapien
37	83.5	2.9	2813	1 VWF_CANFA	Q28295 canis famli
38	83	2.9	853	1 AHR_RAT	P41738 rattus norv
39	83	2.9	1113	1 PHG1_HUMAN	Q9u1l1 homo sapien
40	83	2.9	1499	1 PGF1_HUMAN	Q9v4g8 homo sapien
41	82.5	2.9	374	1 HAT1_YEAST	Q12341 saccharomyc
42	82.5	2.9	495	1 ACH3_BOVIN	Q07263 bos taurus
43	82.5	2.9	647	1 L1K1_RAT	P53669 rattus norv
44	82	2.8	489	1 YEN5_YEAST	P39370 saccharomyc
45	82	2.8	933	1 N106_SCHPO	O14310 schizosacch

#### ALIGNMENTS

##### RESULT 1

ID	RIK2_HUMAN	STANDARD;	PRT;	540 AA.
AC	O43353			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)			
DE	(RIP-like interacting CLARP kinase) (Receptor-interacting protein 2)			
DE	(RIP-2) (CARD-containing interleukin-1 beta converting enzyme			
DE	associated kinase) (CARD-containing IL-1 beta ICE-kinase).			
GN	RIPK2 OR RICK OR RIP2 OR CARDIAC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.			
RX	MEDLINE=98241596; PubMed=9575181;			
RA	Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;			
RT	"RICK, a novel protein kinase containing a caspase recruitment domain,			
RT	interacts with CLARP and regulates CD95-mediated apoptosis.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.			
RC	TISSUE=Endothelial cells;			
RX	MEDLINE=98307936; PubMed=9642260;			
RA	McCarthy J.V., Ni J., Dixit V.M.;			
RT	"RIP2 is a novel NF-kappaB-activating and cell death-inducing			
RT	kinase.";			
RL	J. Biol. Chem. 273:16968-16975 (1998).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.			
RX	MEDLINE=98381580; PubMed=9705938;			
RA	Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,			
RA	Mattmann C., Tschopp J.;			
RT	"Identification of CARDIAC, a RIP-like kinase that associates with			
RT	caspase-1.";			
RL	Curr. Biol. 8:885-888(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Ozersky P., Holmes A., Broy M.;			



```
Db 533 AnLeuLeuGlnAsnLysSerMet 540
RESULT 2
ID RIK2 MOUSE STANDARD; PRT; 539 AA.
AC P58801;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).
GN RIKP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21891093; PubMed=11894097;
RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
RT "Involvement of receptor-interacting protein 2 in innate and adaptive
immune responses.";
RL Nature 416:190-194(2002).
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to CFLAR/CARP and CASP1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex (By similarity). (Probable).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF461040; AAL96436.1; -
CC MGD; MGI:1891456; Rikp2.
CC DR InterPro; IPR001315; CARD.
CC DR InterPro; IPR007019; Prot_kinase.
CC DR InterPro; IPR008271; Ser_thr_kin_AS.
CC DR Pfam; PF00619; CARD; 1.
CC DR Pfam; PF00609; pkinase; 1.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR SMART; SM00114; CARD; 1.
CC DR PROSITE; PS0209; CARD; 1.
CC DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN_KINASE.
FT DOMAIN 431 533 CARD.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP (BY SIMILARITY).
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;

Alignment Scores:
Pred. No.: 5,29e-68 Length: 539
Score: 839.50 Matches: 164
Percent Similarity: 80.70% Conservative: 20
Best Local Similarity: 71.93% Mismatches: 43
Query Match: 29.15% Indels: 1
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RT that activates NF-kappaB.";  
RL J. Biol. Chem. 274:12355-12358(1999).  
RN [2]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.  
RC MEDLINE=99262599; PubMed=10329646;  
RX TISSUE=Breast;  
RA Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrilo R.,  
RA Merino J., Liu D., Ni J., Nunez G.;  
RT "Nod1, an Apaf-1-like activator of caspase-9 and nuclear factor-  
RT kappaB.";  
RL J. Biol. Chem. 274:14560-14567(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=21264704; PubMed=11058605;  
RA Inohara N., Ogura Y., Chen F.F., Muto A., Nunez G.;  
RT "Human Nod1 confers responsiveness to bacterial lipopolysaccharides.";  
RL J. Biol. Chem. 276:2551-2554(2001).  
RC -!- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-  
CC B activity via RICK (CARDIAP, RIP2) and IKK-gamma. Confers  
CC responsiveness to intracellular bacterial lipopolysaccharides  
CC (LPS).  
CC -!- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD  
CC interaction.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal  
CC muscle, pancreas, spleen and ovary. Also detected in placenta,  
CC lung, liver, kidney, thymus, testis, small intestine and colon.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
CC -!- SIMILARITY: Contains 1 NACHT domain.  
CC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.  
CC  
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CC  
CC -----  
CC EMBL; AF126484; AAD29125.1; -;  
CC EMBL; AF149774; AAD43922.1; -;  
CC EMBL; AF113925; AAD28350.1; -;  
CC EMBL; BC040339; AAH40339.1; -;  
CC EMBL; HGNC:16390; CARD4.  
CC MIM; 605980; -;  
CC DR GO; 0008656; F: caspase activator activity; TAS.  
CC DR GO; 0006915; P: apoptosis; TAS.  
CC DR GO; 0007165; P: signal transduction; TAS.  
CC DR InterPro; IPR001315; CARD.

DR InterPro; IPR007091; LRR RNinh.  
DR InterPro; IPR007111; NACHT\_NTPase.  
DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF05729; NACHT; 1.  
DR PROSITE; PS50209; CARD; 1.  
DR PROSITE; PS50837; NACHT; 1.  
KW Apoptosis; ATP-binding; Repeat; Leucine-rich repeat.  
FT DOMAIN 15 105  
FT DOMAIN 196 531  
FT DOMAIN 202 209  
FT REPEAT 632 656  
FT REPEAT 702 725  
FT REPEAT 727 750  
FT REPEAT 755 778  
FT REPEAT 783 806  
FT REPEAT 839 862  
FT REPEAT 867 891  
FT REPEAT 895 918  
FT REPEAT 923 946  
FT MUTAGEN 41  
FT MUTAGEN 208  
FT MUTAGEN 447 447  
FT CONFLICT 953 AA; 107690 MW; 0A9D5FC6487E21A CRC64;  
SQ SEQUENCE 953 AA; 107690 MW; 0A9D5FC6487E21A CRC64;  
V->Q: ABOLISHES CASPASE-9 ACTIVATION AND  
INTERACTION WITH RICK.  
K->R: REDUCES CASPASE-9 ACTIVATION.  
R -> H (IN REF. 3).  
Alignment Scores:  
Pred. No.: 0.00403 Length: 953  
Score: 122.50 Matches: 39  
Percent Similarity: 55.24% Conservative: 19  
Best Local Similarity: 37.14% Mismatches: 36  
Query Match: 4.25% Indels: 11  
DB: 1 Gaps: 6  
US-09-771-161A-2 (1-1669) x CAR4\_HUMAN (1-953)  
QY 707 CAGTGCATCCAGGCAAAAGGGAAGACATTGTGAACCAATGACAGAGCC---TGCCTT 763  
DB 21 GlnLeuLeuLysSerAsnArgGluLeuValThrHisIleArgAsnThrGlnCysLeu 40  
QY 764 AACGAGTCGCTAGATGCCCTTCCTGTCACGGGACTTGATCATGAAAGAGGACTATGAATT 823  
DB 41 -----ValAspAsnLeuLeuLysAsnAspTyrPheSerAlaGluAspAlaGluIle 57  
QY 824 GTTAGTACCAAGCTCAGAGGACCTCAAAAGTCAGCAATTTACTAGACACTACTGACATC 883  
DB 58 ValCysAlaCysProThrGlnProAspLysValArgLysIleLeuAspLeuValGlnSer 77  
QY 884 CAAGGAGAA-----GAATTGCAAAAGTTATAGTACAAAATTTGAAAGATACAA 934  
DB 78 LysGlyGluGluValSerGluPheLeuTyrLeuLeuGlnGlnLeuAlaAsp---Ala 96  
QY 935 CAAATGGTCTTCAGCCTTACCGGAAATACTTGTGGTTCTTAGATCACCATCTTTAAAT 994  
DB 97 TyrValAspLeuArgProTrp-----LeuLeuGluIleGlyPheSerProSerLeu--- 113  
QY 995 TTACTTCAAAATATAA 1009  
DB 114 LeuThrGlnSerLys 118  
RESULT 4  
YLW5 CAEEL STANDARD; PRT; 943 AA.  
AC P34408;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical protein P22B7.5 in chromosome III.  
GN P22B7.5  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]



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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fullon L., Gardner A., Green P., Hawkins J., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonnhammer E., Staden K.,
RA Sulston J., Thierry-Nieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkins-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -!- SIMILARITY: Contains 1 GoLoco domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
CC EMBL; L12018; AAA65459.1; --
CC PIR; S44636; S44636.
CC HSP; P08622; 1XBL.
CC WormPep; F22B7.5; CE00158.
CC InterPro; IPR002939; DnaJ C.
CC InterPro; IPR001305; DnaJ_CXXCXXGXG.
CC InterPro; IPR001623; DnaJ N.
CC InterPro; IPR003109; GoLoco.
CC InterPro; IPR008971; HSF40_DnaJ_pap.
CC InterPro; IPR003095; Hsp DnaJ.
CC InterPro; IPR008941; TPR-like.
CC Pfam; PF00226; DnaJ; 1.
CC Pfam; PF01556; DnaJ C; 1.
CC Pfam; PF00684; DnaJ_CXXCXXGXG; 1.
CC Pfam; PF02188; GoLoco; 1.
CC PRINTS; PR00625; DNAJPROTEIN.
CC SMART; SM00271; DnaJ; 1.
CC SMART; SM00390; GoLoco; 1.
CC PROSITE; PS00636; DnaJ 1; 1.
CC PROSITE; PS50076; DnaJ 2; 1.
CC PROSITE; PS50877; GOLOCO; 1.
KW Hypothetical protein.
FT DOMAIN 424 445 GOLOCO.
FT DOMAIN 531 595 J-DOMAIN.
SQ SEQUENCE 943 AA; 105926 MW; 9847F95977E0418E CRC64;

Alignment Scores:
Pred. No.: 0.394 Length: 943
Score: 100.50 Matches: 45
Percent Similarity: 38.36% Conservative: 44
Best Local Similarity: 19.40% Mismatches: 84
Query Match: 3.49% Indels: 59
DB: 1 Gaps: 10

US-09-771-161A-2 (1-1669) x YLM5_CABEL (1-943)
QY 392 CTGAACATACCTGTAATCATGGTCCACAAAGGAATCATGTGGATCCTCTCAGCTCCAT 451
Db 349 IieAspValAlaWeCAsnGlnGluArgSerGluThrAlaThrAspGlnAspValCysLeu 368
QY 452 GAAATAGTGGTCTCTCTGAACTTCAAGGTCCTGCCAGCTCCTCAAGACATGATTTT 511
Db 369 AlaIleAspSerSerProAspProThrSerSer-----AsnAspMet 382
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCATGTCTCGAATATC 571

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Db 383 IieAsnLys-----PheValValGluLeuGluHieAlaThrAsnValGlu 397
QY 572 AGTTGGATAGTACCACCATTTCTGGA----- 595
Db 398 ThrTrpGluMetIleValAsnGlyIleIleAspAspGlnLysLysProValAlaIleGlu 417
QY 596 -----TCTCAAAGGCTGCA 610
Db 418 LysLysGluAsnGluGluProValAspMetMetAspLeuIlePheSerMetSerArg 437
QY 611 TTCTGTGATCACAAGACACCTCCATGCTCTTCAGCAATAATA-----AATCACTCTCA 664
Db 438 MetAspAspGlnArgThrGluLeuProAlaAlaArgPheIleProProArgProValSer 457
QY 665 ACTGCAGGA-----AACTCAGAACCTGTCAGCCTGTGTATAGCCCGCAGCTGG 712
Db 458 SerAlaSerLysLysThrThrLysSerHisArgIleLeuProGlyLeuArgAlaAsnTrp 477
QY 713 ATCCAGACAAAGGAAGACATGTGAACCAATGACAGAACCTGCTTAAACAGTGG 772
Db 478 ThrLysValGlnSerMetLysValLeuGlyMetPheVal-----LeuAsnArgSer 494
QY 773 CTAGATGCCCTCTCTCCAGGACTTGATCATGAAAGAGGACTATGAACCTGTTAGTACC 832
Db 495 ---SerGlyLeuIleHisArgSerValProLeuLeuAlaGln-----ValSerThr 510
QY 833 AAGCCTACAAGGACCTCAAAAGTACAGACAACTTACTAGACACTTACTGACATCAAGGAGAA 892
Db 511 ProThrThrSerThrThrLysLeuAlaGlnLeuHisThrThrHisAlaLeuSerLysGlu 530
QY 893 GAATTGGCCAAAGTTATA---GTACAAAATTTGAAGATAACAAA----- 934
Db 531 AspTyrTyrLysThrLysLeuGlyValAspLysLysSerAspAlaLysAlaIleLysLysAla 550
QY 935 -----GAAATGGTCTTTCAGCCTTACCGGAAATA 964
Db 551 TyrPheGlnLeuAlaLysLysTyrHisProAspVal 562

RESULT 5
BIR2 HUMAN
ID BIR2 HUMAN STANDARD; PRT; 618 AA.
AC Q13450; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
DE protein 2) (IAP homolog B).
GN BIRC2 OR API1 OR IAP2 OR MIHB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Fetal liver;

```

RX MEDLINE=96209843; PubMed=8643514;  
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
 RT "Cloning and expression of apoptosis inhibitory protein homologs that  
 function to inhibit apoptosis and/or bind tumor necrosis factor  
 receptor-associated factors";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis, and Uterus;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Stapleton M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Kana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP STRUCTURE BY NMR OF 266-363.  
 RX MEDLINE=99332054; PubMed=10404221;  
 RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
 RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)  
 repeat";  
 RL Nat. Struct. Biol. 6:648-651(1999).  
 CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions  
 CC inhibit apoptotic suppressor activity.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -!- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.  
 CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,  
 CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD  
 CC LEUKOCYTES.  
 CC -!- SIMILARITY: Belongs to the IAP family.  
 CC -!- SIMILARITY: Contains 3 BIR repeats.  
 CC -!- SIMILARITY: Contains 1 CARD domain.  
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
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 CC  
 CC EMBL; L49431; AAC41942.1; -;  
 CC EMBL; U45879; AAC50372.1; -;  
 CC EMBL; U37547; AAC50508.1; -;  
 CC EMBL; BC016174; AAH16174.1; -;  
 CC EMBL; BC028578; AAH28578.1; -;  
 CC PIR; S68450; S68450.  
 CC PDB; 1QEH; 20-OCT-99.  
 CC Genbank; HGNC:590; BIRC2.  
 CC MIM; 601712; -;  
 CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.  
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.  
 CC InterPro; IPR001370; BIR.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM01114; CARD; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 KW Apoptosis; Zinc-finger; Repeat; 3D-structure.  
 FT REPEAT 46 113  
 FT BIR 1.  
 FT REPEAT 184 250  
 FT BIR 2.  
 FT REPEAT 269 336  
 FT BIR 3.  
 FT DOMAIN 453 543  
 FT CARD.  
 FT ZN FING 571 606  
 FT RING-TYPE.  
 FT CONFLICT 157 157 S -> P (IN REF. 2).  
 FT CONFLICT 308 308 S -> G (IN REF. 2).  
 FT CONFLICT 414 414 Q -> L (IN REF. 2).  
 FT CONFLICT 514 514 L -> W (IN REF. 2).  
 FT TURN 269 270  
 FT HELIX 271 274  
 FT HELIX 287 293  
 FT TURN 294 294  
 FT TURN 296 297  
 FT TURN 301 304  
 FT TURN 309 309  
 FT STRAND 309 309  
 FT HELIX 322 325  
 FT TURN 326 328  
 FT STRAND 333 333  
 FT TURN 334 343  
 FT HELIX 344 351  
 FT TURN 353 354  
 SQ SEQUENCE 618 AA; 69899 MW; CL778D328063586D CRC64;  
 Alignment Scores:  
 Pred. No.: 0.64 Length: 618  
 Score: 98.00 Matches: 31  
 Percent Similarity: 44.78% Conservative: 29  
 Best Local Similarity: 23.13% Mismatches: 58  
 Query Match: 3.40% Indels: 16  
 DB: 1 Gaps: 3  
 US-09-771-161A-2 (1-1669) x BIR2\_HUMAN (1-618)  
 QY 713 ATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAGAGCCCTGCTTACCACTGCG 772  
 Db 461 ILAAGLYSAsnArgMetAlaLeuPheGlnLeuThr-----CysValLeuProIle 478  
 QY 773 CTGATGCTCTTCTGCTCCAGGACTTGATCATGAAAGAGGACTATGCACTTGTAGTACC 832  
 Db 479 LeuAspAsnLeuLeuLysAlaAsnValIleAsnLysGlnGlnHisAspIleLeuLysGln 498  
 QY 833 AAGCTTCAAGGACCTCAAAAGTCAGACATTTACTAGACACTACTGACATCCAAAGAGAA 892  
 Db 499 LysThrGlnIleProLeuGlnAlaAAGLeuLeuLeuLeuLeuLeuLeuValIleLeuValLysGlyAsn 518  
 QY 893 GAATTTCCCAAGTTATAGTACAAAAATTGCAAGAT----- 928  
 Db 519 AlaAlaAlaAsnIlePheLysAsnCysLeuLysGluIleAspSerThrLeuTyrLysAsn 538  
 QY 929 -----AACAAACAATGGGTCTTTCAGCCTTACCCGGAATACTTGTGTTCTTAGA 979  
 Db 539 LeuPheValAspLysAsnMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 558  
 QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAGAA 1039  
 Db 559 GluGluGlnLeuArgArgLeuGlnGluGluGluGluGluGluGluGluGluGluGlu 578  
 QY 1040 ATGTGTTTCATA-----AAGAGTATTATTATCTCTGT 1072



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RESULT 7
REPI_ZYGBA STANDARD; PRT; 357 AA.
AC REPI_ZYGBA
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Trans-acting factor B (REPI).
GN B.
OS Zygocharomycetes baillii.
OC Plasmid PSB2.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygocharomycetes.
OX NCBI_TaxID=4954;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 1047; PubMed=3680169;
RX MEDLINE=88059763; PubMed=3680169;
RA Utatsu I., Sakamoto S., Imura T., Toh-E A.;
RT "Yeast plasmids resembling 2 micron DNA: regional similarities and
RL J. Bacteriol. 169:5537-5545 (1987)."
CC -!- FUNCTION: PLASMID PARTITION REQUIRE REPI1, REP2, AND A CIS-ACTING
CC DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN
CC THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA
CC REP2.
CC -!- SIMILARITY: TO THE P GENE PRODUCT OF PSR1.
CC
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CC
CC EMBL: M18274; AAA35283.1;
DR InterPro; IPR008897; Yeast_TAF.
DR Pfam; PF05797; Yeast_TAF; 1.
KW Plasmid; Trans-acting factor.
SQ SEQUENCE 357 AA; 40752 MW; 7DF4C06359D4BA35 CRC64;

Alignment Scores:
Pred. No.: 1.41 Length: 357
Score: 94.00 Matches: 61
Percent Similarity: 29.72% Conservative: 53
Best Local Similarity: 21.25% Mismatches: 100
Query Match: 3.26% Indels: 73
DB: 1 Gaps: 12

US-09-771-161A-2 (1-1669) x REPI_ZYGBA (1-357)
QY 275 TTCTATATTCCTAATCATCTCCAGTTAAAGTGATATATATTTATGTTATTCATTACAG 334
Db 95 PheGlnAspHisLysLeuPheAlaAsnLysAsnAlaAspValtyrValgluArgLeuGln 114
QY 335 TTACAGAGGTGTTTCAAGTGCCATTCACCTATGTCAGCAAGAAAGAAATGGAATTATCTG 394
Db 115 ---AsnAlaIleAlaSerGlyIleLysLeuProGluSerLysLys- 128
QY 395 AACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGTCCATGAA 454
Db 129 ---AsnGlu 130
QY 455 AATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCTCCACAGACAATGATTTTAA 514
Db 131 ArgLeuGlyGlnProLysLysThrLysAsnValThrLysGluIleGluThrPheIle 150
QY 515 -----TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCAGTCTCT 562
Db 151 AspAlaThrAsnAlaArgLysGluLeuAspGluItyrPheArgLysLeuGln- 167
QY 563 GGAAATCACAGTGGGATAGACCAATTTCTGGATCTCAAGGGCTGCATCTCTGTCATCAC 622

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Db 168 ---AspGlyThrLeuThrGlyAspLeuGluGlyGlyLeuCysLysVal 182
QY 623 AAGACCTCCATGCTTTCAGCAATATAATCACTCTCAACTGCAGGAACTCAGAA 682
Db 183 LysThrLeuIleSerCysLysAlaLeuPhe- 197
QY 683 CGTCTGCAG-----CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAC 733
Db 198 GluLeuGlnPheMetAlaThrAsnValArgLysValTrpIle-----GlyGlu 213
QY 734 ATTGTGAACCAATACAGAGCCTGCTTAACCGATCGCTAGATGCCCTCTCTGTCAGG 793
Db 214 IleValCysGlyMetVal-----SerAsnLysAsnAlaIleAspAsn 228
QY 794 GACTTGATCATCAAGAGGACTATGAACCTGTGTAGTACCAAGCCTACAGAGCACTCAAAA 853
Db 229 AspLeu-----GluGluGluGluArgAsnAlaSerGlyGluGlnThrThrAlaArg 246
QY 854 GTCAGA---CAATTACTAGACACTACTGAC----- 880
Db 247 GluGluSerGluAlaLeuAspThrThrSerAsnGlyLeuAspAlaLeuAsnThrGlnIle 266
QY 881 -----ATCCAAGGAGAGAATTTCCCAAGTTATTAGTACAAAATTGCAAGATAACAA 934
Db 267 AsnAlaIleGluThrGluGluSerPheTrpGluAlaIleArgAlaLeuHisGlnGlu--- 285
QY 935 CAAATGGGTCTTCAGCCTTACCCGAAATACTGTGTGTTTCTAGATCACTTTTAAAT 994
Db 286 -----LeuArgThrSerProThrGlnLeuGluGlyCysArgLysAlaValPhe 302
QY 995 TTACTTCAAAATAAAGCATGTAAGTGAAGTGTGTTTTCAGAGAAATGTGTTTCATAAA 1054
Db 303 LeuLeuGlyHisLysLysIleLeuGlnThr-PheThrLysGlnLysAspThrAlaArgAl 322
QY 1055 GGATATTTATATCTCTGTT 1073
Db 322 aLeuPheTyriIleAsnLeu 328

RESULT 8
BIR2_MOUSE STANDARD; PRT; 612 AA.
ID BIR2_MOUSE
AC Q82210; O08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
DE protein 2) (MIAP2) (MIAP-2).
DE BIRC2 OR BIRC3 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Roche W., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503 (1997).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions

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CC inhibit apoptotic suppressor activity (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,  
CC liver, skeletal muscle, kidney and testis.  
CC -!- SIMILARITY: Belongs to the IAP family.  
CC -!- SIMILARITY: Contains 3 BIR repeats.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
CC -----  
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CC -----  
DR EMBL: L49433; AAC42078.1; -;  
DR HBB: U88909; AAC53532.1; -;  
DR HSP: Q13490; IQH.  
DR MGD: MGI:1197009; Birc3.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR001315; CARD.  
DR InterPro: IPR001841; Znf\_ring.  
DR Pfam: PF00653; BIR; 3.  
DR Pfam: PF00619; CARD; 1.  
DR Pfam: PF00097; ZF-C3HC4; 1.  
DR SMART: SM00238; BIR; 3.  
DR SMART: SM00114; CARD; 1.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS0209; CARD; 1.  
DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE: PS0089; ZF\_RING\_2; 1.  
DR Apoptosis; Zinc-finger; Repeat.  
KW REPEAT 46 113 BIR 1.  
FT REPEAT 177 243 BIR 2.  
FT REPEAT 262 329 BIR 3.  
FT DOMAIN 447 537 CARD.  
FT ZN FING 565 600 RING-TYPE.  
FT ZN FING 380 380 E -> K (IN REF. 2).  
FT CONFLICT 380 380  
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;  
  
Alignment Scores:  
Pred. No.: 2.23 Length: 612  
Score: 92.00 Matches: 30  
Percent Similarity: 41.04% Conservatives: 25  
Best Local Similarity: 22.39% Mismatches: 63  
Query Match: 3.19% Indels: 16  
DB: 1 Gaps: 3  
  
US-09-771-161A-2 (1-1669) x BIR2\_MOUSE (1-612)  
QY 713 ATCCGAGCAAAAGGGAAGACATTTGAAACCAATGACAGAGCCCTTAACGAGTCG 772  
Db 455 IleArgLysAsnArgMetAlaLeuPheGlnLeuThrHisValLeu-----ProIle 472  
QY 773 CTAGATGCCCTCTGTCCAGGACTGTATCATGAAGAGGACTATCACTTGTAGTACC 832  
Db 473 LeuAspAsnLeuLeuGluAlaSerValIleThrLysGlnGluHisAspIleArgGln 492  
QY 833 AAGCCTACAAGGACCTCAAAAGTCAACAATTAAGACACTACTGACATCAAGAGGAA 892  
Db 493 LysThrGlnIleProLeuGlnAlaArgGluLeuIleAspThrValLeuValLysGlyAsn 512  
QY 893 GAATTTGCCAAGTATAGTACAAAATTTGAAGAT----- 928  
Db 513 AlaAlaAlaAsnIlePheLysAsnSerLeuLysGluIleAspSerThrLeuTyrGluAsn 532  
QY 929 -----AACAAACAATGGCTTTCAGCCCTTACCCGGAATACCTTGCTTCTAGA 979  
Db 533 LeuPheValGluLysAsnMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 552

QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTCACTGTTTTCACAGAAGAA 1039  
Db 553 GluGluGlnLeuArgGlnGluGlnGluArgThrCysLysValCysMetAspArgGlu 572  
QY 1040 ATGCTTTTCATA-----AAAGGATATTATATCTCTGT 1072  
Db 573 ValSerIleValPheIleProCysGlyHisLeuValValCys 586  
  
RESULT 9  
KHS1\_YEAST  
ID KHS1\_YEAST STANDARD; PRT; 708 AA.  
AC P39690;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Killer toxin KHS precursor (Killer of heat sensitive).  
GN KHS1 OR KHS OR YER187W-A. (Baker's yeast).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 37-42.  
RC STRAIN=115;  
RX MEDLINE=92118315; PubMed=1368726;  
RA Goto K., Fukuda H., Kichise K., Kitano K., Hara S.;  
RT "Cloning and nucleotide sequence of the KHS killer gene of  
RT Saccharomyces cerevisiae."  
RL Agric. Biol. Chem. 55:1953-1958(1991).  
CC -!- FUNCTION: Kill sensitive strains of yeast. Optimal pH is 4-4.5  
CC and it is unstable above 30 degrees Celsius.  
CC -!- SUBUNIT: Monomer.  
CC -!- SIMILARITY: TO YEAST YER187W.  
CC -----  
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CC -----  
DR EMBL: S7712; AAC60532.1; -;  
DR PIR: JQ1148; JQ1148.  
DR GerMOnline; I44546; -;  
DR SGD: S0007427; KHS1.  
KW Toxin; Signal; Transmembrane. POTENTIAL.  
FT SIGNAL 1 27  
FT PROPEP 28 36  
FT CHAIN 37 708 KILLER TOXIN KHS.  
FT TRANSMEM 77 97 POTENTIAL.  
FT TRANSMEM 380 400 POTENTIAL.  
FT TRANSMEM 466 486 POTENTIAL.  
SQ SEQUENCE 708 AA; 79535 MW; FB63D9E8C4C27431 CRC64;  
  
Alignment Scores:  
Pred. No.: 3.43 Length: 708  
Score: 90.00 Matches: 43  
Percent Similarity: 37.86% Conservatives: 35  
Best Local Similarity: 20.87% Mismatches: 80  
Query Match: 3.12% Indels: 48  
DB: 1 Gaps: 7  
  
US-09-771-161A-2 (1-1669) x KHS1\_YEAST (1-708)  
QY 230 ATGTAATTTT---GTACAAACATATAAATGCTGTAGATTGTTTACTTCTATATTTTC 286  
Db 454 MetTyrPheGlnLysGlnCysTyrSerSerGlnAsnAsnIleIleTyrIleTyrAsnSer 473  
QY 287 CTAATCATCTCCAGTTAAAGTGTATATATTTATGTTATTCATTACAGTTACAGAGTGT 346  
Db 474 IleHisIleThrCysGlyAlaValIleValIleValHisAspValArgThrProSerVal 493







```
Pred. No.: 4,29 Length: 3130
Score: 89.50 Matches: 68
Percent Similarity: 32.11% Conservative: 28
Best Local Similarity: 22.74% Mismatches: 116
Query Match: 3.11% Indels: 87
DB: 1 Gaps: 14

US-09-771-161A-2 (1-1669) x DPOZ_HUMAN (1-3130)
QY 350 AGTGCCATTCACCTATGTGACAGAGAAAATGGAATTATCTCTGACATACCTGTAAT 409
DB 1631 SerCysTyrSerLeuGluAspSerLeuSerProGluHisAsnTyrAsnPheAspIleAsn 1650
QY 410 CATGGTCCACAGAGGAATCATGT-----GGATCCTCTCAGCTCCATGAAAT 457
DB 1651 ThrIleGlnThrGlyPheCysSerPheTyrSerGlySerGlnPheValProAlaAsp 1670
QY 458 AGTGGTTCCTGAACTTCAAGGTCCTCCAGCTCTCAAGAC----- 502
DB 1671 GlnAsnLeuProGlnPheLeuSer---AspAlaValGlnAspLeuPheProGlyGln 1689
QY 503 -----AATGATTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGACAGCTG 550
DB 1690 AlaIleGlnPheAsnGluPheLeuSerHisAspAsnGlnPheCysAspGluAspPhys 1708
QY 551 CATCACTGTCTCGAAATCACAGTTGG----- 577
DB 1709 HisIleThrThrAspSerAlaSerTyrIleArgSerGlyThrLeuSerProGluIlePhe 1728
QY 578 ---GATAGACCATTTCTGATCTCAAGGGCTGATCTGTGATCAAGACCACTCCA 634
DB 1729 GluLysSerThrIleAspSerAsnGluAsnArgHisAsnGlnTyrLysAsnSer 1747
QY 635 TGCTTTCAGCAATAAATACACTCTCAACTCGACGGAACATCA----- 679
DB 1748 -----PheHisProLeuThrThrArgSerAsnSerIleMetAspSerPhe 1762
QY 680 -----GAAGCTCTG----- 688
DB 1763 CysValGlnGlnAlaGluAspCysLeuSerGluLysSerArgLeuAsnArgSerSerVal 1782
QY 689 -----CAGCTGGTATAGCCAGCGAGTGATGATCCAGAGC 721
DB 1783 SerLysGluValPheLeuSerLeuProGlnProAsn---AsnSerAspTyrIleGlnGly 1801
QY 722 AARAGGAGACATGTGACCAATCAGACAGAGCTGCTTAACAGTCGCTAGATGCC 781
DB 1802 HisThrArgLysGluMetGlyGlnSerLeuAspSerAla---AsnThrSerPheThrAla 1820
QY 782 CTTCTGTCCAGG-----GACTTG-----ATCATGAAAGAGGACTATGAACCTGTT 826
DB 1821 IleLeuSerSerProAspGlyGluLeuValAspValAlaCysGluAspLeuGluLeuTyr 1840
QY 827 AGTACCAAG-----CCTACAGGACCTCAAAAGTCACACAACTACTA 868
DB 1841 ValSerArgAsnAsnAspMetLeuThrProAspSerSerProArgSerThrSer 1860
QY 869 GACACTACTGACATCCCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTCAGAAAT 928
DB 1861 SerProSerGlnSerLysAsnGlySerPheThrProArgThrAlaAsnIleLeuLys--- 1879
QY 929 AACAAACAAATGGGTCTTCAGCTTACCGGAAATCTTGTGGTTCTAGATCACCATCT 988
DB 1880 -----ProLeuMetSerProProArgGluGluIle 1890
QY 989 TTAATTTACTTCAAAATAAAGCATGTAAGTACTGTTCTTTTCAAGAGAAATGCTGT 1045
DB 1891 MetAlaThrLeuLeuAspHisAspLeuSerGluThrIleTyrGlnGluProPheCys 1909

RESULT 12
ANCL_MOUSE
ID ANCL_MOUSE STANDARD; PRT; 1944 AA.
AC P53995; Q8BP33; Q8C772;
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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Anaphase promoting complex subunit 1 (APC1) (Cyclosome subunit 1)
DE (Protein Tsg24) (Mitotic checkpoint regulator).
GN ANAPC1 OR TSG24 OR MCPR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=CBA; TISSUE=Testis;
RX MEDLINE=95014147; PubMed=7929068;
RA Starborg M., Brundell E., Gell K., Hosoe C.;
RT "A novel murine gene encoding a 216-kDa protein is related to a
RT mitotic checkpoint regulator previously identified in Aspergillus
RT nidulans.";
RL J. Biol. Chem. 269:24133-24137 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb, and Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
CC -i- FUNCTION: Component of the anaphase promoting complex/cyclosome
CC (APC/C), a cell cycle-regulated ubiquitin ligase that controls
CC progression through mitosis and the G1 phase of the cell cycle (By
CC similarity).
CC -i- SUBUNIT: The APC/C is composed of at least 11 subunits (By
CC similarity).
CC -i- TISSUE SPECIFICITY: Abundantly expressed in proliferating
CC fibroblasts, juvenile testis, adult brain and epididymis.
CC -i- DEVELOPMENTAL STAGE: Uniformly expressed throughout interphase of
CC the cell cycle.
CC -i- SIMILARITY: Contains 4 PC repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X80169; CAA56450.1; --
DR
```



DR	ENBL; AK052404; BAC34976.1; -.
DR	EMBL; AK077847; BAC37032.1; -.
DR	PIR; A55117; A55117.
DR	MGI; MGI:103097; Mcpr.
DR	InterPro; IPR002015; APC_proteasome.
DR	Pfam; PF01851; PC_rep; 5. Cell cycle; Cell division; Mitosis; Repeat.
KW	Ubl conjugation pathway; Cell cycle; Cell division; Mitosis; Repeat.
FT	REPEAT 1297 1325 PC 1.
FT	REPEAT 1366 1404 PC 2.
FT	REPEAT 1467 1501 PC 3.
FT	REPEAT 1520 1552 PC 4.
FT	CONFLICT 112 112 Q -> A (IN REF. 2).
FT	CONFLICT 348 349 GV -> AA (IN REF. 2).
FT	CONFLICT 643 643 N -> K (IN REF. 2; BAC34976).
FT	CONFLICT 1036 1036 H -> D (IN REF. 2; BAC34976).
SQ	SEQUENCE 1944 AA; 216086 MW; 48FIEEP01053B6C3 CRC64;

  

Alignment Scores:			
Pred. No.:	4.58	Length:	1944
Score:	89.00	Matches:	52
Percent Similarity:	37.56%	Conservative:	25
Best Local Similarity:	25.37%	Mismatches:	72
Query Match:	3.09%	Indels:	56
DB:	1	Gaps:	10

  

US-09-771-161A-2 (1-1669) x ANCI_MOUSE (1-1944)			
QY	326 TCATTACAGTTACACAGTGTTTCAAGTCCGCAAT-----CACCTATGTGCACAAGAAGAA	379	
DB	291 ThrLeuGlnAsnAlaThrSerSerSerLeuThrAlaHisLeuArgSerLeuSerLys	310	
QY	380 ATGGAAATTATCTCTGAACATACCTGTAAATCAT-----GGTCACACAAGAGAA	427	
DB	311 GlyGluSerProValAlaSerProPheGlnAsnTyrSerSerIleHisSerGlnSerArg	330	
QY	428 TCATGTGGATCTCTCAGCTCGATCAAATAAGTAGTGTTCTCTCGAACTTCAGGTCCTCG	487	
DB	331 SerThrSerSerProSerLeuHisSerArgSer-----	341	
QY	488 CAGAGTCCTCAAGACAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAG	547	
DB	342 ProSerIleSerAsnMetGlyValLeuSerArgala-----	353	
QY	548 CTGCATCACTGTCCT-----GGAAATCACAGTTGGGATAGCACCATTCTCGATCTCAA	601	
DB	354 -----HisSerProAlaLeuGlyValHisSerPhe-----SerGlyAlaGln	367	
QY	602 AGGGCTGCATTCGTGATCAACAGACACTCCATGCTCTTCAGCATATAATAATCCACTC	661	
DB	368 ArgPheAsnLeuSerSerHisSerGlnSerProLysArgHisSerIleSerHisSerPro	387	
QY	662 TCAACTGCAGGAAACTCAGAACGCTCGCAGCTCGTATAGCCCAGCAGTCGATCCAGACG	721	
DB	388 SerGlySerPheAsnAspSerPheLeuAlaPro-----	398	
QY	722 AAAAGGGAGACATTGTGAACAAATCACAGAAGCCTGCCCTTAACCAAGTCGCTAGATGCC	781	
DB	399 GluThrGluProIleVal-----ProGluLeuCysile-----	409	
QY	782 CTTCTGTCAGGAGCTTGATCATGAAAGAGACTATGAACCTGTGTAGTACCAAGCCTACA	841	
DB	410 -----AspHisLeuTriphrThrGluThrLeuProAsnIleArgGluLysAsnSer	425	
QY	842 AGGACCTCAAAGCTCAGACAAATTACTAGACACTACTGCATCCAGGAGAGAGATTGCC	901	
DB	426 GlnAlaSerLysVal-----PheIleThrAspLeuCysGlyGlnLysPheLeu	442	
QY	902 AAAGTTATAGTACAA 916		
DB	443 CysPheLeuValGlu 447		

  

RESULT 13  
 PIAP FIG

ID	PIAP_PIG	STANDARD;	PRT;	358 AA.
AC	O62640;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Putative inhibitor of apoptosis.			
GN	PIAP.			
OS	Sus scrofa (pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Aorta;			
RX	MEDLINE=98162622; PubMed=9501011;			
RA	Stehlik C., de Martin R., Binder B.R., Lipp J.;			
RT	"Cytokine induced expression of porcine inhibitor of apoptosis			
RL	protein (iap) family member is regulated by NF-kappa B.";			
RL	Biochem. Biophys. Res. Commun. 243:827-832(1998).			
CC	-!- SIMILARITY: Belongs to the IAP family.			
CC	-!- SIMILARITY: Contains 2 BIR repeats.			
CC	-!- SIMILARITY: Contains 1 CARD domain.			
CC	-!- SIMILARITY: Contains 1 RING-type zinc finger.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
DR	EMBL; U79142; AAC39171.1; --			
DR	PIR; JCS964; JCS964.			
DR	HSSP; Q13490; IQBH.			
DR	InterPro; IPR001370; BIR.			
DR	InterPro; IPR001315; CARD.			
DR	InterPro; IPR001841; Znf_ring.			
DR	Pfam; PF00653; BIR; 2.			
DR	Pfam; PF00619; CARD; 1.			
DR	Pfam; PF00097; zf-C3HC4; 1.			
DR	SMART; SM00238; BIR; 2.			
DR	SMART; SM00114; CARD; 1.			
DR	SMART; SM00184; RING; 1.			
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.			
DR	PROSITE; PS0143; BIR_REPEAT_2; 2.			
DR	PROSITE; PS0209; CARD; 1.			
DR	PROSITE; PS00518; ZF_RING_1; FALSE_NEG.			
DR	PROSITE; PS00089; ZF_RING_2; 1.			
DR	Apoptosis; zinc-finger; Repeat.			
FT	REPEAT 4 70 BIR 1.			
FT	REPEAT 90 157 BIR 2.			
FT	DOMAIN 193 283 CARD.			
FT	ZN_FING 311 346 RING-TYPE.			
SQ	SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;			
Alignment Scores:				
Pred. No.:	4.91	length:	358	
Score:	88.00	Matches:	72	
Percent Similarity:	33.33%	Conservative:	47	
Best Local Similarity:	20.17%	Mismatches:	135	
Query Match:	3.06%	Indels:	103	
DB:	1	Gaps:	18	
US-09-771-161A-2 (1-1669) x PIAP_PIG (1-358)				
Qy	76	GATTTTCGAGGATGAAGCTCTGAGACACTGAGAGAAGGTAA	CCAATTAAATGAGCCAGGA	135
Db	55	AspAlaMetThrGluHisLeuArgHis-	-----	63
Qy	136	TTCAAGTCTGCTGTTNCTAAAGTATTATTC	CCGTTCTC	171
Db	64	PheProAsnCys-	-----	77

RESULT 13  
PIAP PIG

```
QY 172 -----TACACTGCTCTTTCTCCTCAGTTATATGTTATATCTCAACTCTTTATATTCT 225
Db 78 SerArgTyrThrValSerAsnLeuSerMetGlnThrTyrAlaAla-----Arg 93
QY 226 TTCCATGTTATTTGTACAAACATATAAATGTGTTAGATTGTTATTTTACTTCTATAATTT 285
Db 94 PheLysThrPheCys-----AsnTyrProSerSerIleProVal-----His 107
QY 286 CTTAATCATCTCCAGTTAAAGTGTATATATATATTTATGTTATCTTACAGTTACAGAGTGT 345
Db 108 ProGluGlnLeuAlaSerAlaGlyPheTyrTyrMetGlyHisSerAspValLysCys 127
QY 346 TTTCAAGTGCCATTACCTATGTGACAAAGAAATGGAATTATCTCTGAACATACCTGT 405
Db 128 PheCysCys-----AspGlyGlyLeu-----134
QY 406 AAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATCAAAATAGTGGTTC 465
Db 135 ArgCysTrpGluSerGlyAspAspProTyrValGluHisAlaLys-----TrpPhe 151
QY 466 TCTGAACTTCAAGTCCCTCCAGCTCTCAAGCAATGATTTTATCTAGAAAGC 525
Db 152 -ProArg---CysGluTyrLeuIleArgIleLysGlyGlnGluPheIleSerArg---Va 169
QY 526 TCAAGACTGTATTTATGAAGCTGCATCATCTGCTCGGAAATCAACAGTTGGATAGCAC 585
Db 169 GlnAlaSerTyr-----ProHisLeuLeuGlnLe 180
QY 586 CATTTCTGGATCTCAAGGCTGCATTTCTGTGATCAACAGCACCTCATGCTTTCAGC 645
Db 180 uLeuSerThrSerAsp-----185
QY 646 AATATAAATCCACTCTCAACTGCAGGAATCAAGACTCTGCAGCTCGGTATAGCCCA 705
Db 186 -----AsnPro-----GluAspGluAsnAlaGluProProAsnAspLe 198
QY 706 GCAGTGTGATCAGACGAAAGGAAAGACTGTGTGAACCAATGACAGAGCCCTGCTTAA 765
Db 198 uSerLeuIleArgLysAsnArgMetAlaLeuPheGlnHisLeuThr-----CysValle 216
QY 766 CCAGTCTGATAGCTCTTCTGTCAGGAGCTGATCATGAAAGAGACTATGAACCTGT 825
Db 216 uProIleLeuAspSerLeuLeuIleAlaArgValIleSerGluGlnGluHisAspValII 236
QY 826 TAGTACCAAGCCTACAGAGACCTCAAAGTCAAGATTTACTAGACACTACTGACATCCA 885
Db 236 eLysGlnLysThrGlnThrSerLeuGlnAlaArgGluLeuIleAspIleLeuVally 256
QY 886 AGGAGAAAGATTTTGCCAAAGTTATAGTACAAAATTTGAAAGAT-----AA 930
Db 256 sGlyAsnTyrAlaAlaThrIlePheLysAsnSerLeuGlnGluIleAspProMetLeuTy 276
QY 931 CAACAAATGGTCTTCAG-----CCTTACCCGGAATATCTTGGT 972
Db 276 rLysHisLeuPheValGlnGlnAspIleLysTyrIleProThrGluAsnValSerAspLe 296
QY 973 TTCTAGATCACCATCTTTAAATTTTACTTCAAAATPAAAGCATGTAAAGTGTGTTTTC 1032
Db 296 uSerMetGluGlnLeuArgGluLeuGlnGluArgThrCysLysValCysMetAs 316
QY 1033 AGAAGAAATGTGTTTCATA-----AAAGGATATTTATCTCTGT 1072
Db 316 pLysGluValSerIleValPheIleProCysGlyHisLeuValValCys 332
RESULT 14
T2FA_XENLA
ID T2FA_XENLA STANDARD; PRT; 524 AA.
AC Q04870;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Transcription initiation factor IIF, alpha subunit (TFIIF-alpha)
```

```
DE (Transcription initiation factor RAP74).
GN RAP74.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93126122; PubMed=1480494;
RA Gong D.-W., Hasegawa S., Wada K., Roeder R.G., Nakatani Y.,
RA Horikoshi M.;
RT "Elucidation of three putative structural subdomains by comparison of
RL Nucleic Acids Res. 20:6736-6736(1992).
CC -!- FUNCTION: TFIIF IS A GENERAL TRANSCRIPTION INITIATION FACTOR THAT
CC BINDS TO RNA POLYMERASE II AND HELPS TO RECRUIT IT TO THE
CC INITIATION COMPLEX IN COLLABORATION WITH TFIIB. IT PROMOTES
CC TRANSCRIPTION ELONGATION.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: TO OTHER TRANSCRIPTION FACTOR IIF, ALPHA SUBUNIT.
CC
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CC
CC EMBL; Z17426; CAA78999.1; -
CC PIR; S35551; S35551.
CC TRANSFAC; T02171; -
CC InterPro; IPR008851; TFIIF-alpha.
CC Pfam; PF05793; TFIIF-alpha; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
SQ SEQUENCE 524 AA; 58699 MW; 8CF3A74A3BF77BB0 CRC64;

Alignment Scores:
Pred. No.: 5 07 Length: 524
Score: 88.00 Matches: 54
Percent Similarity: 33.63% Conservative: 22
Best Local Similarity: 23.89% Mismatches: 90
Query Match: 3.06% Indels: 60
DB: 1 Gaps: 9

US-09-771-161A-2 (1-1669) x T2FA_XENLA (1-524)
QY 398 ATACCTGTTAAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAAAT 457
Db 290 LeuProGlyLysIleLysProAlaLysGluGluGluGlyProLysGlyLeuAspGluGln 309
QY 458 AGTGGTCTCTCTGAACTTCA-----478
Db 310 SerGluSerGluSerGluSerGluGluLysAlaGluGluGluGluGluGlu 329
QY 479 AGGTCTCCCTGCCAGCTCTCTCAAGACAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTAT 538
Db 330 LysLysAlaProThrProGlnAspAsnLys-----LysLysLysLysGlyAsp-----345
QY 539 TTTATGAAGCTGCATCAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
Db 346 -----SerSerAspGluSerGluThrSerGluAspSerAspIleAspGlyAla 361
QY 599 CAAAGGGCTCATTTCTGTGATCAACAGCCACTCCA-----634
Db 362 SerSerSerLeuPheMetGlnLysLysThrProProLysLysAspLysLysGlyGly 381
QY 635 ---TGCTCTTTCAGCAATAATAAAT-----CCACTCTCAACTGCAGGAAC 676
Db 382 SerAsnSerSerSerArgGlyAsnSerArgProGlyThrProSerProAspThrGlyAsn 401
```

QY 677 TCAGAACGTCGACGCTGGTATAGCCAGCAGCGATGATCCAGAGCAAGGAAGGACATT 736  
 Db 402 ThrSerSerThrLeuArgAlaalaSerLysLeuGluGlnSerLysArgGlyThrVal 421  
 QY 737 GTGAACCAATGACAGACGCTGCCTTAACCAAGTCGCTAGATGCC----- 781  
 Db 422 SerAsn-----ThrProAlaLysArgLeuLysMetGluAlaGlyProGlnAsnThr 439  
 QY 782 -----CTTCTGTCCAGGACTTG 799  
 Db 440 SerGlyLysSerThrProGlnProGlnSerGlyLysSerThrProSerSerGlyAspIle 459  
 QY 800 ATCATGAAGAGGAC-----TATGACTTGTAGTACCAAGCCTACAGGACCTCAAAA 853  
 Db 460 GlnLeuThrGluGluAlaValArgArgTyrLeuThrArgLysProMetThrThrLysAsp 479  
 QY 854 GTCAGACAATTACTAGACACT-----ACTGACATCCAAAGGAGAGAATTGCCAAAGTT 907  
 Db 480 LeuLeuLysLysPheGlnThrLysLysThrGlyLeuSerSerGluGlnThrValAsnVal 499  
 QY 908 ATAGTACAAAATTGAAA 925  
 Db 500 LeuAlaGlnIleLeuLys 505

RESULT 15

SNEL\_HUMAN  
 ID SNEI\_HUMAN STANDARD; PRT; 8797 AA.  
 AC Q8NF91; Q8NF97; Q8TQCP1; Q8WMW6; Q8WMW7; Q8WKF6; Q96NL7;  
 AC Q9COA7; Q9H525; Q9H536; Q9NS316; Q9NU50; Q9UJ06; Q9UJ07; Q9ULF8;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Nesprin 1 (Nuclear envelope spectrin repeat protein 1) (Synaptic  
 DE nuclear envelope protein 1) (Syn-1) (Myocyte nuclear envelope protein  
 DE 1) (Wyne-1) (Enaptin).  
 GN SYNE1 OR MYNE1 OR KIAA0796 OR KIAA1756 OR KIAA1262.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), CHARACTERIZATION, AND  
 RP MUTAGENESIS OF 8758-LEU-CYS-8763.  
 RC TISSUE=Heart, Placenta, Skeletal muscle, Spleen, and Testis;  
 RX MEDLINE=21652858; PubMed=11792814;  
 RA Zhang Q., Skepper J.N., Yang F., Davies J.D., Hegyi L., Roberts R.G.,  
 RA Weissberg P.L., Ellis J.A., Shanahan C.M.;  
 RT "Nesprins: a novel family of spectrin-repeat-containing proteins that  
 RT localize to the nuclear membrane in multiple tissues.";  
 RL J. Cell Sci. 114:4485-4498(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SUBCELLULAR LOCATION.  
 RC TISSUE=Heart, Spleen, and Testis;  
 RX MEDLINE=2296983; PubMed=12408964;  
 RA Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.;  
 RT "The nesprins are giant actin-binding proteins, orthologous to  
 RT Drosophila melanogaster muscle protein MSP-300.";  
 RL Genomics 80:473-481(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT GLY-8323.  
 RA Braune S., Abraham S., Padmakumar V., Tunggal B., Noegel A.A.,  
 RA Kornebaum E.;  
 RT "The longest isoform of enaptin/Syne-1, a nuclear envelope associated  
 RT protein, binds actin cytoskeleton via the alpha-actinin-like actin-  
 RT binding domain.";  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).  
 RA Zhang Q., Shanahan C.M.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Almeida J., Clark S., Griffiths C., Lloyd D., Parker A., Smith M.,

Tracey A., Williams S.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 1-856 FROM N.A.  
 RC TISSUE=Kidney;  
 RA Gough I., Fan J., Lisa G., Chu S., Winnick S., Beck K.A.;  
 RT "Golgi localization of syne-1.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 28-778 AND 2901-3476 FROM N.A.  
 RC TISSUE=Adrenal gland, and Teratocarcinoma;  
 RA Nimmiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,  
 RA Furuya I., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,  
 RA Otsuka N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato K., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,  
 RA Kanehori K., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B.,  
 RA Takemoto M., Ota T., Suzuki Y., Sugano S., Nagahari K., Masuho Y.,  
 RA Nagai K., Isogai T.;  
 RT "NED0 human cDNA sequencing project.";  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE OF 443-8797 FROM N.A. (ISOFORM 5).  
 RC TISSUE=Brain;  
 RX MEDLINE=21082932; PubMed=11214970;  
 RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XIX.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 7:347-355(2000).  
 RN [9]  
 RP SEQUENCE OF 743-8797 FROM N.A. (ISOFORM 6).  
 RC TISSUE=Brain;  
 RA Anseorge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE OF 4219-8797 FROM N.A. (ISOFORM 7).  
 RC TISSUE=Brain;  
 RX MEDLINE=20039619; PubMed=10574462;  
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 6:337-345(1999).  
 RN [11]  
 RP SEQUENCE OF 6922-8797 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99087487; PubMed=9872452;  
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,  
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XI.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 5:277-286(1998).  
 RN [12]  
 RP REVISIONS.  
 RC TISSUE=Brain;  
 RX MEDLINE=22158633; PubMed=12168954;  
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual  
 RT curation of 330 KIAA cDNA clones.";  
 RL DNA Res. 9:99-106(2002).  
 RN [13]  
 RP SEQUENCE OF 7631-8797 FROM N.A., AND CHARACTERIZATION.  
 RX MEDLINE=21659781; PubMed=11801724;  
 RA Mislow J.M.K., Kim M.S., Davis D.B., McNally E.M.;  
 RT "Wyne-1, a spectrin repeat transmembrane protein of the myocyte inner  
 RT nuclear membrane, interacts with lamin A/C.";  
 RL J. Cell Sci. 115:61-70(2002).  
 RN [14]  
 RP SEQUENCE OF 8406-8797 FROM N.A.



Qy 1030 T-----CAAGAGAAATGTGTTTCATAAA 1054  
| : : : ||| : : : |||  
Db 2021 eAsnGlnLeuGluAspGluLeuAsnSerHisGluHisGluLeuCysTrpLeuLys 2039

Search completed: March 29, 2004, 14:20:36  
Job time : 44.5 secs

**This Page Blank (uspto)**

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:14:57 ; Search time 87.5 Seconds

(without alignments)  
12036.569 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880

Sequence: i acctagttattaccagata.....caacagcgtgtgtgtaaaa 1669

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO scool\_p/US09771161/runat\_29032004.124825.13679/app\_query.fasta\_1.1863  
-DB=SPTREMBL\_25 -QFMT=fastcan -SUFFIX=n2p.ispt -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CGN 1.1.95 @runat\_29032004.124825.13679 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvrius:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	335	11.6	584 13 Q8JHU4	Q8JHU4 brachydanio

	2	105.5	3.7	791	16	Q8A9V6
	3	101.5	3.5	1309	5	Q8IJE8
	4	101	3.5	734	5	Q8I1Z1
	5	100.5	3.5	461	12	Q9J861
	6	100	3.5	589	11	Q9QZC6
	7	100	3.5	589	11	Q9ESE8
	8	99.5	3.5	799	5	Q8IN63
	9	99.5	3.5	829	5	Q9VDR7
	10	99.5	3.5	830	5	Q45116
	11	99.5	3.5	830	5	Q44224
	12	99.5	3.5	869	10	Q9FTV4
	13	99	3.4	949	5	Q8I0W9
	14	99	3.4	1029	4	Q9C099
	15	98.5	3.4	537	11	Q8R489
	16	98	3.4	2381	5	Q8IKD7
	17	97	3.4	285	13	Q8JFU4
	18	96.5	3.4	243	16	Q8CSO9
	19	96	3.3	1169	16	Q7ZA11
	20	95.5	3.3	264	8	Q9G8N6
	21	95.5	3.3	293	5	Q8ICV6
	22	95.5	3.3	2063	11	Q80TB4
	23	95	3.3	731	10	Q9AW75
	24	94.5	3.3	896	11	Q91X10
	25	93.5	3.2	571	16	Q87L04
	26	93.5	3.2	1229	16	Q8D169
	27	93	3.2	692	5	Q965M1
	28	92.5	3.2	923	13	Q90ZT7
	29	92.5	3.2	956	5	Q8IBI0
	30	91.5	3.2	411	13	Q7SYF5
	31	91.5	3.2	618	4	Q8IUL4
	32	91.5	3.2	718	4	Q9BYH8
	33	91.5	3.2	846	2	Q93U47
	34	91.5	3.2	1096	5	Q8ICM0
	35	91	3.2	1386	8	Q9XMS2
	36	90.5	3.1	241	10	Q9XHB9
	37	90.5	3.1	776	2	Q9RAA7
	38	90.5	3.1	956	3	Q94717
	39	90.5	3.1	1627	5	Q8IAN6
	40	90.5	3.1	1672	5	Q8IEL8
	41	90	3.1	338	10	Q9FKN7
	42	90	3.1	592	5	Q86B11
	43	90	3.1	597	16	Q9PR58
	44	90	3.1	628	5	Q8I578
	45	90	3.1	1205	12	Q56300

#### ALIGNMENTS

RESULT 1

Q8JHU4  
ID Q8JHU4 PRELIMINARY; PRT; 584 AA.  
AC Q8JHU4;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Protein kinase RICK.  
OS RICK.  
GN Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP MEDLINE=98241596; PubMed=9575181;  
RX Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;  
RT "RICK, a novel protein kinase containing a caspase recruitment domain,  
interacts with CIARP and regulates CD95-mediated apoptosis.";  
RL J. Biol. Chem. 273:12296-12300(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Muto A., Ruland J., McAllister-Lucas L.M., Lucas P.C., Yamaoka S.,  
Chen F.F., Lin A., Mak T.W., Nunez G., Inohara N.;

RT "PKK mediates Bcl10-independent NF-kappa B activation induced by  
phorbol ester";

RL J. Biol. Chem. 0:0-0(2002).  
DR EMBL; AF487540; AAW76920.1; --  
DR GO; GO:0003622; C:intracellular; IEA.  
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR InterPro; IPR008271; Ser Thr\_pkin\_AS.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF00669; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TYRKc; 1.  
DR PROSITE; PS50209; CARD; 1.  
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 584 AA; 66124 MW; 7A4BFFCB65DEB9C0 CRC64;

## Alignment Scores:

Pred. No.: 1.66e-24 Length: 584  
Score: 335.00 Matches: 84  
Percent Similarity: 52.58% Conservative: 28  
Best Local Similarity: 39.44% Mismatches: 45  
Query Match: 11.63% Indels: 56  
DB: 13 Gaps: 7

US-09-771-161A-2 (1-1669) x Q8JHU4 (1-584)

QY 380 ATGGAATTATCTGTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCC 439  
DB 396 MetSerLeuProLeuMetAspProPro-----LysProLeuMetAspCysSerPro 412  
QY 440 TCTCAGCTCCATGAAATAGTGTCTCTCTGAA-----ACTTCA 478  
DB 413 AsnAsnLeu-----SerProGluTyrGlnThrAlaGlnValSerAsp 427  
QY 479 AGTCCCTGCGCA-----GCTCCTCAAGACAAATGATTTTATCTAGAAAAGCT 526  
DB 428 LeuAsnIleProPheLysAlaHisAlaProGlnSerGluLeuAlaLeuAlaIle 447  
QY 527 CAAGACTGTTATTTATGAAGCTGCATCTGCTGCTGGAATCACAGTTGGGATAGCACC 586  
DB 448 GlnPro-----LeuThrLeuHisProHisProGlnAspPheVal----- 460  
QY 587 ATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAGACCACTCCATGCTCTCTAGCA 646  
DB 461 -----ThrAlaPheAspGln----- 466  
QY 647 ATATATAATCCACTCAACTGCGAGGAATCAGAGCTCTGCGACCTGGTATAGCCAG 706  
DB 467 -----GlyProAlaAla 470  
QY 707 CAGTGGATCCAGACAAAGGAGACATTTGAAACCAATGACAGAGCTCTGCTTAAC 766  
DB 471 ArgTrpIleAlaAlaArgGluGluValValArgGlnMetThrGluAlaCysLeuAsn 490  
QY 767 CAGTCCGTAGATGCCCTTCTGTCAGGAGCTTGCATGATGAAGAGGACTATGAACCTTGT 826  
DB 491 GlnSerLeuAspAlaLeuLeuSerArgGluLeuLeuMetArgGluLeuVal 510  
QY 827 AGTACCAAGCTTCAAGGACTCAAAAGTACAGCAATTACTAGACTACTGACATCCAA 886  
DB 827 ----- 886

Db 511 ValAsnGlnThrArgThrAlaLysValArgLysLeuLeuAspThrCysGluArgHis 530  
QY 887 CGAGAAGATTGGCCAAAGCTTATAGTACAAATAATTGAAAGATAACAAACAAATGGGTCTT 946  
Db 531 SerGluGluPheCysArgValValValArgLysLeuGlnAspAsnLysGlnMetGlyLeu 550  
QY 947 CAGCCTTACCCCGAAATACTTGTGTTCTAGATCACCA 985  
Db 551 GlnProTyrProAspLeuSerThrThrSerSerProPro 563

## RESULT 2

Q8A9V6 PRELIMINARY; PRT; 791 AA.  
AC Q8A9V6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
OS Bacteroides thetaiotaomicron.  
GN Bt0709.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VPI-5482 / ATCC 29148;  
RX MEDLINE=22550858; PubMed=12663928;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";  
RL Science 299:2074-2076(2003).  
DR EMBL; AB016928; AAO75816.1; --  
DR InterPro; IPR001364; Hemagglutn.  
DR ProDom; PD000225; Hemagglutn. 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 791 AA; 88443 MW; 7C72011D0CD93232 CRC64;

## Alignment Scores:

Pred. No.: 0.166 Length: 791  
Score: 105.50 Matches: 64  
Percent Similarity: 32.73% Conservative: 44  
Best Local Similarity: 19.39% Mismatches: 97  
Query Match: 3.66% Indels: 125  
DB: 16 Gaps: 14

US-09-771-161A-2 (1-1669) x Q8A9V6 (1-791)

QY 323 TATTCATTACAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATG 382  
Db 452 TyrThrLeuSerLeuGlnAlaIle-----ArgLysLysAsn 463  
QY 383 GAATTATCTCTGAACATACCT----- 403  
Db 464 ThrAlaAlaThrAsnLeuProAspGluProGluProLysLeuAlaPheProLeuIle 483  
QY 404 -----GTAATCATGTGTCACAGAGGAATCATGTGGA 436  
Db 484 ProAlaAspIleSerArgAlaGlnLeuIleThrHisLeuIleAsnAsnGlnSerCysSer 503  
QY 437 TCTCTCAGCTCCATGAAAATAGTGTCTCTGTAACCTCAAGTCCCTGCCAGCTCCT 496  
Db 504 SerLeuLeuThrSerThrGluAlaSerSerValSerThrAlaArgAsnGlnAspTyrGly 523  
QY 497 CAAGCAATGATTTTATCTAGAAAAGCTGTTATTTATGAAGCTGCATCAC 556  
Db 524 HisPheAspIleLeuCysLysAlaPheGluHisGluLeuLeuSerSerTyrLys 543  
QY 557 TGTCTCGAAATCAC-----AGTTGGATAGACCATTTCTGGA 595  
Db 544 IleAsnGlyArgHisProLeuLysValGluTyrProSerLeuSerAlaPheLeuThrGly 563  
QY 596 TCTCAAGGGCTCCATCTCTGTGATCACAGACCATCTCCATGCTCTTCAGCAATAATAAT 655  
Db 596 ----- 655



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Db 564 -----ThrProSerSerLeuLeuPheile 572
QY 656 CCACCTCTCACTGCAGGA-----AACTCAGAACTCTG----- 688
Db 573 ProThrMetGluThrGlyLeuTyraAsnArgPheLeuLeuAsnThrPheArgLeuProAla 592
QY 689 -----CAGCCTGGTATAGCCAGCAGTGATCCAGAGCAAAAGGAGACATTTGTGAAC 742
Db 593 AlaTrpGlnAspValPheAlaGluGluysValaIrgAla-----AspAspLeuPheAsn 610
QY 743 CAATGACAGAGAGCTGCCTTAAACAGTCGTAGATGCCCTTCTGTCAGGAGCTGATC 802
Db 611 GluLeuSerMetArgPheAlaGlnMetAlaLeu----- 621
QY 803 ATCAAGAGGAGCTATGAACCTTGTAGTACCAAGCCTTACAGGACCTCAAAAGCTCAGACAA 862
Db 622 -----PheLeuLysAspSerProThrGlu----- 629
QY 863 TTACTAGACACTACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATG 922
Db 630 ---ValLysLeuThrAspThrGlnLysLysGluPheAsnArgValPheThrGlnLeuLeu 648
QY 923 AAAGATAACAACAATGGTCTTACGCTTACCCGGAATACTT---GTGGTTTCTAGA 979
Db 649 LysAspThrAspGlnLeuGly-----AsnAspAspLeuLeuGlyValValLysArg 665
QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTGAAGTCTTTTCAAGAGAA 1039
Db 666 -----TyrGlyValIleThrAlaArg 672
QY 1040 ATGTGTTTCAATA-----AAAGA----- 1057
Db 673 IleCysCysIlePheSerAlaIleAspLysGlyThrMetArgMetGluThrProGluVal 692
QY 1058 -----TATTTATATCTCTGTGTTGCTTGTGACTTT 1084
Db 693 TyrCysSerAspAlaHisPheLysAlaAlaLeuAlaIleValLeuLysCysPheGluHis 712
QY 1085 TTTTATATAAATCCGTGAGTATTAAAGCT 1114
Db 713 SerLysLeuValSerThrSerValLysSer 722

RESULT 3
Q81JEB
ID AC Q81JEB PRELIMINARY; PRT; 1309 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN PF10_0250.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Paine A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perle M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., R.W.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014833; AN35447.1; --
KW Hypothetical protein.
SQ SEQUENCE 1309 AA; 158469 MW; 5FF6811DE127D910 CRC64;

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Alignment Scores:
Pred. No.: 0.449 Length: 1309
Score: 101.50 Matches: 82
Percent Similarity: 38.46% Conservative: 73
Best Local Similarity: 20.35% Mismatches: 143
Query Match: 3.52% Indels: 105
DB: 5 Gaps: 18

US-09-771-161A-2 (1-1669) x Q81JEB (1-1309)
QY 176 CTGCTTTTCTCCTTCAGTTATATATATCTCAACTCTTTATATTTCTTCTTC----- 229
Db 46 LeuCysTyrAspLysMetIleMetPheTyrCysAsnThrPheAspTyrLeuLysAspAsn 65
QY 230 -----ATGTATTTTCTACAAACA-----TATAAAATGTTAGATTGTA 268
Db 66 ValValIleCysIleAspThrPheLeuGlnThrLysLysTyrMetLeuLysLysLeuIle 85
QY 269 TTTTACTTCTATAATTTCTCAATCATCTCCAGTTAAAGTGTATATATATTTATGTTATCA 328
Db 86 ValAspLysLysAsnPheValTyrIleLys-----TyrGluTyrPheTyrLys 101
QY 329 TTACAGTTACAGAGTGTTCAGT---GCCATTACCTATGTGAC----- 370
Db 102 IleLysLeuSerSerTyrSerThrAspHisIleAsnIleCysAspLysIleCysAspAsp 121
QY 371 ---AAGAAGAAATGGAATTTATCTCGAATATCTCGAATATCTCGAATATCTCGAATATCT 427
Db 122 GluLysAsnLysLysLys-Tyr-----IleMetLysAsnAs 133
QY 428 TCATGTGATCTCTCAGCTCCATCCATGAAATAGTGTCTCTGAAACTTCAAGGTCCTCG 487
Db 133 nHisIleAspAsn----- 137
QY 488 CAGCTCTCTCAAGACAATGATTTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAG 547
Db 138 -----PheIleAsnLysLeuLysLysPheAsnAsnGluAs 149
QY 548 CTGCATCACTGTCCTGGAA---ATCACAGTTGGGATAGCACCATTCTTCGATCTCAAAGG 604
Db 149 nCysTyrLeuIlePheGlnGlyValAspGlnAsnIleTyrThrIleLeuLysGlnAsnAs 169
QY 605 GCTGCATCTGTGATCAAGAACCACTCCATCTCTTACAGCAATAATAATCACTCTCA 664
Db 169 nLeuAsnArgile-----Tyr-IlePheLeuAsnAspIleAsnLysIleA 184
QY 665 ACTGCAGGAATCTAGAACGCTGCGAGCTGTATAGCCACAGCTGGATCCAGACAA 724
Db 184 snLeuAsnLysIleAsnThrHis-----TyrHisValIleMet-CysAsnTyrThr 200
QY 725 AGGGAAGACATTTGTAACCAATATGACAGAACCTCGCTTAACACAGTCGCTAGATGCCCTT 784
Db 201 LysGluAsnIleIleAsnLeuIleLysTyrTyrTyrGluLysGluLysGlnTyrVal 220
QY 785 CTGTCAGGAGCTTCATCATGAAGAGGACTAT----- 817
Db 221 GlnGlnAsnAspGluIleAsnGlnGluAspTyrGlnGluArgValMetAsnLeuTyrAsn 240
QY 818 GAACCTGTTAGTACCAAGCCTACAGGACCTCAAAGTCAGACAAATTACTAGACACTACT 877
Db 241 GluCysLeuAsnAsnGluLysThrLysGluValValLysGluIleSerGluGluLys 260
QY 878 GACATCCAGGAGAA-----GAATTTTGCACAA 904
Db 261 GluLysHisAsnGlnHisIleLysAsnSerAsnThrLysAspGluLysGluPheAlaLeu 280
QY 905 GTT-----ATAGTACAAAATTCAAA---GATAACAAAACAAATGGTCTTT 946
Db 281 IleTyrValPheTyrLeuLeuIleGluSerLeuLysTyrIleAsnGlnGlnTyrIle 300
QY 947 ---CAGCCTTACCCGGAATATCTTGTGTTTCTAGATCACCATCTTTAATTTACTTCAA 1003
Db 947 ---CAGCCTTACCCGGAATATCTTGTGTTTCTAGATCACCATCTTTAATTTACTTCAA 1003

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301 CysAsnThrPheLeuLysIleValLysSerPheSerArgHisPheAsnIleMetAsn 320  
 1004 AATAAAGCAGTAAGTACTGTTTCAAGAGAAATGTTTCAATAAAGGATATTTA 1063  
 321 AsnLys-----GlnAlaGluIle-----TyrIleLeuAsnTyrPhe 332  
 1064 TATCTCTGTTGCTTGCATTTTATATAAATCCGTGAGTA-----TT 1108  
 333 TyrPheTyrIleLeuSerLeuIleTyrAsnLysAspIle-LeuThrValAsnPheIleLeu 352  
 1109 AAAGCTTTATGAAGGTTCTTGGGTAATATTAGTCTCCCTCCATGACACATGATTT 1168  
 352 uSerIleTyrIleAspIlePheValAsnAsnLeuIleLysTyrIleAspIlePheLeuPh 372  
 1169 TTTTAAATTAATACAAAGTTTGAATTTTCTACATAGTTCAATTTTATGCTT 1228  
 372 ePheLysThrPheThrAsnGlnAsnLysGluLysCysIleGlnLysTyrIleAsnLeu 392  
 1229 C 1229  
 392 u 392

RESULT 4

Q811Z1 PRELIMINARY; PRT; 734 AA;  
 AC Q811Z1;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein, conserved.  
 GN PF0185C.  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RX MEDLINE=2255708; PubMed=12369867;  
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
 Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
 Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
 Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
 Cronin A., Davies P., Davis P., Dear P., Dearden F., Doggett J.,  
 Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
 Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,  
 Humphrey S., Jagels K., James K.D., Johnson D., Kerhornou A.,  
 Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
 Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,  
 Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
 Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
 Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,  
 Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
 Sulston J.E., Craig A., Newbold C., Barrell B.G;  
 "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13";  
 Nature 419:527-531(2002).  
 RL Nature 419:527-531(2002).  
 DR EMBL; AL034557; CAD49130.1;  
 DR GO; GO:0003824; F:catalytic activity; IDA.  
 DK InterPro; IPR000379; Ser\_estrs.  
 KW Hypothetical protein.  
 SQ SEQUENCE 734 AA; 83360 MW; 7ADBBD4F3D8F69EC CRC64;

Alignment Scores:

Pred. No.: 0.463 Length: 734  
 Score: 101.00 Matches: 76  
 Percent Similarity: 35.65% Conservat: 73  
 Best Local Similarity: 18.18% Mismatches: 163  
 Query Match: 3.51% Indels: 106  
 DB: 5 Gaps: 17

US-09-771-161A-2 (1-1669) x Q811Z1 (1-734)

QY 5 AGTTTATACCAGATATTTTATATATAGGTCATCTAGAACCATCTGCCATGTA 64  
 DB 249 SerValTyr---AspIleSerAsnIleAsnThrGlnLysLeuArgAsnMetPheIleLeu 267

QY 65 GGTAAATTGTTAGATTTCGAGGATGAAGCTCTGAGACACTGAGAGAGGTAACCAATTAT 124  
 DB 268 AsnAsnThrGluLysLeuLysAspLysLeu-----LysGluLysIleGly 282  
 QY 125 ATGAGCCAGGATCAAGTCTGTGTCTAAGATTATTCCCGTCTACACTGCTCTTT 184  
 DB 283 AspLysGluLysLysAspLeuThrSerLysIleLysLysAsnGluLysValIleLeu 302  
 QY 185 CTTTCAGTTATATATATATT-----CTCAACTCTTTATATTTCTTTCCATGTAT 235  
 DB 303 AsnAsnLysIleProLysLysLysAspValAsnSerTyrTyrSerSerMetGlu 322  
 QY 236 TTTGTA-----CAAAACATATAAATGTGTTAGATT-----GTATTTTACTTCTAT 280  
 DB 323 GlyIleGlySerSerThrGlnAsnIleCysLysValGlnSerSerThrGluSerSerTyr 342  
 QY 281 AATTCTCTTAATCATCTCCAGTTAAAGTGTATATATATTTATGTATTCATTACAG----- 334  
 DB 343 AsnSerLeuThr-----SerValSerThrIleLeuAlaSerIleGluSerIle 358  
 QY 335 TTACAGAGTGTTCGAGTCCCATTCACCTATGTGCAAGAGAAATGAATATATCTCTG 394  
 DB 359 MetLysGlyIleProAspSerAsnThrLeuCysGluLysAsnSerValGlnArgAsnAsn 378  
 QY 395 AACATACCTGTAAATCATCGTCCACAAGAG-----GAATCATGT----- 433  
 DB 379 AsnIleLysLysAsnAsnSerSerAsnGluIleTyrSerAspCysAsnProGlyTyrAsn 398  
 QY 433 ----- 433  
 DB 399 TyrTyrThrAsnAsnLysTyrAspAsnLeuTyrSerProAsnLysValThrSerIleAsn 418  
 QY 434 -----GGATCTCTCTCAGCTCCAT 451  
 DB 419 AsnAsnLysMetAspGlnLysAsnHisLysLysGlyAsnAsnLysSerSerAsnAsn 438  
 QY 452 GAAATAGTGTCTCTCTGAACTTCAAGTCTCCAGCTCCCTCAACACATGATTTT 511  
 DB 439 AsnAsnAsnAsnAsnAsnAsnAsnAsnSerSerSerSerSerSerSerSerMet 458  
 QY 512 ---TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCTCTCTCGAAAT 568  
 DB 459 SerLeuAsnMetLysThrLeuSerSerTyrThrLeuLysAsnLysAsnThrGlnGlyAsn 478  
 QY 569 CACAGTTGGGATAGCACCACTTTCTGCATCTCAAGGGCTGCATCTGTGATCAAGACC 628  
 DB 479 SerAsnHisAspAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnSerAsnSerAsn 498  
 QY 629 ACTCCATGCTCTTACAGCAATAATAATCCACTCTCA-----ACTCGAGAAAC----- 676  
 DB 499 SerThrCysSerSerHisSerLysAsnAsnLeuSerTyrAsnAsnLysGlyAsnGlyLeu 518  
 QY 677 -----TCAGAACCTGTGACGCTGTATAGCCAGCAGTGCATCCAG 718  
 DB 519 IleAsnThrAsnIleGlySerSerAsnValLysProAsnIle-----ArgIleLeuGln 536  
 QY 719 AGCAAAAGGAGACATTT-----GTGAACCAATGACA 751  
 DB 537 ThrLysArgAsnSerTyrLysValAspLysValProArgIleAsnPheAspAsnMetLys 556  
 QY 752 GAAGCTGCTTAACGAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAAGAG 811  
 DB 557 LysAsnIleIleSerGluGlnIleAspSer-----AsnIleValTyrAsnAsn 572  
 QY 812 GACTATGAATCTGTATTAGTACCAAGCCCTACAGGACCTCAAAAGTCAGACAATTACTAGAC 871  
 DB 573 SerTyrGluLeuIleLysAspGlyValTyrIleLysLysLysIleAsnAsnAsnAsn 592  
 QY 872 ACTACTGACATCCAGAGGAAGAAATTGGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 DB 593 AsnAsnAsnIleLys---GlnGluSerSerSerLeuValTyrAsnAsnLeuSer----- 609

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QY 932 AAACAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACAATCTTTA 991
Db 610 -----SerProHisille 613
QY 992 AATTACTTCAAAATAAAGCATGTAAGTACTGTTTTCACAGAAATGTGT 1045
Db 614 AsnGlnGlyLeuAsnAsnThrArgTyrValSerCysGluLysAlaLysLeuCys 631

RESULT 5
Q9J861
ID Q9J861 PRELIMINARY; PRT; 461 AA.
AC Q9J861;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ORF76 CG30.
OS Spodoptera exigua nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10454;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036646; PubMed=10567663;
RA IJkel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
RA Goldbach R.W., Viak J.M.;
RT "Sequence and organization of the spodoptera exigua multicapsid
RT nucleopolyhedrovirus genome."
RL J. Gen. Virol. 80:3289-3304 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA IJkel W.F., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.,
RA Goldbach R.W., Viak J.M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF169823; RAF33605.1; -.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 461 AA; 50820 MW; 6C062A3B43DD5D06 CRC64;

Alignment Scores:
Pred. No.: 0.484 Length: 461
Score: 100.50 Matches: 72
Percent Similarity: 36.23% Conservative: 53
Best Local Similarity: 20.87% Mismatches: 121
Query Match: 3.49% Indels: 99
DB: 12 Gaps: 13

US-09-771-161A-2 (1-1669) x Q9J861 (1-461)
QY 189 CAGTTATATGTTATCTCACTCTTATATTTCTTCCATGTTATTTGTACAAACAT 248
Db 27 GlnMetPheVal-----ProLeuPheIleLeuAspGluCys-----LysHis 41
QY 249 ATAAATGTGT-----AGATTGTTATTTTACTTCT 278
Db 42 ValLeuCysLeuMetCysCysLysSerIleGlnAspGlyArgArgAlaIleThrCys 61
QY 279 ATAAATTCCTAATCATCTCCAGTTAAAGTGTTATATATTTATTTATTTATTTACAGTTAC 338
Db 62 ProThrCysArgValSerSerGluLysLeuPheSerTyr-----PheTyrGlySerAsn 79
QY 339 AGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTCTGAACA 398
Db 80 GlyLeuValLysPheAsnPheThrLeuAsnSerAlaGluLysPheAspMetArgAlaAsn 99
QY 399 TACCTGTGAATCATGTCACCAAGAGGAATCAT-----GTGGATCTCTTC 443
Db 100 -----IleuAlaHisValAsnGluArgPheLysPheAlaIleValAspSerLeu 116
QY 444 AGCTCCATGAAATAGTGTCTCTCGTGAACCTTCAAGGTCCTG----- 487
```

## RESULT 6

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Q9QZC6
ID Q9QZC6 PRELIMINARY; PRT; 589 AA.
AC Q9QZC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RT Cloning of cDNA for rat inhibitor of apoptosis protein 2.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1; -.
DR HSP; Q13490; IQBH.
DR GO: GO:0005622; C:intracellular; IEA.
```

DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.  
 DR GO; GO:0006916; P:anti-apoptosis; IEA.  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00184; RING; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS0209; CARD; 1.  
 DR PROSITE; PS0089; zf-RING\_2; 1.  
 KW Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 589 AA; 66777 MW; E6812FFB3EA34142 CRC64;

Alignment Scores:  
 Pred. No.: 0.564 Length: 589  
 Score: 100.00 Matches: 32  
 Percent Similarity: 42.54% Conservative: 25  
 Best Local Similarity: 23.88% Mismatches: 61  
 Query Match: 3.47% Indels: 16  
 DB: 11 Gaps: 3

US-09-771-161A-2 (1-1669) x Q9QZC6 (1-589)

QY 713 ATCCAGAGCAAAAGGAGACATTTGCAACCAATGACAGAACGCTTCCTTACCAGTCG 772  
 DB 432 IleArgLysAsnArgMetalalaLeuPheGlnLeuThr-----CysValIleProIle 449  
 QY 773 CTAGATGCCCTTCTGTCCAGGGACTTGATCATCAAGAGGACTATGAACTTGTAGTACC 832  
 DB 450 LeuAspLeuLeuGluAlaSerValLeuThrLysGluHisAspIleIleArgGln 469  
 QY 833 AAGCTCAAGAGCACTCAAAAGTCAGCAATTAAGTACACTGACATCTGACATCCAGAGAA 892  
 DB 470 LysThrGlnIleProLeuGlnAlaArgGluLeuIleAspThrIleLeuValLysGlyAsn 489  
 QY 893 GAATTTGCCAAAGTTATAGTACAAAATTCAGAGAT----- 928  
 DB 490 AlaAlaSerValPheLysAsnSerLeuLysGluValAspSerThrLeuTyrGluHis 509  
 QY 929 -----AACAAACAAATGGGTCTTCAGCCTTACCCTCCGGAATATCTTGTGGTTCTAGA 979  
 DB 510 LeuPheValGluLysThrMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 529  
 QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAA 1039  
 DB 530 GluGluGlnLeuArgArgLeuGlnGluArgThrCysLysValCysMetAspArgGlu 549  
 QY 1040 ATGTGTTTCATA-----AAAGGATATTTATCTCTGT 1072  
 DB 550 ValSerIleValPheIleProCysGlyHisLeuValValCys 563

RESULT 7

Q9ESE8 PRELIMINARY; PRT; 589 AA.  
 ID Q9ESE8  
 AC Q9ESE8  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Inhibitor of apoptosis protein 2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;  
 RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of  
 Apoptosis Protein 1, 2, and 3 Genes.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR HSSP; Q13490; 1QBH.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.  
 DR GO; GO:0006916; P:anti-apoptosis; IEA.  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS0209; CARD; 1.  
 DR PROSITE; PS0089; zf-RING\_2; 1.  
 KW Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B .CRC64;

Alignment Scores:  
 Pred. No.: 0.564 Length: 589  
 Score: 100.00 Matches: 32  
 Percent Similarity: 42.54% Conservative: 25  
 Best Local Similarity: 23.88% Mismatches: 61  
 Query Match: 3.47% Indels: 16  
 DB: 11 Gaps: 3

US-09-771-161A-2 (1-1669) x Q9ESE8 (1-589)

QY 713 ATCCAGAGCAAAAGGAGACATTTGCAACCAATGACAGAACGCTTCCTTACCAGTCG 772  
 DB 432 IleArgLysAsnArgMetalalaLeuPheGlnLeuThr-----CysValIleProIle 449  
 QY 773 CTAGATGCCCTTCTGTCCAGGGACTTGATCATCAAGAGGACTATGAACTTGTAGTACC 832  
 DB 450 LeuAspLeuLeuGluAlaSerValLeuThrLysGluHisAspIleIleArgGln 469  
 QY 833 AAGCTCAAGAGCACTCAAAAGTCAGCAATTAAGTACACTGACATCTGACATCCAGAGAA 892  
 DB 470 LysThrGlnIleProLeuGlnAlaArgGluLeuIleAspThrIleLeuValLysGlyAsn 489  
 QY 893 GAATTTGCCAAAGTTATAGTACAAAATTCAGAGAT----- 928  
 DB 490 AlaAlaSerValPheLysAsnSerLeuLysGluValAspSerThrLeuTyrGluHis 509  
 QY 929 -----AACAAACAAATGGGTCTTCAGCCTTACCCTCCGGAATATCTTGTGGTTCTAGA 979  
 DB 510 LeuPheValGluLysThrMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 529  
 QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAA 1039  
 DB 530 GluGluGlnLeuArgArgLeuGlnGluArgThrCysLysValCysMetAspArgGlu 549  
 QY 1040 ATGTGTTTCATA-----AAAGGATATTTATCTCTGT 1072  
 DB 550 ValSerIleValPheIleProCysGlyHisLeuValValCys 563

RESULT 8

Q8IN63 PRELIMINARY; PRT; 799 AA.  
 ID Q8IN63  
 AC Q8IN63  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CG12249-PB (LD02989p).  
 GN MIRA OR CG12249.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea: Drosophilidae; Drosophila.  
 RN NCBI\_TaxID=7227;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Hoskins R.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Gallie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brokstein P.,  
 RA Chertkov K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glöckle A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Barzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of *Drosophila melanogaster* genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Mitra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clump M., Drysdale R., Emert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of *Drosophila melanogaster* genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Guarin H., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003728; AANI3815.1; -;  
 DR EMBL; BT004903; AAO47881.1; -;  
 DR FlyBase; FBgn0021776; mira;  
 DR GO; GO:0045180; C:basal cortex; NAS;  
 DR GO; GO:0008105; P:asymmetric protein localization; IGI;  
 SQ SEQUENCE 799 AA; 89816 MW; AE00B9F2C7F654B6 CRC64;  
 Alignment Scores:  
 Pred. No.: 0.662 Length: 799  
 Score: 99.50 Matches: 59  
 Percent Similarity: 37.50% Conservative: 49  
 Best Local Similarity: 20.49% Mismatches: 111  
 Query Match: 3.45% Indels: 69  
 DB: 5 Gaps: 10  
 US-09-771-161a-2 (1-1669) x Q8IN63 (1-799)  
 QY 353 GCCATTACCTATGTGACAAAGAAATGGAAATTCTCTGAACATACCTGTAAATCAT 412  
 DB 64 AlavalArgPheAlaSerSerSerLysGluAlaLysGluPheAlaIlePro----- 80  
 QY 413 GGTCCACAGAGGAATCATGTGGATCTCTAGCTCCATGAAATAGTGGTCTCTCTGAA 472  
 DB 81 ---LysGluAspLysLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGin 99  
 QY 473 ACTTCAAGGTCCCTCCAGCTCTCTCAAGACATGATTTTATCTAGAAAGCTCAAGAC 532  
 DB 100 ArgLeuArgPheArgProThrProSerHisThrAspThrAlaThrGlySerGly----- 117  
 QY 533 TGTATTATTAAGCTGCATCACTCTCTGGAATACAGTTGGATAGCACCATTCTT 592  
 DB 118 -----Ser 118  
 QY 593 GGATCTCAAGGGCTGCATTCTGTGATCAAGACACCTCCATGCTCTTTCAGCAATAATA 652  
 DB 119 GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133  
 QY 653 ATCCACTCTCACTGCAGGAACCTCAGAACCTCTGCAGCTGTATATGCCAGCAGTGG 712  
 DB 134 ThrProValLysGluAlaLysSerAlaSerArgLysGlyLysGluAlaLeuGlnTyr 153  
 QY 713 --ATCCAGCAAAAGGAAGACATTTGTGAACCAATGACAGAGGCC---TGCCTTAAC 766  
 DB 154 GluIleArgHisLysAsnGluLeuLeuGluSerGlnLeuSerGlnLeuAspValLeuArg 173  
 QY 767 CAGTCGTAGTACCTCTGTCCAGGGACTTGTATCATGAAAGAGCATTATGAACCTGTT 826  
 DB 174 ArgHisValAspGlnLysGluAlaLysLeuArgLysGluLysGluLeuAla 193  
 QY 827 AGTACCACGCTACAGG-----ACCTCAAAAGTCAGACAATTACTAGAC 871  
 DB 194 ThrSerLysThrAspArgLeuLeuGluAlaLeuThrSerGlnAsnLeuSerHisLysAla 213  
 QY 872 ACTACTGACATCCAAGGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 DB 214 LeuAsnGluGlnMetGlyGlnGluHisAlaAsp---LeuLeuGluArgLeuAlaMet 232



Db 119 GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133  
QY 653 AATCCACTCTCAACTGCAGAACTCAGAACGCTGCGACCTGGTATAGCCAGCAGTGG 712  
Db 134 ThrProValGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnTyr 153  
QY 713 ---ATCCAGAGCAAAAGGAGACATTGTGAACCAATGACAGAGCC---TGCCTTAAAC 766  
Db 154 GluIleArgHisLysAsnGluLeuIleGluSerGlnLeuSerGlnLeuAspValLeuArg 173  
QY 767 CAGTCGCTAGATGCCCTCTGCTCCAGGAGCTTGATCATGAAAGAGGACTATCACTTGT 826  
Db 174 ArgHisValAspGlnLeuLysGluAlaGluAlaLysLeuArgGluHisGluLeuAla 193  
QY 827 AGTACCAAGCCTTACAAG-----ACCTCAAAAGTCCAGCAATTAAGTACAG 871  
Db 194 ThrSerLysThrAspArgLeuIleGluAlaLeuThrSerGluAsnLeuSerHisLysAla 213  
QY 872 ACTACTGACATCCAGGAGCAAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATTAAC 931  
Db 214 LeuAsnGluGlnMetGlyGlnGlnHisAlaAsp---LeuLeuGluArgLeuAlaMet 232  
QY 932 AAACAAATGGGTCTTCAGCCTTACCCTGAA-----ATATTACTTCAAAATAAAGTGA 1024  
Db 233 GluGlnGlnLeuGlnGlnHisAspGluHisGluArgGlnValGluAlaLeuValAla 252  
QY 977 AGATCACCATCTTTA-----AATTACTTCAAAATAAAGTGAAGTGA 1024  
Db 253 GluSerGluAlaLeuArgLeuAlaAsnGluLeuGlnThrAlaAsnGluAspArgGln 272  
QY 1025 GTTTTTCAGAGAAATGTGTTTCAATAAAGGATATTATATCTCTGTGCTTGTGACTTT 1084  
Db 273 LysValGluGluGln----- 277  
QY 1085 TTTTATATAAATCCGTGAGTATTAAAGCTTTATTGAAGTCTTCTTGGTAAATATTAGT 1144  
Db 278 -----LeuGlnAlaGlnLeuSerAlaLeuGlnAlaAspValAla 290  
QY 1145 CTCCTCCATGACACTGCAGTATT 1168  
Db 291 GlnAlaArgGluHisCysSerLeu 298  
RESULT 10  
O45116 PRELIMINARY; PRT; 830 AA.  
ID AC O45116;  
DT 01-JUN-1998 (TREMELrel. 06, Created)  
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE MIRANDA.  
GN MIRA OR CG12249.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CANTON-S;  
RX MEDLINE=97410310; PubMed=9267025;  
RA Shen C.P., Jan L.Y., Jan Y.N.;  
RT "Miranda is required for the asymmetric localization of Prospero during mitosis in Drosophila.";  
RL Cell 90:449-458(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CANTON-S;  
RA Shen C.P., Jan L.Y., Jan Y.N.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF045771; AAC02621.1; --  
DR Flybase; FBgn0021776; mira.  
DR GO; GO:0045180; C:basal cortex; NAS.  
DR GO; GO:0008105; P:asymmetric protein localization; IGI.

SQ SEQUENCE 830 AA; 93112 MW; 72F80EDC3FE6113B CRC64;  
Alignment Scores:  
Pred. No.: 0.666 Length: 830  
Score: 99.50 Matches: 59  
Percent Similarity: 37.50% Conservative: 49  
Best Local Similarity: 20.49% Mismatches: 111  
Query Match: 3.45% Indels: 69  
DB: 5 Gaps: 10  
US-09-771-161A-2 (1-1669) x O45116 (1-830)  
QY 353 GCCATTACCTATGTGACAGAGAAATGGAATATTCTCTGAACATACCTGTAAATCAT 412  
Db 64 AlaValArgPheAlaSerSerLysGluAlaLysGluPheAlaIlePro----- 80  
QY 413 GGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTCTCTCTGAA 472  
Db 81 ---LysGluAspLysLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGln 99  
QY 473 ACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTATCTAGAAAAGCTCAAGAC 532  
Db 100 ArgLeuArgPheArgProThrProSerHisThrAspThrAlaThrGlySerGly----- 117  
QY 533 TGTATTTTATGAAGCTGCATCACTGTCTGCTGAAATCACAGTTGGATAGCACCATTCT 592  
Db 118 ----- 118  
QY 593 GGATCTCAAGGGCTGCATTCTGTGATCAAGACCACCTCCATGCTCTTTCAGCAATAATA 652  
Db 119 GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133  
QY 653 AATCACCCTCTCACTGCGAGAACTCAGAACGCTCTGACGCTGGTATAGCCAGCAGTGG 712  
Db 134 ThrProValLysGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnTyr 153  
QY 713 ---ATCCAGAGCAAAAGGAGACATTGTGAACCAATGACAGAGCC---TGCCTTAAAC 766  
Db 154 GluIleArgHisLysAsnGluLeuIleGluSerGlnLeuSerGlnLeuAspValLeuArg 173  
QY 767 CAGTCGCTAGATGCCCTCTGCTCCAGGAGCTTGATCATGAAAGAGGACTATCACTTGT 826  
Db 174 ArgHisValAspGlnLeuLysGluAlaLysLeuArgGluHisGluLeuAla 193  
QY 827 AGTACCAAGCCTTACAAG-----ACCTCAAAAGTCCAGCAATTAAGTACAG 871  
Db 194 ThrSerLysThrAspArgLeuIleGluAlaLeuThrSerGluAsnLeuSerHisLysAla 213  
QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATTAAC 931  
Db 214 LeuAsnGluGlnMetGlyGlnGlnHisAlaAsp---LeuLeuGluArgLeuAlaMet 232  
QY 932 AAACAAATGGGTCTTCAGCCTTACCCTGAA-----ATATTACTTCAAAATAAAGTGA 1024  
Db 253 GluSerGluAlaLeuArgLeuAlaAsnGluLeuGlnThrAlaAsnGluAspArgGln 272  
QY 1025 GTTTTTCAGAGAAATGTGTTTCAATAAAGGATATTATATCTCTGTGCTTGTGACTTT 1084  
Db 273 LysValGluGluGln----- 277  
QY 1085 TTTTATATAAATCCGTGAGTATTAAAGCTTTATTGAAGTCTTCTTGGTAAATATTAGT 1144  
Db 278 -----LeuGlnAlaGlnLeuSerAlaLeuGlnAlaAspValAla 290  
QY 1145 CTCCTCCATGACACTGCAGTATT 1168  
Db 291 GlnAlaArgGluHisCysSerLeu 298  
RESULT 11



```
O04224
ID O04224 PRELIMINARY; PRT; 830 AA.
AC O4224;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MIRANDA.
GN MIR OR CG12249.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=9605952; PubMed=9403694;
RA Ikeshima-Kataoka H., Skeath J.B., Nabeshima Y., Doe C.Q.,
RA Matsuzaki F.;
RT "Miranda directs Prospero to a daughter cell during Drosophila
RL asymmetric divisions.";
RL Nature 390:625-629(1997).
DR ENBL; AB005861; BAA24111.1; -.
DR PIR; T00029; T00029.
DR FlyBase; FBgn0021776; mira.
DR GO; GO:0045180; C:basal cortex; NAS.
DR GO; GO:0008105; P:asymmetric protein localization; IGI.
SQ SEQUENCE 830 AA; 93171 MW; F7AD159AA58F178A CRC64;

Alignment Scores:
Pred. No.: 0.666 Length: 830
Score: 99.50 Matches: 59
Percent Similarity: 37.50% Conservative: 49
Best Local Similarity: 20.49% Mismatches: 111
Query Match: 3.45% Indels: 69
DB: 5 Gaps: 10

US-09-771-161A-2 (1-1669) x O4224 (1-830)
QY 353 GCCATTACCTATGTGACAGAGAAATGGAATATCTCTGAACATACCTGTAAATCAT 412
Db |||...|||
64 AlaValArgPheAlaSerSerLysGluAlaLysGluPheAlaLysPro----- 80
QY 413 GGTCCACAGAGGAATCATGTGGCTCTCAGCTCCATGAAATAGTGTCTCTCGTAA 472
Db |||...|||
81 ---LysGluAspLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGln 99
QY 473 ACTTCAGGTCCTGCCAGCTCTCAGACAGAAATGTTTATCTAGAAAGCTCAAGAC 532
Db |||...|||
100 ArgLeuArgPheArgProThrProSerHisThrAlaThrGlySerGly----- 117
QY 533 TGTATTATTTAAGCTGCATCACTGTCTCGGAAATCACAGTTGGGATAGCACCATTCT 592
Db |||...|||
118 -----Ser 118
QY 593 GGATCTCAAGGGCTGCATTCTGTGATCACAGACCACTCCATCTCTCAGCAATAATA 652
Db |||...|||
119 GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133
QY 653 AATCCATCTCACTCAGGAAACTCAGACGCTGCAGCTGTGTATAGCCAGCAGTGG 712
Db |||...|||
134 ThrProValLysGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnTyr 153
QY 713 ---ATCCAGAGCAAAAGGAGACATGTGAAACCAATGACAGAGCC---TGCCCTTAAC 766
Db |||...|||
154 GluLeuArgHisLysAsnGluLeuLeuLeuSerGlnLeuSerGlnLeuAspValLeuArg 173
QY 767 CAGTCGTAGATGCCCTTCTGTCCAGGACTTATGATCAAGAGAGCACTAGCACTGTT 826
Db |||...|||
174 ArgHisValAspGlnLeuLysGluAlaGluAlaLysLeuArgGluGluHisGluLeuAla 193
QY 827 AGTACCAGCCTACAAG-----ACCTCAAAAGCTCAGACAATTACTAGAC 871
Db |||...|||

RESULT 12
Q9FTV4 PRELIMINARY; PRT; 869 AA.
ID Q9FTV4;
AC Q9FTV4; (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0407B12.26 protein.
GN P0407B12.26. (Rice).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0407B12.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF002843; BAB17189.1; -.
DR Gramene; Q9FTV4; -.
SQ SEQUENCE 869 AA; 97064 MW; E2E59640E0BE63B2 CRC64;

Alignment Scores:
Pred. No.: 0.67 Length: 869
Score: 99.50 Matches: 59
Percent Similarity: 37.83% Conservative: 42
Best Local Similarity: 22.10% Mismatches: 83
Query Match: 3.45% Indels: 83
DB: 10 Gaps: 14

US-09-771-161A-2 (1-1669) x Q9FTV4 (1-869)
QY 317 TTTATGTATTCATACAGTTTCAAGTGCCTTCACTTACCTATGTGACAGAAG 376
Db |||...|||
298 PheGluHisGlnLeuAsnGluPheAlaAsnSerAlaPheArgLeuAsnGluHisSer 317
QY 377 AAAATCGAATTA-----TCTCTGAACATACCTGTAAATCAT 412
Db |||...|||
318 SerMetGlnLeuAsnLeuAspPheGlyAspAspHisSerSerSerSerHis 337
QY 413 GGTCCACAGAGGAATCATGTGATGCTCTCT-----CAGCTCCATGAAATAGTGT 463
Db |||...|||
338 AspArgThrGluLysGlyCysGlySerArgSerIleGlnLeu---LysThrAspGly 356
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QY 464 -----TCTCTGAAACTTCAAGGTCCTCCAGCTCTCTCAAGACAAATGATTTT 514  
 Db 357 LeuLeuLeuSerProSerArgSerGlyAspIleGluSerProLys-----AspIleLeu 374  
 QY 515 TCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCACTGTCTGGAATCACAGT 574  
 Db 375 CysGluArgAspAlaGluCys----- 381  
 QY 575 TGGGATAGCACCATTCTGATCTCAAGGGCTGCATCTGTGATCACAGACCACTCCA 634  
 Db 382 -----GlnValGluProSerAspAlaArgValSerPro 392  
 QY 635 TGCTCT-----TCAGCAATAATAATCACTCTCAACTGCA-----GGA 673  
 Db 393 CysSerProValLeuGluAspLysLeuValAspProLeuCysSerGlnGlnLysAspAsn 412  
 QY 674 AACTCAGAAGCTGTCAGCTGTATAGCCAG---CAGTGGATCCAGAGCAAGGGA 730  
 Db 413 AsnSerGluAspLeu-----GlyMetAlaAsnIleSerAspValAsnCysLysGlyGlu 430  
 QY 731 GACATTGTGAACCAATGACAGAGCGCTGCCTTAACCACTCGCTA----- 775  
 Db 431 HisLysValAsnAspAspAspGlySerLeuSerMetGlySerGluGlnLysArgLys 450  
 QY 776 -----GATCCCTTCTGTCAGGACTTGATC-----ATG 805  
 Db 451 GluCysAspGluAspSerLeuValAspGluSerMetCysLysThrHisGluGlnLysSer 470  
 QY 806 AAAGAGGAC-----TATCACTTGTAGTACCAAG 835  
 Db 471 LysAspAspHisSerSerProGluAspValSerLysThrHisGluPheAspSerThrLys 490  
 QY 836 CCTCAAGGACCTCAAAAGTC-----AGACAAATTA 868  
 Db 491 AspAsnIleSerSerAlaValAspGlyAsnGluLysHisGluPheGluSerLysLysAsp 510  
 QY 869 GACACTACTGACATCAAGAGAGAAATTTGCCAAGTTATATGACAAAATTTGAAAGAT 928  
 Db 511 AspThrAsnSerLysGluGluGluSerLeuAsnLysGluHisGluGlnLysSerLysGlu 530  
 QY 929 AACAAACAATGGCTTTCAG 949  
 Db 531 AspGluAsnSerGlyLeuGlu 537

RESULT 13  
 Q810W9 PRELIMINARY; PRT; 949 AA.  
 ID Q810W9  
 AC Q810W9  
 DT 01-MAR-2003 (TEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Stearoyl-CoA desaturase (Acyl-CoA desaturase, fatty acid desaturase),  
 DE putative (EC 1.14.99.5).  
 GN PF0555W.  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 ON NCBI\_TaxID=36329;  
 RX NCBI\_Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,  
 RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;  
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2255708; PubMed=12368867;  
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,  
 RA Feitwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,  
 RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
 RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,  
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
 RA Sultston J.E., Craig A., Newbold C., Barrell B.G;  
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."  
 RL Nature 419:527-531 (2002).  
 DR EMBL; AL929352; CAD51476.1;  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0003677; E:DNA binding; IEA.  
 DR GO; GO:0005506; F:iron ion binding; IEA.  
 DR GO; GO:0008170; F:N-methyltransferase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0004769; F:stearoyl-CoA 9-desaturase activity; IEA.  
 DR GO; GO:0006306; P:DNA methylation; IEA.  
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
 DR InterPro; IPR001522; Desaturase.  
 DR InterPro; IPR005804; FA desat. fam.  
 DR InterPro; IPR002052; N6 Mtase.  
 DR Pfam; PF00487; FA desaturase; 1.  
 DR PRINTS; PR00075; FACDSDSSTRASE.  
 DR ProDom; PD002221; Desaturase; 1.  
 DR PROSITE; PS00092; N6\_MTASE; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 949 AA; 114072 MW; CB8C77E6A60DA605 CRC64;  
 Alignment Scores:  
 Pred. No.: 0.762 Length: 949  
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 Query Match: 3.44% Indels: 149  
 DB: 5 Gaps: 18

US-09-771-161A-2 (1-1669) x Q810W9 (1-949)  
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 Db 16 ValLeuHisThrLeuAsnLysSerThrLeuAspIleLysAspIleValThrLysLeu 35  
 QY 206 CTCAACTCTTATATTTCCTCCAGTATTTTTCACAAACATATAAAATGTTAGATT 265  
 Db 36 ThrTyrrPheIlePheLeuIleSerCysTyrrLeuLeuLysAsnTyr-----Phe 51  
 QY 266 GTATTTTACTTCTATAATTCTCTAATCATCTCCAGTTAAAGTGATATATATTTATGTAT 325  
 Db 52 SerPheLysPheLeuAsnPheIleArgIleValLysSerSerIleValLeuIleLysCys 71  
 QY 326 TCATTACAGTTACAGAGTGTTTCAAGTGCCATTCCACTATGTGACAAAGAGAAATGGAA 385  
 Db 72 LeuIleSerLeu-----LysTyrrLeuAsp 79  
 QY 386 TTATCTCTGAACATACCTGTAATCATGTGTCCAAAGAGAAATCATGTGATCTCTCAG 445  
 Db 80 LeuAsnLeuThrLeuSerIleAsnPhe----- 88  
 QY 446 CTCATGAAATAGTGGTGTCTCTGAAACTTCAAGGTCCTGCCAGCTCTCTCAAGACAAT 505  
 Db 88 ----- 88  
 QY 506 GATTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCTGTCTCTGGA 565  
 Db 89 PheTyrrLeuTyrrAsnIleLeuGlnLeuSerAsnPheLeuGlu----- 102  
 QY 566 AATCAGTGGGATAGCACCATTTCTGGATCTCAAGGGGCTGCATTTCTGTGATCAAG 625  
 Db 103 -----ValSerThrSerGlnAsnLysLys---SerAsnAsnLys 114  
 QY 626 ACCACTCCATGCTCTTCCAGCAATAATAATCCACTCTCACTCACTGACGAAACATCAGACGT 685  
 Db ----- 685



Db 208 uileasnSerSerGlnLeuGlnCysLeuGluGlyLeuLeuAspAsnLeuValSerSerAs 228  
QY 796 C-----TTGATCATGAAGAGCATATGAATCTGTAGTACCAAGCCTACCAAGACCTC 849  
Db 228 pSerProLeuAsnIleSerGluAsp---GluIleIleAspArgMetProValIleThrAl 247  
QY 850 AAAAGTCAGACAATTACTAGACACTACTGACATCCCAAGGAGGAAGAAATTGCC 901  
Db 247 aProIleAspGluLeuValProLeu-----GluGlnPheAla 259  
RESULT 15  
Q8R489 PRELIMINARY; PRT; 537 AA.  
AC Q8R489;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Syntaxin-interacting protein OCSYN.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Safieddine S., Ly D., Wang Y.-X., Wang C.-Y., Kachar B., Petralia R.,  
RA Wenthold R.;  
RT "OCSYN, A novel syntaxin-interacting protein enriched in the subapical  
RT region of inner hair cells."  
RL Mol. Cell. Neurosci. 0:0-0(2002).  
DR EMBL; AF494296; AM14616.1; -  
SQ SEQUENCE 537 AA, 58735 MW, EASDFPD9AADDECD4 CRC64;

## Alignment Scores:

Pred. No.: 0.786 Length: 537  
Score: 98.50 Matches: 51  
Percent Similarity: 41.81% Conservative: 46  
Best Local Similarity: 21.98% Mismatches: 76  
Query Match: 3.42% Indels: 59  
DB: 11 Gaps: 12

US-09-771-161A-2 (1-1669) x Q8R489 (1-537)

QY 407 AATCATGTGTCACAGAGAGAAATCATGTGATCCTCTCAGCTCATCAAAATAGTGTCT 466  
Db 54 AsnArgGlyProHisGlyArgSerAsnGlyAlaSer---LeuHisLysProGlySerSer 72  
QY 467 CCTGAACCTTCAAGGTCCTCCAGCTCCTCAAGACAATGATTTTATCTAGAAAAAGCT 526  
Db 73 Pro-----ProSerProArgGluLysAspLeuLeuSerMetLeuCys 86  
QY 527 CAAGACTGTTATTTT---ATGAAGCTGCATCACTGTCTCGAAATCACAGATTGGGATAGC 583  
Db 87 ArgAsnGlnLeuGlyProIleAsnValHisProSerTyrAlaProSerSerProSerSer 106  
QY 584 ACCATTCTGGATCTCAAGGGCTGATCTGTGATCAAGACCACTCCATCTCTTCA 643  
Db 107 SerAsnSerGlySer-----TyrLysGluSerAspCysSerPro 119  
QY 644 GCAATAATAATCCA-----CTCTCAACTCGAGGAACCTCAGACGCTCGCAGCTGCT 697  
Db 120 ValMetArgProGlyArgTyrMetSerCysGlyGluAsnHisGlyValLysProPro 139  
QY 698 ATAGCCACAGCAGTGGATCCAGAGC-----AAAAGGAGACATTTGTGAACCAAAATGACAGAA 754  
Db 140 AsnProGluGlnThrProLeuGlnLysGluValThrValArgHisLeuLys 159  
QY 755 GCGTGCCTTAACCATGTCG-----CTA 775  
Db 160 ThrLysLeuLysGluSerGluArgArgLeuHisGluArgGluSerGluIleValGluLeu 179  
QY 776 GATGCCCTTCTGTCAGGGACTTGATCATCAAGAGGACTAT----- 817  
Db 180 LysSerGlnLeuAlaArg-----MetArgGluAspIrpIleGluGluCysHis 196

QY 818 -----GAACTTGTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTA 868  
Db 197 ArgValGluAlaGlnLeuAlaLeuLysGluAlaArg---LysGluIleLysGlnLeu--- 214  
QY 869 GACACTACTGACATCCAAAGGAGAGAATTTCGCAAAAGTTATAGTACAAAAAATTGAAAGAT 928  
Db 215 -----LysGlnValIleGluThrMetArgAsp 223  
QY 929 AAC-----AAACAAATGGCTTTCAGCCTTACCGGAAATACTTGTGTGTTTCTTGA 979  
Db 224 AsnLeuAlaAspLysAspLysGlyIleGlnLysTyrPheValAspIleAsnIleGlnAsn 243  
QY 980 TCACCATCTTTAAATTTTACTTCAAAATAAAAGCATG 1015  
Db 244 LysLysLeuGluAlaLeuLeuGlnSerMetGluMet 255

Search completed: March 29, 2004, 14:23:34  
Job time : 101.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 12, 2004, 11:14:14 ; Search time 292 Seconds  
(without alignments)  
3.125 Million cell updates/sec

Title: AF027706  
Perfect score: 4369  
Sequence: 1 ggcaccagtctctagaaag.....aaagtcaacagcctgatgtg 2501

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0  
Searched: 874 seqs, 182427 residues

Total number of hits satisfying chosen parameters: 1748

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 7 summaries

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-OUT=af027706.pep -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1  
-END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=7 -DOALIGN=200  
-THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=7 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO XLPXY  
-NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : \*pep\*  
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2: /home/sdavid/sdavid-tmp/apr04/swopel61/6348573.pep:\*  
3: /home/sdavid/sdavid-tmp/apr04/swopel61/6033855.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2849	65.2	544	1	US-09-925-301-1015
2	2827	64.7	540	3	US-09-069-023-27
3	2821	64.6	540	3	US-09-019-942-1
4	2778	63.6	531	2	US-09-069-023-1
5	2749.5	62.9	530	2	US-09-069-023-3
6	2501	57.2	478	2	US-09-069-023-4
7	1475	33.8	284	2	US-09-069-023-5

ALIGNMENTS

RESULT 1  
US-09-925-301-1015  
; Sequence 1015, Application US/09925301  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106

; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1015  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1015  
Alignment Scores:  
Pred. No.: 1.13e-190 Length: 544  
Score: 2849.00 Matches: 544  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 65.21% Indels: 0  
DB: 1 Gaps: 0  
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Qy 213 GCGCCGGGACCATGAACGGGGAGGCCATCTGAGCGCCCTGCCACCATTCCCTACCAC 272  
Db 1 AlaProGlyThrMetAsnGlyGluAlaIleCysSerAlaLeuProThrIleProTyrHis 20  
Qy 273 AAACCTCCGCGACCTGCGCTACCTGAGCGGGCGGCGCTGCGACCTGCTGCTCGCCCGC 332  
Db 21 LysLeuAlaAspLeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerAlaArg 40  
Qy 333 CACGACGACGCGCGCTCCAGGTCGCGCTGAAGCACCTGCACATCCACACTCCGCTGCTC 392  
Db 41 HisAlaAspTrpArgValGlnValAlaValIleHisLeuHisIleHisThrProLeuLeu 60  
Qy 393 GACAGTGAAGAAAGAGATGCTTAAAGAGAGCTGAAATTTTACACAAAGCTAGATTAGT 452  
Db 61 AspSerGluArgIysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSer 80  
Qy 453 TACATCTCTCCAAATTTGGGAATTTGCAATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 512  
Db 81 TyrIleLeuProIleLeuGlyIleCysAsnGluProGluPheLeuGlyIleValThrGlu 100  
Qy 513 TACATGCAATGATGATCAATTAATGAATCTCTACATAGGAAATCAATATCTCTGATGT 572  
Db 101 TyrMetProAsnGlySerLeuAsnGluLeuHisArgIysThrGluTyrProAspVal 120  
Qy 573 GCTTGGCCATTGAGATTTGCGATCTCTGCATGAAATTCGCCCTTGGTGTAAATTACCTGCAC 632  
Db 121 AlaTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHis 140  
Qy 633 AATATGACTCTCTCTTACTTCATCATGACTTGAAGACTCAGATATCTTATTCGACAAT 692  
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Qy 693 GAATTTTCATGTTAAGATTGACAGATTTTGGTTTATCAAGTGGCGCATGATGCTCTCTCA 752  
Db 161 GluPheHisValIysIleAlaAspPheGlyLeuSerIysTrpArgMetMetSerLeuSer 180  
Qy 753 CAGTCACGAAGTAGCAAAATCTGCACACAGAGAGGAGGACAATTATCTATATGCCACCTGAA 812  
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Qy 813 AACTATGACCTGACAAAATCAAGGCCAGTATCAAGCAGCATATATATAGCTATGCA 872  
Db 201 AsnTyrGluProGlyGlnIysSerArgAlaSerIleIysHisAspIleTyrSerTyrAla 220  
Qy 873 GTTATCATCGGGAAGTGTATTCAGAAAAACAGACCTTTTGAAGATGTCAACCAATCCTTTG 932  
Db 221 VallIleThrTrpGluValLeuSerArgIysGlnProPheGluAspValThrAsnProLeu 240  
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Qy 1053 CCAGATGAAGAACCATCTTCTTAAATGTTTAAATAGAACTTGAACAGTTTGAAGACA 1112  
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Qy 1113 TTTGAAGAGATAAATCTTCTTGAAGCTGTTATTCAGCTTAAGAAAAACAAAGTTACAGAGT 1172  
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Qy 1173 GTTTCAGTGCATTCACCTATGACAAAGAAATGGAATATCTCTGAACATACCT 1232  
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Qy 1593 RACCACTGCATAGTCCCTCTCTGTCAGGACTTGATCAAAAGAGACTATGAACTT 1652  
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Qy 1713 CAAGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAAACAATGGGT 1772  
Db 501 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 520  
Qy 1773 CTTACAGCTTACCCGGAATACTCTGTGGTTTCTAGATCACCATCTTTAAATTTACTCAA 1832  
Db 521 LeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuGln 540  
Qy 1833 AATAAAGCATG 1844  
Db 541 AsnLysSerMet 544

RESULT 2

US-09-069-023-27  
Sequence 27, Application US/09069023A  
Patent No. 6348573  
GENERAL INFORMATION:  
APPLICANT: Nunez, Gabriel  
APPLICANT: Inohara, Naohiro  
APPLICANT: Koseki, Takeyoshi  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

FILE REFERENCE: UM-03333  
CURRENT APPLICATION NUMBER: US/09/069,023A  
CURRENT FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 27  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-069-023-27  
Alignment Scores:  
Pred. No.: 3,69e-189 Length: 540  
Score: 2827.00 Matches: 540  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 64.71% Indels: 0  
DB: 2 Gaps: 0  
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Qy 285 CTGCGCTACCTGAGCGCGCGCTCTGCGACTGTGTCTGCCCTCCGCCCGCCACGAGACTGG 344  
Db 21 LeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTyr 40  
Qy 345 CGGTCAGAGTGGCGTGAAGACCTGCACATCCACATCCGCTCGCAGCTGGAAGA 404  
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Qy 465 ATTTTGGGAATTTGCAATGAGCTGAAATTTTGGGAATAGTTACTGTAATCATGCGCAAT 524  
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Qy 525 GGATCATAAATGAACTCTACATAGAAACCTGAAATATCTGATGTTGCTTGGCCATTG 584  
Db 101 GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTyrProLeu 120  
Qy 585 AGATTTGCGCATCTGCGCATGAAATTCCTTGGTGTAAATTAACCTGCAATATGACTCCT 644  
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Qy 645 CTTTACTTTCATCATGACTTGAAGACTCAGAAATCTTATTTGGCAATGAATTTTCATGTT 704  
Db 141 ProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisVal 160  
Qy 705 AAGATTCAGATTTTGGTTTATCAAGTGGCGCATGATGTCCTCTCACAGTTCACGAAGT 764  
Db 161 LysIleAlaAspPheGlyLeuSerLysTyrArgMetMetSerLeuSerGlnSerArgSer 180  
Qy 765 AGCAAACTGCACAGAGGAGGACAAATATCTATATGCCCACCTGAAAACTATGAACCT 824  
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Db 241 SerValSerGlnGlyHisArgProValIleAsnGluSerLeuProTyrAspIlePro 260

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QY 1065 CCATCTTTCTTAATGTTTAAATGAACTTGAACAGTTTGGAGACATTTGAGAGNATA 1124
Db 281 ProSerPheLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 300
QY 1125 ACTTTTCTTGAAGTGTATTATTCAGTAAAGAAAACAAAGTTTACAGAGTGTTCAGTGCC 1184
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## RESULT 3

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US-09-019-942-1
; Sequence 1, Application US/09019942
; Patent No. 603855
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; ADDRESS: Fish & Richardson P. C.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA: US/09/019,942
APPLICATION NUMBER: 06-FEB-1998
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
SEQUENCE CHARACTERISTICS:
SEQUENCE FOR SEQ ID NO: 1:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-019-942-1
Alignment Scores:
Pred. No.: 9,53e-189 Length: 540
Score: 2821.00 Matches: 539
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 64.57% Indels: 0
DB: 3 Gaps: 0
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QY 345 CGCTCCAGGTGGCGGTGAAGACCTGCACATCCACACTCCGCTGCCTGCAGCAGTGAAGA 404
Db 41 ArgValGlnValAlaValLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60
QY 405 AAGGATCTCTTAAGAGAGCTGAAATTTTACAAAGCTAGATTAGTTAGTACATCTTCCA 464
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QY 465 ATTTTGGGAATTTGCAATGACCTGAATTTTGGGAATAGTTACTGATGATGATGATGATGAT 524
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QY 525 GGATCATTAATAAGACTCTACATAGGAAACTGAATATCTGATGTTGTTGGCCATTG 584
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QY 585 AGATTTCCGATCTCCATGAAATTTGCCCTTGGTGTAAATTTACCTGCGCAATATGACTCCT 644
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Db 161 LysIleAlaAspPheGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSer 180
QY 765 AGCAATCTGCACCAAGAGGAGGCAATTTATCTATATGACCCTGAAACACTATGAACCT 824
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181 SerLysSerAlaProGluGlyGlyThrIleIleTyrMetProGluAsnTyrGluPro 200
QY 825 GGACAAAATCAAGGCCAGTATCAAGCACATATATACCTATGACGTTATCACATGG 884
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QY 885 GAAGTGTATCCAGAAACACGCTTTGAAGATGTCACCAATCTCTTTCAGATATATGAT 944
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Db 241 SerValSerGlnGlyHisArgProValIleAsnGluSerLeuProTyrAspIlePro 260
QY 1005 CACGAGACGATGATCTCTTAATAGAAAGTGGTGGGACAAAATCCAGATGAAGA 1064
Db 261 HisArgAlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArg 280
QY 1065 CCATCTTTCTTAAATGTTTAAAGAACTTGAACCTGCAACAGTTTGAAGAACATTTGAAGAGATA 1124
Db 281 ProSerPheLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 300
QY 1125 ACTTTTCTTGAAGCTGTTTATTACGCTAAAGAAACAAAGTTTACAGAGTGTTCAGTGCC 1184
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QY 1185 ATTCACTATGTGACAGAAGAAATGAATATCTCTGAACATACCTGTAAATCATGGT 1244
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QY 1485 CCATCTCAACTGCAGGAACTCAGAACGCTGTGCAAGCCTGGATAGCCACGAGTGATC 1544
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QY 1545 CAGACAAAGGAGACATCTGTAACCAATGACAGAGCTGCTTAACCAAGTCGCTA 1604
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QY 1605 GATGCCCTTCTGCCAGGACTTGATCATGAAGAGGACTATGAACCTGTTAGTACCAAG 1664
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QY 1665 CCTAAGAGCCTCAAAAGTCAGACAAATTAAGACACTACTGACATCCAGGAGAGAA 1724
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QY 1725 TTTGCCAAGTTATAGTACAAAATTTGAAGATAACAAACAAATGGGCTTCAGCCTTAC 1784
Db 501 PheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyr 520
QY 1785 CCGAAATACCTGTGGTCTTAGATCACCATCTTTAAATTTTACTTTCAAAATAAAGCATG 1844
Db 521 ProGluIleLeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 540
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RESULT 4

US-09-069-023-1

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; Sequence 1, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Takeyoshi
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-1

Alignment Scores:
Pred No.: 8.6e-186 Length: 531
Score: 2778.00 Matches: 530
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.81% Mismatches: 0
Query Match: 63.58% Indels: 0
DB: 2 Gaps: 0

AF027706 (1-2501) x US-09-069-023-1 (1-531)
QY 252 CTGCCACCAATTCCTTACCAAACTCGCGACTCGCTACCTGAGCGGGCGCTCT 311
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QY 312 GGCACTGTGCTCGCGCCGCGCAGACTGGCGCTCCAGGTGGCGCTGAAGCACCTG 371
Db 21 GlyThrValSerSerAlaArgHisAlaAspTrpArgValGlnValAlaValLysHisLeu 40
QY 372 CACATCCACACTCGCGCTCGACAGTCAAGAAAGGATGCTTTAAGAGAGAGCTGAAT 431
Db 41 HisIleHisThrProLeuLeuAspSerGluArgLysAspValLeuArgGluAlaGluIle 60
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Db 121 LeuGlyValAsnTyrLeuHisAsnMetThrProProLeuLeuHisAspLeuLysThr 140
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Db 141 GlnAsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyLeuSerLys 160
QY 732 TGGCGCATGATGTCCTCTCACATGTCAGAAAGTAGCAAAATCTGCACGAGAGGAGACA 791
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QY 792 ATTATCTATATGCCACCTGAAAATCTGAACCTGCACAAAATCAAGGCCAGCTATCAAG 851
Db 181 IleIleTyrMetProProGluAsnTyrGluProGlyGlnLysSerArgAlaSerIleLys 200
QY 852 CACGATATATAGCTATGCAAGTTTATCACATGGGAAGTGTATTCCAGAAAAACAGCTTTT 911
Db 201 HisAspIleTyrSerTyrAlaValIleThrTrpGluValLeuSerArgLysGlnProPhe 220
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QY 912 GAAGATGTCACCAATCTTTGGCAGATAATGTTATAGTGTCTCAGAGCATCGACTGTT 971
Db 221 GluAspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGlyHisArgProVal 240
QY 972 ATTAATGAAGAAGTTTGCATATATATACCTCAGGAGCAGTATGATCTCTCTAATA 1031
Db 241 IleAsnGluSerLeuProTyrAspIleProHisArgAlaArgMetIleSerLeuIle 260
QY 1032 GAAAGTGAATGGGCACAAATCCAGATGAAAGACCATCTTTCTTAAATGTTTAAAGAA 1091
Db 261 GluSerGlyTyrAlaGlnAsnProAspGluArgProSerPheLeuLysCysLeuIleGlu 280
QY 1092 CTTGAACCACTTTTGAACATTTGAAGAGATAACTTTCTTGAAGCTGTATTTCAGCTA 1151
Db 281 LeuGluProValLeuArgThrPheGluGluIleThrPheLeuGluAlaValIleGlnLeu 300
QY 1152 AAGAAACAAAGTTTACAGAGTCTTCAAGTGCCTTCACTATGTGACAGAGAAAGATG 1211
Db 301 LysLysThrLysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMet 320
QY 1212 GAATTATCTCTGAACATACCTGTAATCATGTCTCACAAGAGGAATCATGTGATCCTCT 1271
Db 321 GluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSer 340
QY 1272 CAGCTCCATGAAATAGTGGTCTCTGTAACCTTCAAGTCTCCTCCAGCTCCTCAAGAC 1331
Db 341 GlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAsp 360
QY 1332 ATGATTTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCTGCTCT 1391
Db 361 AsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysPro 380
QY 1392 GAAATTCACAGTTGGATGACCACTTCTGCTTCTCAAGGCTGCATCTCTGTCATCAC 1451
Db 381 GlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHis 400
QY 1452 AAGACCACTCCATGCTCTTACAGCAATAATAATCACTCTCAACTGCAGGAAACTCGAA 1511
Db 401 LysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGlu 420
QY 1512 CQCTGACGCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATCTGTAAC 1571
Db 421 ArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsn 440
QY 1572 CAAATTCACAGAGCCTGCTTAAACAGTGGCTAGATGCCCTTCTCTCCAGGACTTGTATC 1631
Db 441 GlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIle 460
QY 1632 ATGAAAGAGGACTATGAATCTTTAGTACCAAGCCTCAAGGACCTCAAAAGTCCAGACAA 1691
Db 461 MetLysGluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGln 480
QY 1692 TTACTAGACACTACTGACATCCAAAGGAGAGATTTGCCAAGTTATAGTACAAAATTG 1751
Db 481 LeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeu 500
QY 1752 AAAGATAACAAACAAATGGCTTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCA 1811
Db 501 LysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSer 520
QY 1812 CCATCTTAAATTTACTTCAAAATAAAGCATG 1844
Db 521 ProSerLeuAsnLeuLeuGlnAsnLysSerMet 531
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## RESULT 5

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US-09-069-023-3
; Sequence 3, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
```

```
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069, 023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-3
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## Alignment Scores:

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Pred. No.: 7,84e-184 Length: 530
Score: 2749.50 Matches: 528
Percent Similarity: 99.62% Conservative: 1
Best Local Similarity: 99.44% Mismatches: 1
Query Match: 62.93% Indels: 1
DB: 2 Gaps: 1
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AF027706 (1-2501) x US-09-069-023-3 (1-530)

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QY 312 GGCACCTGTGCTCGCCGCCGCCAGCAGCAGCTGGCGCGTCCAGGTGGCGCTGAAGCACCTG 371
Db 20 GlyThrValSerSerAlaArgHisAlaAspTrpArgValGlnValAlaValLysMetLeu 39
QY 372 CACATCCACACTCCGCTGCTCGACAGTGAAGAAAGAGTGTCTTAAAGAGAAGCTGAAATT 431
Db 40 HisIleHisThrProLeuLeuAspSerGluArgLysAspValLeuArgGluAlaGluIle 59
QY 432 TTACACAAAGCTAGATTAGTTACATCTTCCAAATTTGGGAATTTGCAATGAGCTGAA 491
Db 60 LeuHisLysAlaArgPheSerTyrIleLeuProIleLeuGlyIleCysAsnGluProGlu 79
QY 492 TTTTGGGAATAGTTACTGAATACATGCAAAATGGATCATTTAAATGAACTCTCATATAGG 551
Db 80 PheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeuLeuHisArg 99
QY 552 AAAACTGAATATCTGTATGTTGCTTGGCCATTGAGATTTGCGATCTCGATGAAATTGCC 611
Db 100 LysThrGluTyrProAspValAlaTrpProLeuArgPheArgIleLeuHisGluIleAla 119
QY 612 CTTGCTGTTAAATTTACCTGCAATATGACTCTCTCTTTTACTTCTCATGACTTGAGACT 671
Db 120 LeuGlyValAsnTyrLeuHisAsnMetThrProProLeuLeuHisAspLeuLysThr 139
QY 672 CAGAAATATCTTATGGACAATGAATTTTCATGTTAAGATTGAGATTTTGGTTTATCAAG 731
Db 140 GlnAsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyLeuSerLys 159
QY 732 TGGCGCATGATGTCCTCTCAGCTCAGAGTAGTACAAATCTGCACCAAGAGAGGGACA 791
Db 160 TrpArgMetSerLeuSerGlnSerArgSerLysSerAlaProGluGlyGlyThr 179
QY 792 ATTATCTATATGCCACCTGAAACTATGCACTGCACAAATAATCAAGGCCAGTATCAAG 851
Db 180 IleIleTyrMetProProGluAsnTyrGluProGlyGlnLysSerArgAlaSerIleLys 199
QY 852 CACGATATATATAGCTATGCAAGTTATCACATGGGAAGTGTATTCCAGAAAAACAGCTTTT 911
Db 200 HisAspIleTyrSerTyrAlaValIleThrTrpGluValLeuSerArgLysGlnProPhe 219
QY 912 GAAGATGTCACCAATCTTTTGCAGATAATGTATAGTGTGTGCACAAAGGACATCGACTGTT 971
Db 220 GluAspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGlyHisArgProVal 239
QY 972 ATTAATGAAGAAGTTTGGCCCATATGATATACCTCAGCAGCAGCATGATCTCTCTAATA 1031
Db 240 IleAsnGluGluSerLeuProTyrAspIleProHisArgAlaArgMetIleSerLeuIle 259
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; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-4

Alignment Scores:
Pred. No.: 9,4e-167 Length: 478
Score: 2501.00 Matches: 478
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.24% Indels: 0
DB: 2 Gaps: 0

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QY 471 GGAATTTGCAATGAGCTGAAATTTTGGGAATAGTTACTGAATACATGCAAAATGATCA 530
Db 21 GlyLeuCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsnGlySer 40
QY 531 TTAATGAACTCCTACATAGGAAACTGAATATCCTGATGCTGCTGGCCATTGAGATTT 590
Db 41 LeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 60
QY 591 CGATCTCGCATGAAATTTGCTTGGTGTAAATTTACTGACCAATATGACTCTCTCTTTA 650
Db 61 ArgLeuLeuHisGluLeuAlaLeuGlyValAsnTyrLeuHisAsnMetThrProLeu 80
QY 651 CTTCATCATGACTTTGAGACTCAGAATATCTTATGGACAATGAATTCATGTTAAGATT 710
Db 81 LeuHisHisAspLeuLysThrGlnAsnLeuLeuAspAsnGluPheHisValLysIle 100
QY 711 GCAGATTTGGTTTATCAAGTGGCGCATGATCTCCTCTCACAGTCACCAAGTAGCAAA 770
Db 101 AlaAspPheGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSerLys 120
QY 771 TCTCCACAGAGGAGGAGCAATTTATCTATATGACCTGACCTGAAAACCTATGAACCTGGCAA 830
Db 121 SerAlaProGluGlyThrIleLeuTyrMetProGluAsnTyrGluProGlyGln 140
QY 831 AAATCAAGGCGCATGATCAAGCAGATATATATAGCTATGCTATGATGAGGAGTG 890
Db 141 LysSerArgAlaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTrpGluVal 160
QY 891 TTATCCAGAAACAGCCTTTTGAAGATGTCACCAATCCTTTGCAGATAATGTATAGTGTG 950
Db 161 LeuSerArgLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrSerVal 180
QY 951 TCACAGACATCGACCTGTTTATTAATGAAGAAAGTTTGCATATATATACCTCACCGA 1010
Db 181 SerGlnGlyHisArgProValIleAsnGluSerLeuProTyrAspIleProHisArg 200
QY 1011 GCAGTATGATCTCTTAATAGAAAGTGGATGGCCACAAATCCAGATGAAGACCATCT 1070
Db 201 AlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSer 220
QY 1071 TTCTTAAATGTTTAAATAGAACTTGAACCTTTTGAACATTTGAGAGATAACTTTT 1130
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QY 1131 CTGGAAGCTGTTTATTCAGCTAAAGAAACCAAGTTTACAGAGTGTTCAGAGTGCATTCAC 1190
Db 241 LeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerValSerSerAlaIleHis 260
QY 1191 CTATGTGACAAGAAATGCAATTTATCTCTGACATACCTGTAAATCATGGTCCCAAA 1250
Db 261 LeuCysAspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGln 280
QY 1251 GAGGAATCATGTGGATCTCTCAGCTCCATGAAATAGTGTCTCTCTGAAACTTCAAGG 1310
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1032 GARAGTGGATGGGCACAAAATCCAGATGAAGACATCTTTCTTAAATGTTTAAATAGAA 1091
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QY 1092 CTTGAACAGATTTTGAAGACATTTTGAAGAGATAACTTTCTTGAAGCTGTTTATTCAGCTA 1151
Db 280 LeuGluProValLeuArgThrPheGluGluIleThrPheLeuGluAlaValIleGlnLeu 299
QY 1152 AAGAAAAACAAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAGAAAGAAATG 1211
Db 300 LysLysThrLysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysLysMet 319
QY 1212 GAAATTTATCTCAACATACCTGCTAAATCATGCTGCACAAAGAGGAATCATGTGGATCTCT 1271
Db 320 GluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSer 339
QY 1272 CAGCTCCATGAAAATAGTGGTTTCTCTGAAAATCTCAAGGTCCCTGCCAGCTCCTCAAGAC 1331
Db 340 GlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAsp 359
QY 1332 AATGATTTTATCTAGAAAAGCTCAAGCTGTTATTTTATGAAGCTGCATCCTGCTCT 1391
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Db 380 GlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHis 399
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Db 420 ArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsn 439
QY 1572 CAAATGACAGAGCTGCTTAAACAGTGCCTGATGATGCTCTCTCCAGGAGCTTGATC 1631
Db 440 GlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIle 459
QY 1632 ATGAAAGAGGACTATGAATCTTGTATACCAAGCTTACCAAGCTTCAAGGACCTCAAAAGTCAAGAA 1691
Db 460 MetLysGluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGln 479
QY 1692 TTACTAGACACTACTGACATCCAGAGAGAGAAATTTGCCAAGTTATAGTACAAAAATG 1751
Db 480 LeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeu 499
QY 1752 AAAGATAACAAACAAATGGTCTTCAAGCCTTACCCGGAATAACTGTGTTTCTAGATCA 1811
Db 500 LysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSer 519
QY 1812 CCATCTTTAAATTTACTTCAAAATAAAAGCATG 1844
Db 520 ProSerLeuAsnLeuGlnAsnLysSerMet 530

RESULT 6
US-09-069-023-4
; Sequence 4, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069, 023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
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QY 1371 ATGAAGCTGCATCACTGCTCGGAATACACAGTTGGGATAGACCATTTCTGGTTCTCAA 1430
Db 321 MetLysLeuHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGln 340
QY 1431 AGGCGTCAATCTGTGATCACAGACCACTCATGCTCTCTCAGCAATATAAATCCACTC 1490
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QY 1491 TCAACTGCAGGAACTCAGAACGCTGCGAGCCTGTATAGCCCAAGCTGGATCCAGAGC 1550
Db 361 SerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSer 380
QY 1551 AAAAGGGAAGCATTTGTGAACCAATGACAGAGCTGCTTAAACCAGTCCGCTAGATGCC 1610
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Db 421 ArgThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluPheAla 440
QY 1731 AAAGTTATAGTACAAAAATTGAAGATAACAAATAATGGGTCTTACGCTTACCCGGAA 1790
Db 441 LysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGlu 460
QY 1791 ATACTTGGTGTCTTACAGTACCATCTTAATTTACTTCAATAAAGCATG 1844
Db 461 IleLeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 478

RESULT 7
US-09-069-023-5
; Sequence 5, Application US/09069023A
; Patent No.: 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-5
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Pred. No.: 2,98e-96 Length: 284
Score: 1475.00 Matches: 284
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.76% Indels: 0
DB: 2 Gaps: 0
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Db 61 ValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeuAsnIlePro 80
QY 1233 GTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAAAAATAGTGGT 1292
Db 81 ValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGluAsnSerGly 100
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QY 1773 CTTCAAGCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAA 1832
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Db 281 AsnLysSerMet 284
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Search completed: April 12, 2004, 11:24:10  
Job time : 303 secs

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XX 3

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Qy 1140 GTTATTCAGCTAAAGAAACAAAGTTTACAGAGTGTTCAGAGTCCATTCACCTATGTGAC 1199  
Db 1141 GTTATTCAGCTAAAGAAACAAAGTTTACAGAGTGTTCAGAGTCCATTCACCTATGTGAC 1200  
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1381 CATCACTGCTCTGGAATCACAGTTGGGATAGACACATTTCTGGTTCTCAAGGGCTGCA 1440  
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Qy 1560 GACATTTGTGAAACCAATGACAGAGCCTGCCTTAAACAGTCCGTAGATGCCCTTCTGTCC 1619  
Db 1561 GACATTTGTGAAACCAATGACAGAGCCTGCCTTAAACAGTCCGTAGATGCCCTTCTGTCC 1620  
Qy 1620 AGGACTTGTATGATGAAGAGGACTATGAATCTTGTAGTACCAAGCTCAAGGACCTCA 1679  
Db 1621 AGGACTTGTATGATGAAGAGGACTATGAATCTTGTAGTACCAAGCTCAAGGACCTCA 1680  
Qy 1680 AAAGTCAGACAAATTTACTAGACACTACTGACATCCAAAGGAGAGAAATTTGCAAGTTATA 1739  
Db 1681 AAAGTCAGACAAATTTACTAGACACTACTGACATCCAAAGGAGAGAAATTTGCAAGTTATA 1740  
Qy 1740 GTACAAAATTTGAAGATTAACAAACAAATGGGCTTTCAGCCTTACCCGGAAATACTTTGTG 1799  
Db 1741 GTACAAAATTTGAAGATTAACAAACAAATGGGCTTTCAGCCTTACCCGGAAATACTTTGTG 1800  
Qy 1800 GTTCTTAGATCACCATCTTTTAAATTTTACTTCAAAAATAAAGCATGTAAGTGAATGTTTT 1859  
Db 1801 GTTCTTAGATCACCATCTTTTAAATTTTACTTCAAAAATAAAGCATGTAAGTGAATGTTTT 1860  
Qy 1860 CAAGAGAAATGTGTTTCATAAAAGGATATTTATATCTCTGTTGCTTTGACTTTTTTAT 1919  
Db 1861 CAAGAGAAATGTGTTTCATAAAAGGATATTTATATCTCTGTTGCTTTGACTTTTTTAT 1920  
Qy 1920 ATAAATCCGAGTATTAAGCTTTTATTCAGAGCTTTTGGGTAATATAGTCTCCCT 1979  
Db 1921 ATAAATCCGAGTATTAAGCTTTTATTCAGAGCTTTTGGGTAATATAGTCTCCCT 1980  
Qy 1980 CCATGACACTGCAGTATTTTTTAAATTAACAAGTAAAGTGAATGTAATTTGGTGTGAAT 2039  
Db 1981 CCATGACACTGCAGTATTTTTTAAATTAACAAGTAAAGTGAATTTGGTGTGAAT 2040  
Qy 2040 TGCTACATAGTTCATTTTATGCTCTTTTGTGTACAGAAACCACTTTTAAAGGATAGT 2099  
Db 2041 TGCTACATAGTTCATTTTATGCTCTTTTGTGTACAGAAACCACTTTTAAAGGATAGT 2100  
Qy 2100 AATTTTCTTGTTTTATTAACAGTGCCTTTAAGTATGATTTCTGATGGAAGCCTTTT 2159  
Db 2101 AATTTTCTTGTTTTATTAACAGTGCCTTTAAGTATGATTTCTGATGGAAGCCTTTT 2160  
Qy 2160 CACATTCATGTTCTTCAATGATTTTGTGTTTACTGTTCTAAGATGCAATTTGATTTATGA 2219  
Db 2161 CACATTCATGTTCTTCAATGATTTTGTGTTTACTGTTCTAAGATGCAATTTGATTTATGA 2220  
Qy 2220 AGTATATACCTTTTACCCAGAGACAGTACAGAACTCCCTGCCCTAAAATCCCAGGCTT 2279  
Db 2221 AGTATATACCTTTTACCCAGAGACAGTACAGAACTCCCTGCCCTAAAATCCCAGGCTT 2280  
Qy 2280 AATTTGCCCTACAAAGGTTTAAATTTAAATCTCCATTTATGAGTATCAATTTTAAAGTT 2339  
Db 2281 AATTTGCCCTACAAAGGTTTAAATTTAAATCTCCATTTATGAGTATCAATTTTAAAGTT 2340  
Qy 2340 TTATTTATGATTTCCCTTTTAAATGATTTTCAAGGTAAGAAACCAATATAAAGAA 2399  
Db 2341 TTATTTATGATTTCCCTTTTAAATGATTTTCAAGGTAAGAAACCAATATAAAGAA 2400  
Qy 2400 AAAATAAATATAATATACCGGCTTCTGTCCCAATTTTTTAACTCAGGCTTCCCTACT 2459  
Db 2401 AAAATAAATATAATATACCGGCTTCTGTCCCCCAATTTTTTAACTCAGGCTTCCCTACT 2460  
Qy 2460 GTCCACCAACCAAGCTTAAATTAAGTCAACAGGCTGATGTG 2501  
Db 2461 GTCCACCAACCAAGCTTAAATTAAGTCAACAGGCTGATGTG 2502

RESULT 2  
AA02558  
ID AAX02558 standard; cDNA; 2098 BP.  
XX  
AC AAX02558;  
XX  
DT 07-MAY-1999 (first entry)  
XX  
DE Human B1 cDNA.  
XX  
KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
KW cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO985507-A2.  
XX  
PD 10-DEC-1998.  
XX  
PF 01-JUN-1998; 98WO-IL000255.  
XX  
PR 05-JUN-1997; 97IL-00121011.  
PR 30-JUN-1997; 97IL-00121199.  
PR 11-SEP-1997; 97IL-00121746.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Wallach D, Boldin M, Malinin N;  
XX  
DR WPI; 1999-070258/06.  
DR P-PSDB; AAW92795.  
XX  
PT New B1 protein regulates cell death and cell survival pathways -  
PT derivatives, DNA and antibodies, also regulate intracellular inflammation  
PT ; for treating AIDS, cancer.  
XX  
PS Claim 4; Fig 3B; 90pp; English.  
XX  
CC This invention describes the isolation of a novel human B1 protein which  
CC can interact with, intracellular mediators or modulators of inflammation,  
CC cell death and/or cell survival pathways, directly or indirectly. Cells  
CC can be modulated or mediated in inflammation, cell death or cell survival  
CC pathways or another intracellular signalling activity using B1.  
CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
CC oligonucleotides and ribozymes can also be used to regulate the above  
CC pathways  
XX  
SQ Sequence 2098 BP; 649 A; 452 C; 449 G; 539 T; 0 U; 9 Other;  
  
Query Match 80.7%; Score 2017.8; DB 3; Length 2098;  
Best Local Similarity 99.3%; Pred. No. 1.1e-06;  
Matches 2016; Conservative 9; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 GGCACCACTCTCTAGAAAAGAGTCAAGTCTGGTTTCGGAGAACAGCGGCTGGCGTGGGC 60  
Db |||||  
Qy 36 GGCACCACTCTCTAGAAAAGAGTCAAGTCTGGTTTCGGAGAACAGCGGCTGGCGTGGGC 95  
Db |||||  
Qy 61 CATCCGGGAATGGCGCCCTCGTGACCTAGTGTTCGGGGGCAAAAAGGGTCTTTCGGCGC 120  
Db |||||  
Qy 96 CATCCGGGAATGGCGCCCTCGTGACCTAGTGTTCGGGGGCAAAAAGGGTCTTTCGGCGC 155  
Db |||||  
Qy 121 CTCGCTGTGAGGGGCGTATCTGGCGCCTGAGCGGCAGTGGAGCCCTTGGAGCGGC 180  
Db |||||  
Qy 156 CTCGCTGTGAGGGGCGTATCTGGCGCCTGAGCGGCAGTGGAGCCCTTGGAGCGGC 215  
Db |||||  
Qy 181 CGCAGCAGGGGGCACACCCGGAACCGGCTGAGCGCCCGGACCATGAACGGGAGGCCA 240  
Db |||||  
Qy 216 CGCAGCAGGGGGCACACCCGGAACCGGCTGAGCGCCCGGACCATGAACGGGAGGCCA 275  
Db |||||  
Qy 241 TCTCAGCGCCCTCGCCCAACCAATCCCTACCAAACTCGCGCACTCGCGTACCTGAGCC 300  
Db |||||

276 TCTGCAGCGCCCTGCCCAACCAATCCCTACTCCACAAACTCGCGAGCCTCGCTACCTGAGCC 335  
Qy |||||  
301 GCGGCGCTCTGGCACTGTGTGTCGCCGCCGACGAGAGCTGGCGGTCCAGGTGGCGC 360  
Db |||||  
336 GCGGCGCTCTGGCACTGTGTGTCGCCGCCGACGAGAGCTGGCGGTCCAGGTGGCGC 395  
Qy |||||  
361 TGAAGCACCTGCACATCCACACTCCGCTCGTCTGAGAGTGAAGAAAGAGATCTTTAAGAG 420  
Db |||||  
396 TGAAGCACCTGCACATCCACACTCCGCTCGTCTGAGAGTGAAGAAAGAGATCTTTAAGAG 455  
Qy |||||  
421 AAGCTGAATTTTACACAAAGCTAGATTTAGTTACATTTCTCCAAATTTTGGGAATTTGCA 480  
Db |||||  
456 AAGCTGAATTTTACACAAAGCTAGATTTAGTTACATTTTCCAAATTTTGGGAATTTGCA 515  
Qy |||||  
481 ATGAGCCTGAAATTTTGGGAATAGTTACTGATACATGCAATGCAATGCAATGCAATGCAAT 540  
Db |||||  
516 ATGAGCCTGAAATTTTGGGAATAGTTACTGATACATGCAATGCAATGCAATGCAATGCAAT 575  
Qy |||||  
541 TCCTACATAGGAAACCTGAAATATCCTGATGTGTGGCCATGAGATTTTCGCAATCTCTGC 600  
Db |||||  
576 TCCTACATAGGAAACCTGAAATATCCTGATGTGTGGCCATGAGATTTTCGCAATCTCTGC 635  
Qy |||||  
601 ATGAAATTTGCTGGTGAATTTACCTGCACATATGATCTCTCTCTCTCTCTCTCTCTCTCT 660  
Db |||||  
636 ATGAAATTTGCTGGTGAATTTACCTGCACATATGATCTCTCTCTCTCTCTCTCTCTCTCT 695  
Qy |||||  
661 ACTTGAAGACTCAGAATATCTTATTGGACAAATGAAATTTCAATGTTAAGATTCAGATTTTG 720  
Db |||||  
696 ACTTGAAGACTCAGAATATCTTATTGGACAAATGAAATTTCAATGTTAAGATTCAGATTTTG 755  
Qy |||||  
721 GTTTATCAAAAGTGGCGCATGATGTCCTCTCACAGTCACGAAGTAGCAAAATCTGCACAG 780  
Db |||||  
756 GTTTATCAAAAGTGGCGCATGATGTCCTCTCACAGTCACGAAGTAGCAAAATCTGCACAG 815  
Qy |||||  
781 AAGAGGGCAATATCTATATGACCACTGAAACTATGAACTGGAACCTGGAGCAAAATCAAGG 840  
Db |||||  
816 AAGAGGGCAATATCTATATGACCACTGAAACTATGAACTGGAACCTGGAGCAAAATCAAGG 875  
Qy |||||  
841 CCAGTATCAAGACGATATATATAGCTATGAGTTATCACATGGGAAGTGTATTCCAGAA 900  
Db |||||  
876 CCAGTATCAAGACGATATATATAGCTATGAGTTATCACATGGGAAGTGTATTCCAGAA 935  
Qy |||||  
901 AACAGCCTTTTGAAGATGTCAACCAATCCTTTGACAGATAATGATGATGTGTGTCAAGGAC 960  
Db |||||  
936 AACAGCCTTTTGAAGATGTCAACCAATCCTTTGACAGATAATGATGATGTGTGTGTCAAGGAC 995  
Qy |||||  
961 ATGACCTGTATTATTAAGAAAGTGTGCAATATGATATACCTCACGAGCAGTATGA 1020  
Db |||||  
996 ATGACCTGTATTATTAAGAAAGTGTGCAATATGATATACCTCACGAGCAGTATGA 1055  
Qy |||||  
1021 TCTCTCTAATAGAAAGTGGGACAAATCCAGATGAAAGACCACTCTTCTTTAAAT 1080  
Db |||||  
1056 TCTCTCTAATAGAAAGTGGGACAAATCCAGATGAAAGACCACTCTTCTTTAAAT 1115  
Qy |||||  
1081 GTTTAATAGAACTTGAACCAAGTTTGAAGACATTTTGAAGAGATACTTTTCTGAAGCTG 1140  
Db |||||  
1116 GTTTAATAGAACTTGAACCAAGTTTGAAGACATTTTGAAGAGATACTTTTCTGAAGCTG 1175  
Qy |||||  
1141 TTATTAGCTTAAGAAACAAAGTTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACA 1200  
Db |||||  
1176 TTATTAGCTTAAGAAACAAAGTTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACA 1235  
Qy |||||  
1201 AGAAGAAATAGGAATTTCTCTGAACATCTGTGAAATGATGTGTGTGTGTGTGTGTGTGTGT 1260  
Db |||||  
1236 AGAAGAAATAGGAATTTCTGTGAACATCTGTGAAATGATGTGTGTGTGTGTGTGTGTGTGT 1295  
Qy |||||  
1261 GTGATCCTCTCAGCTCCATGAAATAGTGGTCTCTCTGAAATTTCAAGGTCCCTGCCAG 1320  
Db |||||  
1296 GTGATCCTCTCAGCTCCATGAAATAGTGGTCTCTCTGAAATTTCAAGGTCCCTGCCAG 1355  
Qy |||||  
1321 CTCCTCAAGACATGATTTTCTAGAAAGCTCAAGACTGTTATTTATGAGCTGC 1380  
Db |||||  
1356 CTCCTCAAGACATGATTTTCTAGAAAGCTCAAGACTGTTATTTATGAGCTGC 1415



1381 ATCACTGTCTGGAAATCACAGTTGGGATAGCACCAATTTCTGGTTCTCAAGGGCTGCAT 1440  
1416 ATCACTGTCTGGAAATCACAGTTGGGATAGCACCAATTTCTGGATCTCAAGGGCTGCAT 1475  
1441 TCTGTGATCAAGACCACTCCATGCTCTTCCAGCAATAATAATCACTCTCAACTGCAG 1500  
1476 TCTGTGATCAAGACCACTCCATGCTCTTCCAGCAATAATAATCACTCTCAACTGCAG 1535  
1501 GAAACTCAGAACGCTCTGAGCCTGGTATAGCCAGCAGTGGATCCAGCAAAAGGGAAG 1560  
1536 GAAACTCAGAACGCTCTGAGCCTGGTATAGCCAGCAGTGGATCCAGCAAAAGGGAAG 1595  
1561 ACATTGTGAACCAATGACAGAGCCTGCTTACCAAGTCTGCTAGATGCCCTCTGTCCA 1620  
1596 ACATTGTGAACCAATGACAGAGCCTGCTTACCAAGTCTGCTAGATGCCCTCTGTCCA 1655  
1621 GGGACTTGATCATGAAGAGGACTATGAATCTGTTAGTACCAAGCCTACAGGACCTCAA 1680  
1656 GGGACTTGATCATGAAGAGGACTATGAATCTGTTAGTACCAAGCCTACAGGACCTCAA 1715  
1681 AAGTCAGACCAATTAAGTACTGACACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAG 1740  
1716 AAGTCAGACCAATTAAGTACTGACACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAG 1775  
1741 TACAAAATTTGAAGATTAACAAACAAATGGCTCTTCCAGCTTACCCGGAAATACTTGTGG 1800  
1776 TACAAAATTTGAAGATTAACAAACAAATGGCTCTTCCAGCTTACCCGGAAATACTTGTGG 1835  
1801 TTTCTAGATCACTCTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1860  
1836 TTTCTAGATCACTCTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1895  
1861 AAGAGAAATGGTTTCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1920  
1896 AAGAGAAATGGTTTCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1955  
1921 TAAATTCGTGAGTAAAGCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1980  
1956 TAAATTCGTGAGTAAAGCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2015  
1981 CATGACACTGCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2031  
2016 CATGACACTGCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2066

RESULT 3  
AAZ09246  
ID AAZ09246 standard; cdna; 1931 BP.  
AC AAZ09246;  
XX  
XX  
XX 25-OCT-1999 (first entry)  
DT  
XX  
DE Human CARD-3 cdna.  
DE  
XX  
KW CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
KW caspase activation; detection; screening; therapy; diagnosis; disease;  
KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
KW spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;  
KW myelodysplastic syndrome; myocardial infarction; cell proliferation;  
KW cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;  
KW human; ds.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
CDS 214..1836  
FT /\*tag= a

/product= "CARD-3"  
WO9940102-A1.  
12-AUG-1999.  
05-FEB-1999; 99WO-US002544.  
06-FEB-1998; 98US-00019942.  
17-JUN-1998; 98US-00093041.  
08-DEC-1998; 98US-00207359.  
(MILL-) MILLENNIUM PHARM INC.  
Bertin J;  
WPI; 1999-494269/41.  
P-PSDB; AAY31140.  
Novel CARD-3 and CARD-4 genes and polypeptides used or treating  
regulation of cellular proliferation and differentiation and cell  
survival.  
Example 2; Fig 1; 181pp; English.  
This invention describes the isolation of novel human caspase recruitment  
domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial  
murine CARD-4L protein and genes. The genes and proteins of the invention  
are involved in the regulation of caspase activation. The caspase  
recruitment domain (CARD) polynucleotides, polypeptides, homologues and  
antibodies can be used in screening assays, detection assays, predictive  
medicine and therapeutic and prophylactic methods of treatment. The  
methods may be used to diagnose and treat patients which are suffering  
from a disorder associated with abnormal level or rate of apoptotic cell  
death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
activity of the TNF receptor complex, or abnormal activity of a caspase.  
Diseases that may be treated/include cancer (particularly follicular  
lymphoma, carcinomas associated with mutations in p53 and hormone-  
dependent tumours), autoimmune disorders (e.g. systemic lupus  
erythematosus, immune-mediated glomerulonephritis), viral infections,  
Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,  
anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.  
CARD-3 protein interacts with other cellular proteins, and so can be used  
for regulation of cellular proliferation and differentiation and cell  
survival. The CARD proteins may also be used to for screen drugs or  
compounds which modulate their activity. The CARD-4 gene can express a  
long transcript that encodes CARD-4L, a short transcript that encodes  
CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence  
encodes the human CARD-3 protein described in the method of the invention  
Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;  
Query Match 74.5%; Score 1864; DB 4; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 5.3e-06;  
Matches 1867; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 23 GTCAGCTCTGTTTCGAGAAACACGCGTGGCGCATCCGGGAATGGGGCCCTC 82  
Db 12 GTCAGCTCTGTTTCGAGAAACACGCGTGGCGCATCCGGGAATGGGGCCCTC 71  
QY 83 GTGACCTAGTCTTTCGGGGGAAAAGGCTTTGCCGCTCGCTCGTCAGGGGCGTATC 142  
Db 72 GTGACCTAGTCTTTCGGGGGAAAAGGCTTTGCCGCTCGCTCGTCAGGGGCGTATC 131  
QY 143 TGGGCGCTTGAGCGCGGCGGCTTGGAGCGCTTGGAGCGCGCGGAGGCGGCGG 202  
Db 132 TGGGCGCTTGAGCGCGGCGGCTTGGAGCGCTTGGAGCGCGCGGAGGCGGCGG 191  
QY 203 ACCGCGCTTGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 262  
Db 192 ACCGCGCTTGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 251



QY 263 TCCCTACCAAACTCGCGGACCTGCGCTACTGAGCGCGCGGCGCTCTGGACATGTGTC 322  
Db 252 TCCCTACCAAACTCGCGGACCTGCGCTACTGAGCGCGCGGCGCTCTGGACATGTGTC 311  
QY 323 GTCGCGCGCGCAGCAGACTCGCGGCTGCGGCTGAGGAGCAGCAGCAGCAGCAGCAGC 382  
Db 312 GTCGCGCGCGCAGCAGACTCGCGGCTGCGGCTGAGGAGCAGCAGCAGCAGCAGCAGC 371  
QY 383 TCCGCTGCTCGACAGTGAAGAAAGGATGTCTTAAGAGAAGCTGAATAATTTTACAAAGC 442  
Db 372 TCCGCTGCTCGACAGTGAAGAAAGGATGTCTTAAGAGAAGCTGAATAATTTTACAAAGC 431  
QY 443 TAGATTAGTTACATCTTCCATTTTGGGAATTTGGAATGAGCCTGAATTTTGGGAAT 502  
Db 432 TAGATTAGTTACATCTTCCATTTTGGGAATTTGGAATGAGCCTGAATTTTGGGAAT 491  
QY 503 AGTTACTGAATACATGCGCAATGGAATCAATTAATGAACCTCTACATAGGAAATCTGAATA 562  
Db 492 AGTTACTGAATACATGCGCAATGGAATCAATTAATGAACCTCTACATAGGAAATCTGAATA 551  
QY 563 TCCTGATGTTGCTGGCCATTTGAGATTTTGCATCTCTGATGAAATTTGCTTGTGTA 622  
Db 552 TCCTGATGTTGCTGGCCATTTGAGATTTTGCATCTCTGATGAAATTTGCTTGTGTA 611  
QY 623 TTACTGCAATATGACTCTCTCTTACTTCAATGACTTGAAGACTCAGATATCTT 682  
Db 612 TTACTGCAATATGACTCTCTCTTACTTCAATGACTTGAAGACTCAGATATCTT 671  
QY 683 ATTGACAAATGAATTTTCAATTTAGATTCAGATTTTGGTTTATCAAGATGCGCATGAT 742  
Db 672 ATTGACAAATGAATTTTCAATTTAGATTCAGATTTTGGTTTATCAAGATGCGCATGAT 731  
QY 743 GTCCCTCTCACAGTCACGAAGTAGCAATCTGCAACGAGAGGAGGACAAATATCTATAT 802  
Db 732 GTCCCTCTCACAGTCACGAAGTAGCAATCTGCAACGAGAGGAGGACAAATATCTATAT 791  
QY 803 GCCACCTGAAACTATGAACTGGAACAAATCAAGGCGCAGTATCAAGACGATATATA 862  
Db 792 GCCACCTGAAACTATGAACTGGAACAAATCAAGGCGCAGTATCAAGACGATATATA 851  
QY 863 TAGCTATGCTATCATACATGCGGAGTGTATCCAGAAACAGCCTTTTGAAGATGTCAC 922  
Db 852 TAGCTATGCTATCATACATGCGGAGTGTATCCAGAAACAGCCTTTTGAAGATGTCAC 911  
QY 923 CAATCTTTGAGATAATGATAGTGTGTCAAGGACATCGACCTGTTTATTAATGAAGA 982  
Db 912 CAATCTTTGAGATAATGATAGTGTGTCAAGGACATCGACCTGTTTATTAATGAAGA 971  
QY 983 AAGTTTGCATATGATATACCTACCGAGCAGTATGATCTCTTAATAGAAAGTGGATG 1042  
Db 972 AAGTTTGCATATGATATACCTACCGAGCAGTATGATCTCTTAATAGAAAGTGGATG 1031  
QY 1043 GGCACAAATCCAGATGAAGACCATCTTTCTTAAATGTTTAAATAGAACTTGAACCACT 1102  
Db 1032 GGCACAAATCCAGATGAAGACCATCTTTCTTAAATGTTTAAATAGAACTTGAACCACT 1091  
QY 1103 TTTGAGAACTTTGAGAGATAAATCTTTCTTGAAGCTGTTTATTCAGCTTAAAGAAACAA 1162  
Db 1092 TTTGAGAACTTTGAGAGATAAATCTTTCTTGAAGCTGTTTATTCAGCTTAAAGAAACAA 1151  
QY 1163 GTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAAATGGAATATCTCT 1222  
Db 1152 GTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAAATGGAATATCTCT 1211  
QY 1223 GAAATACCTCTTAATCATGCTCCACAGAGGATCATGTGATCTCTCAGCTCCATGA 1282  
Db 1212 GAAATACCTCTTAATCATGCTCCACAGAGGATCATGTGATCTCTCAGCTCCATGA 1271  
QY 1283 AAATAGTGTGTTCTCTGAAACTTCAAGTCTCTGCAAGCTCTCTCAAGACAAATGATTTTT 1342  
Db 1272 AAATAGTGTGTTCTCTGAAACTTCAAGTCTCTGCAAGCTCTCTCAAGACAAATGATTTTT 1331  
QY 1343 ATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGATCACTGTCTCTGGAATCAAG 1402

Db 1332 ATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTCATCACTGTCTCTGGAATCAAG 1391  
QY 1403 TTGGGATAGACCACTTTCTGGTTCTCAAGGGCTGCAATTTCTGTGATCACAAGACCACTCC 1462  
Db 1392 TTGGGATAGACCACTTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCACAAGACCACTCC 1451  
QY 1463 ATGCTTTAGCAATAATAATCACTCTCAACTGCGAGAACTCAGAACTCTGCGACCC 1522  
Db 1452 ATGCTTTAGCAATAATAATCACTCTCAACTGCGAGAACTCAGAACTCTGCGACCC 1511  
QY 1523 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTAACCAAAATGACAGA 1582  
Db 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTAACCAAAATGACAGA 1571  
QY 1583 AGCCTGCTTTAAACCACTGCTAGATGCCCTCTCTGCGAGGACTTGTATCATGAAAGAGA 1642  
Db 1572 AGCCTGCTTTAAACCACTGCTAGATGCCCTCTCTGCGAGGACTTGTATCATGAAAGAGA 1631  
QY 1643 CTATGAATCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGAAATTTACTAGACAC 1702  
Db 1632 CTATGAATCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGAAATTTACTAGACAC 1691  
QY 1703 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAATTTGAAAGATAACAA 1762  
Db 1692 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAATTTGAAAGATAACAA 1751  
QY 1763 ACAATGGCTCTCAGCGCTTACCGGAAATCTTGTGTTTCTAGATCACCATCTTTAAA 1822  
Db 1752 ACAATGGCTCTCAGCGCTTACCGGAAATCTTGTGTTTCTAGATCACCATCTTTAAA 1811  
QY 1823 TTTACTTTCAAAATAAAAGCATGTAAGTACTGTTTTCAGAGAAATTTGTTTCATAAA 1882  
Db 1812 TTTACTTTCAAAATAAAAGCATGTAAGTACTGTTTTCAGAGAAATTTGTTTCATAAA 1871  
QY 1883 AGGATATTATTA 1894  
Db 1872 AGGATATTATTA 1883

RESULT 4  
AC004003  
LOCUS AC004003 116650 bp DNA linear PRI 21-DEC-1999  
DEFINITION Homo sapiens BAC clone CTA-437L15 from 8q21, complete sequence.  
ACCESSION AC004003  
VERSION AC004003.1 GI:2772557  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 116650)  
Ozeresky, P., Holmes, A. and Broy, M.  
The sequence of Homo sapiens BAC clone CTA-437L15  
Unpublished  
2 (bases 1 to 116650)  
Waterston, R.  
Direct Submission  
Submitted (15-JAN-1998) Department of Genetics, Washington  
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
3 (bases 1 to 116650)  
Waterston, R.  
Direct Submission  
Submitted (27-JUN-1998) Department of Genetics, Washington  
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
4 (bases 1 to 116650)  
Waterston, R.  
Direct Submission  
Submitted (21-DEC-1999) Department of Genetics, Washington  
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
-----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)  
 ----- Summary Statistics -----  
 Center project name: H RG437L15

**NOTICE:** This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

**MAPPING INFORMATION:**  
This chromosome 8 clone was provided by Dr. Patrick Concannon (patrickc@ummc.org) at the Virginia Mason Research Institute.

**SOURCE INFORMATION:**  
Clone CTA-437115 is from a release of the human BAC library CTRB-HS-A. The library contains cloned DNA from human sperm. See Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).

RESEARCH GENETICS, INC.: (INC)  
VECTOR: pBelobAC11  
selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is CTA-237G1. The actual start of  
this clone is at base position 1 of CTA-437L15; actual end is at  
116650 of CTA-437L15.

This clone contains STS HS275YF1 (NID:q1051703).

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repeat_region		498. .649
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repeat_region		673. .1096
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repeat_region		3188. .3348
		/rpt_family="LI"
repeat_region		3605. .3726
		/rpt_family="(TA)n"
repeat_region		3845. .4563
		/rpt_family="LI"
repeat_region		5641. .6075
		/rpt_family="Retroviral"
repeat_region		6133. .6433
		/rpt_family="Alu"
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		/note="CPG_island (GC=69.1, o/e=0.80, #CPGs=93)"
Gene		7872. .40218
		/gene="WUGSC:H_RG437LI15.1"
CDS		join(7872. .8044,12642. .12795,15154. .15309,19584. .19741,21552. .21601,22478. .22639,29890. .29975,33855. .33944,33935. .36488,39123. .39284,39881. .40218)
		/gene="WUGSC:H_RG437LI15.1"
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Query Match 38.8%; Score 969.2; DB 5; Length 116650;

Best Local Similarity 98.9%; Pred. NO. 0.00049;

Matches 985; Conservative 0; Mismatches 3; Indels 8; Gaps 1;

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Qy 1506 TCAGACGCTCGACGCTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGAGACATT 1565
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Qy 1566 GTGAACCAAAATGACAGAGCTGCTTAAACAGTCGCTAGATGCTTCTCTCCAGGGAC 1625
Db 39937 GTGAACCAAAATGACAGAGCTGCTTAAACAGTCGCTAGATGCTTCTCTCCAGGGAC 39996
Qy 1626 TTGATCATGAAAGGAGTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 1685
Db 39997 TTGATCATGAAAGGAGTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 40056
Qy 1686 AGCAATTTACTAGACACTGACATCAAGGAGAGAAATTTGCAAAAGTTATAGTACAA 1745
Db 40057 AGCAATTTACTAGACACTGACATCAAGGAGAGAAATTTGCAAAAGTTATAGTACAA 40116
Qy 1746 AAATTTGAAAGTAAACAAATGCTTCCAGCTTACCCGGAATATCTTGTGTTTCT 1805
Db 40117 AAATTTGAAAGTAAACAAATGCTTCCAGCTTACCCGGAATATCTTGTGTTTCT 40176
Qy 1806 AGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAAGAA 1865
Db 40177 AGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAAGAA 40236
Qy 1866 GAAATGTTTTTCAAAAGGATATTTATCTCTGTTGCTTGTGCTTTTATATATAAA 1925
Db 40237 GAAATGTTTTTCAAAAGGATATTTATCTCTGTTGCTTGTGCTTTTATATATAAA 40296
Qy 1926 TCCGTGAGTATTAAGCTTTTAAAGGTTCTTTGGGTAAATATATAGTCTCCCTCAATGA 1985
Db 40297 TCCGTGAGTATTAAGCTTTTAAAGGTTCTTTGGGTAAATATATAGTCTCCCTCAATGA 40356
Qy 1986 CACTGCAATTTTTTTTTTAAATTAATACAAAGTAAAGTTGAATTTGGTTGAATTTGCTAC 2045
Db 40357 CACTGCAATTTTTTTTTTAAATTAATACAAAGTAAAGTT-----TGAATTTTGTCTAC 40408
Qy 2046 ATAGTTCAATTTTTTATGCTCTTTTGTAAACAGAAACCACTTTTAAAGGATAGTAATAT 2105
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Qy 2106 TCTTGTTTTATAACAGTGGCTTAAAGTATGATGATTTCTGATGAAAGCATTTCACATT 2165
Db 40469 TCTTGTTTTATAACAGTGGCTTAAAGTATGATGATTTCTGATGAAAGCATTTCACATT 40528
Qy 2166 CATGTTCTTCATGGATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATA 2225
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Db 40529 CATGTTCTTCATGGATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATA 40588
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Db 40589 TACCTTTTACCACACAGACAGTACAGAAATCCCTGCCCTAAAAATCCAGGCTTAATTGC 40648
Qy 2286 CCTACAAAGGGTTATTAATTTAAATCCATTTATTAGGATTACATTTTAAAGTTTATTT 2345
Db 40649 CCTACAAAGGGTTATTAATTTAAATCCATTTATTAGGATTACATTTTAAAGTTTATTT 40708
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Qy 2406 AAATATATTAAATACCGGCTTCTGCTGCCCATTTTAACTCAGCTTCCCTACTGTACACC 2465
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Qy 2466 AACAAACCAAGCTAAATAAAGTCAACAGCTGATGTG 2501
Db 40829 AACAAACCAAGCTAAATAAAGTCAACAGCTGATGTG 40864
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#### RESULT 5

AI824070/c

LOCUS

DEFINITION

AI824070

wj35907.x1 NCI CGAP Kid12 Homo sapiens cdna clone IMAGE:2404860 3'

similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ;, mRNA

sequence.

AI824070

AI824070.1 GI:5444741

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 738)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 432 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 460.

Location/Qualifiers

1..738

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clones="IMAGE:2404860"

/tissue\_type="2 pooled tumors (clear cell type)"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Kid12"

/note="Organ: kidney; Vector: pT3D-Pac (Pharmacia) with

a modified polylinker; Site: 1: Not 1; Site 2: Eco RI;

Plasmid DNA from the normalized library NCI CGAP Kids was

prepared, and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(clones 1323912-1325831, 1471368-1472903 and

1492104-1493255). Subtraction by Bento Soares and M.

Fatima Bonaldo. "

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Query Match      28.3%; Score 709; DB 1; Length 738;
Best Local Similarity 98.0%; Pred. No. 0.96;
Matches 726; Conservative 0; Mismatches 7; Indels 8; Gaps 1;
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Qy 1761 AAACAAATGGGTCTTCAGCCCTTACCGGAAATACITGTGGTTCTAGATACCAATCTTTA 1820
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Qy 1821 AATTACTTCAAAATAAAGCATGTAGTGAAGTGTCTTTCAAGAGAAATGTCTTCATA 1880
Db 678 AATTACTTCAAAATAAAGCATGTAGTGAAGTGTCTTTCAAGAGAAATGTCTTCATA 619
Qy 1801 AAAGGATATTTATATCTCTGTCTTCTGACCTTTTATATAAAATCCGTGAGTATTAAA 1940
Db 618 AAAGGATATTTATATCTCTGTCTTCTGACCTTTTATATAAAATCCGTGAGTATTAAA 559
Qy 1941 GCTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 2000
Db 558 GCTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 499
Qy 2001 TTTAATTAATCAAGTAAATGTTGAATTTGGTTGAATTTGCTACATAGTTCATTTTAA 2060
Db 498 TTTAATTAATCAAGTAAATGTT-----TGAATTTTGTACATAGTTCATTTTAA 447
Qy 2061 TGTCTCTTTTGTAAACAGAAACCACTTTTAAAGGATAGTAAATTTCTTTTATAACAG 2120
Db 446 TGTCTCTTTTGTAAACAGAAACCACTTTTAAAGGATAGTAAATTTCTTTTATAACAG 387
Qy 2121 TGCCTTAAGGTATGATGATTTCTGATGGAAGCCATTTTCACATTCATGTTCTTCATGGA 2180
Db 386 TGCCTTAAGGTATGATGATTTCTGATGGAAGCCATTTTCACATTCATGTTCTTCATGGA 327
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Db 326 TTAATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTACCCACC 267
Qy 2241 AGAGACAGTACAGAAATCCCTGCCCTFAAAATCCAGGCTTAATTTGCCCTACAAAGGTTAT 2300
Db 266 AGAGACAGTACAGAAATCCCTGCCCTFAAAATCCAGGCTTAATTTGCCCTACAAAGGTTAT 207
Qy 2301 TAAATTAACACTCCATTTATAGGATTACATTTTAAAGTTTATTTATGAATTCCTTTTAA 2360
Db 206 TAAATTAACACTCCATTTATAGGATTACATTTTAAAGTTTATTTATGAATTCCTTTTAA 147
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Db 86 GGCTTCCTGTCCCAATTTTAACTCAGCTCCCTACTGTCAACCAACCAAGCTAAA 27
Qy 2481 TAAAGTCAACAGCCTGTGTG 2501
Db 26 TAAAGTCAACAGCCTGTGTG 6
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